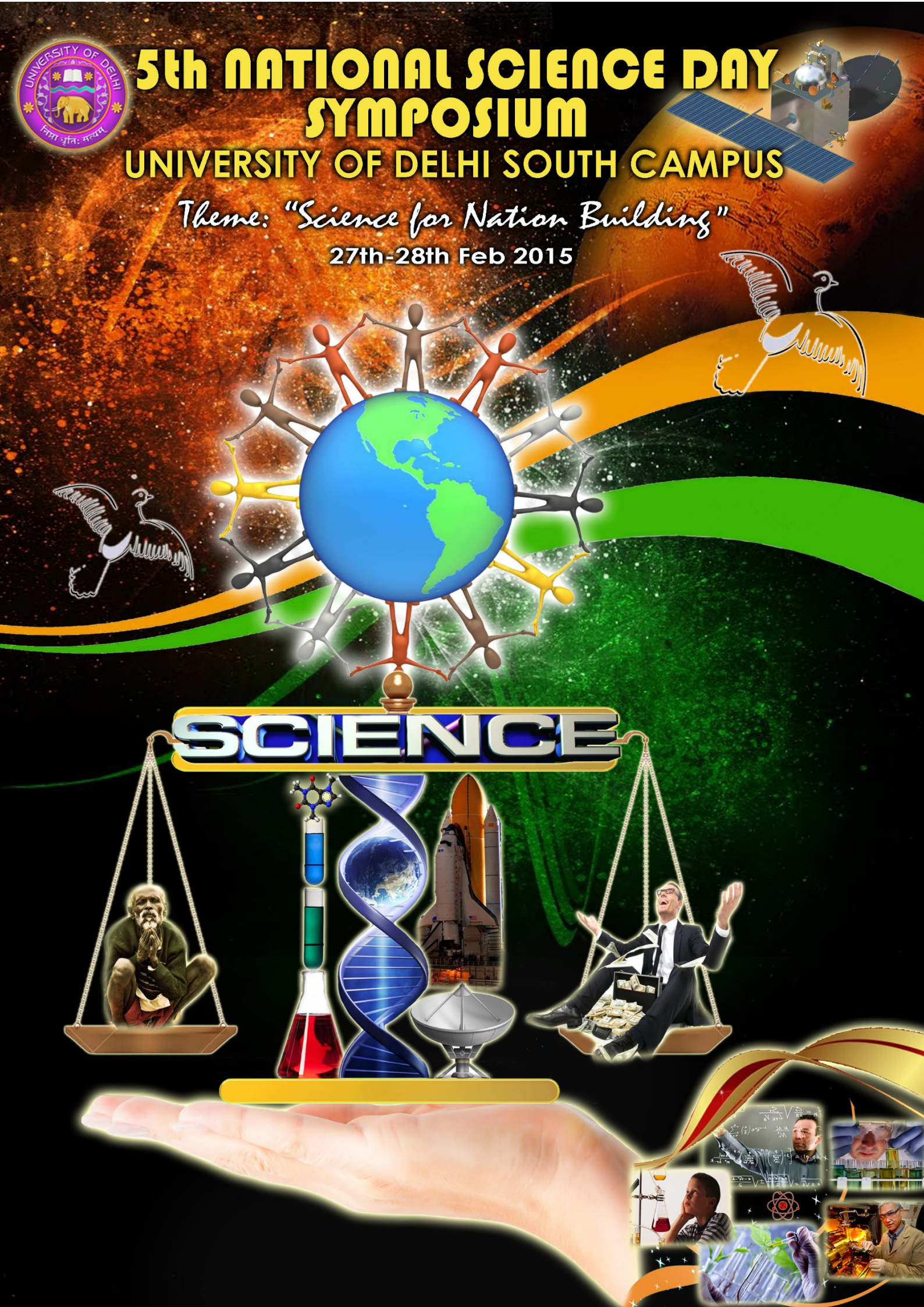
5th NATIONAL SCIENCE DAY SYMPOSIUM

UNIVERSITY OF DELHI SOUTH CAMPUS

Theme: "Science for Nation Building"

27th-28th Feb 2015



Cover Page Designed by T. James Khashim, M.Sc (F), Dept. of Plant Molecular Biology

This year theme: "SCIENCE FOR NATION BUILDING"

With this cover page I want to bring forth the immense contributions science has given to mankind in all spheres of life since time immemorial. It is said that nation achievements and progresses are measured by their scientific progresses. It will make an endless lists if we enumerate the role of science in building nation. We are where we are because of science. I would like to call A Nation, a well-built/progressive nation only when there is equality among its citizens. With equality brings unity and with unity brings peace and there will be no greater nation than a nation built on equality, Unity and Peace. This is what science is doing- bringing equality among people.

The Hand depicts the selfless collective work of scientists in their respective field, which help in bringing equality among the privileged and the non-privileged, the capable and the helpless. It is because of their sacrifices that makes the world a better place to live in.

The globe with people hand-in-hand depicts happiness, unity, love and peace around the world, which is the result of equality-the equality brought about by science.

The background represent our National flag and our recent achievement in space science, Mangalyaan**.**

*** This Cover Page has been selected as the "Best Cover Page Design" for NSD-2015.**

5th National Science Day Symposium

(27th-28th February, 2015)

Organized Jointly by

University of Delhi South Campus

&

INSA-TWAS India Chapter

Abstract book


5th Year Celebration
UDSC - National Science Day Symposium

The Preamble

Slowly but steadily the students of life sciences departments of South Campus are creating a niche and an identity for themselves through an annual scientific cum cultural festival to commemorate the National Science Day on February 28. An "idea", a "concept" that nucleated in 2011, thanks to a group of enterprising and enthusiastic students, – to assemble teachers and students of the campus on a single platform – has crystallized into a soulful event that we all fondly look forward to from the moment the curtain drops on the evening of the programme. Simply called the "National Science Day Symposium (NSDS)", the two day compact event, has since then remained an event of the students, by the students, for the students. The year 2015 marks a landmark in the short but significant life of NSDS in that it has reached its fifth year!

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

While a festival on a larger scale runs the risk of losing relevance and compromise on quality, NSDS has been able to maintain very high standards in all respects. This has been exemplified by the key note lectures NSDS has been able to provide. Luminaries like Dr. G.P. Talwar, Dr. Manju Sharma and Dr. K. Vijayaraghavan have enthralled us in the last few years with their wisdom, vision and high quality oration. They have provided food for thought and sparks of

excellence. NSDS 2015 will witness yet another impactful lecture by an eminent scientist and able administrator Dr. S.K. Sarin, Director, Institute of Liver and Biliary Sciences, New Delhi. NSDS 2015 has also achieved a boost with the plenary lecture being hosted and organized by INSA-TWAS India Chapter. The INSA-TWAS association has surely added a distinction to NSDS 2015.

The key note lecture will be followed by exciting talks by faculties, one from each of the five life sciences department. Students eagerly wait for these talks, which provide a peek into the research activities of the respective labs. This opportunity allows M.Sc. students to decide whether they would be willing to take up Ph.D positions in these labs. Two students from each department also get an opportunity to share the platform along with faculties. This is an eagerly awaited event since the oral presentations are assessed and prizes awarded. NSDS is not all about talks though and a repertoire of other events adds to its aura. Poster presentations by students represent the landscape of life science research in the campus. Team events like quiz competitions are immensely popular and commands full house. The novelty of NSDSs also lies in the "idea" presentations, which is a fiercely competed team event as well, with each team coming out with a novel concept in science. These presentations are awesome and provide an insight into the fertile brains of students. Awards in each of these events promote healthy competition and helps sustain high quality. Cultural programme at the end of the final day adds color, vibrancy and dynamism to the NSDS. It has the ability to stir up our souls after year long slogging in the labs. It provides an avenue for talents to flourish and a snapshot of our cultural strength. NSDS 2015 has added excitement to all the events by announcing "Champions Trophy" for the department of the year. This brings more cheer to the whole programme. In addition, realizing how CPR can be a life-saving exercise, NSDS 2015 has arranged for CPR training for one and all to be conducted by FORTIS hospital. An e- abstract book will capture the event in all its hues, with students competing to win the coveted cover page design. NSDS 2015 thus leaves no stone unturned to make this a memorable event.

It needs no mention that an event of such magnitude needs help and support from all quarters. The event would not have survived without the generous financial, infrastructural and moral support from the administration. The Director of South Campus, Prof. Umesh Rai and Vice-

Chancellor Prof. Dinesh Singh have been magnanimous in their support to NSDS. The finance and academic sections have helped in all possible ways. We are sure we will receive help from all other staff of South Campus including security on those days of the event. Prof. J.P. Khurana conceived the idea of INSA-TWAS key note lecture and his help as Dean, FIAS has been phenomenal. All heads of the departments and teachers have been instrumental to NSDS success. Financial support has also been provided by students themselves in terms of contributions. Several corporate establishments came forward with generous support as well and their help is appreciated.

It is dreamt that NSDS from South Campus will create a brand value of its own, much like the IIT Delhi or DU college fests, but with a difference, with a more academic flavour for pure pursuit of science and higher learning. It is hoped that NSDS will quench the thirst for knowledge and help develop leadership and management skills for the future generation of the country. May NSDS survive the test of time – let this landmark (5th year) be the beginning of many more milestones to achieve.

Prof. SumanKundu
Faculty Coordinator, Department of Biochemistry

Dr. Yogender Pal Khasa
Faculty Coordinator, Department of Microbiology

Dr. SaurabhRaghuvanshi
Faculty Coordinator,Department of Plant Molecular Biology

Dr. Surajit Sarkar
Faculty Coordinator, Department of Genetics


5th Year Celebration
UDSC - National Science Day Symposium

Chief Patrons

Prof. Dinesh Singh, Vice Chancellor, University of Delhi

Prof. Umesh Rai, Director, University of Delhi South Campus

Patrons

Prof. P. C. Ghosh, HOD, Department of Biochemistry

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

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

Prof. R.K. Saxena, HOD, Department of Microbiology

Faculty Coordinators

Prof. Suman Kundu, Department of Biochemistry

Dr. Yogender Pal Khasa, Department of Microbiology

Dr. Saurabh Raghuvanshi, Department of Plant Molecular Biology

Dr. Surajit Sarkar, Department of Genetics

Organizing Secretaries

Sanjay Kumar Dey, Biochemistry

Sujit Kashyap, Genetics

Naveen Sharma, Plant Molecular Biology

Aarti Yadav, Microbiology


5th Year Celebration
UDSC - National Science Day Symposium

Schedule

February 27, 2015

Session: 1

09.30 A.M- 09.55 A.M.: **Registration & High Tea**

10.00 A.M- 11.00 A.M.: **Welcome Address: Prof. J.P. Khurana**, PMB

Introductory Remarks:**Prof. R. Ramaswamy,** Vice President, INSA

INSA-TWAS Key Note Lecture **by Dr. S.K. Sarin,** Director, ILBS: **'Heart of liver'**

11.00 A.M.-11.30 A.M.: Tea

Session: 2

11.30 A.M. - 11.55 A.M.**: Prof. R. K. Saxena,** Dept. of Microbiology

11.55 A.M. – 12.15 P.M.:**Ms. Richa Arya,** Dept. of Biochemistry

12.15 P.M. – 12.35 P.M.: **Ms. Namrata**, Dept. of Genetics

12.35 P.M. – 01.00 P.M.: **FORTIS -CPR Training**

1.00 P.M. – 02.00 P.M.: Lunch & CPR Demo

Session: 3

02.00 P.M.- 03.00 P.M.: **Poster Session 1**

03.00 P.M. - 03.25 P.M.: **Dr. ArunaNaorem**, Dept. of Genetics

03.25 P.M. - 03.45 P.M.: **Ms. NainiBurman,** Dept. of Plant Molecular Biology

03.45 P.M. – 04.05 P.M.: **Ms. ShrutiBindal**, Dept. of Microbiology

04.15 P.M.-04.45 P.M.: Tea

Session: 4

04.45 P.M. - 06.00 P.M.: **Quiz (Prelims)**

06.00 P.M. – 06.15 P.M.: Concluding remarks of first day

February 28, 2015

Session: 1

09.30 A.M- 09.50 A.M.: High Tea

09.50 A.M.- 10.15 A.M.: **Prof. Indranil Dasgupta**, Dept. of Plant Molecular Biology

10.15 A.M. – 10.40 A.M: **Prof. Alo Nag,** Dept. of Biochemistry

10.40 A.M. – 11.00 A.M**.: Dr. Marcio Pocas**, Dept. of Microbiology

11.00 A.M.-11.20 A.M.: Tea

Session: 2

11.20 A.M. – 11.45 A.M.: **Dr. Manish Kumar**, Dept. of Biophysics

11.45 A.M. – 12.05 P.M.: **Ms. Sumedha,** Dept. of Genetics

12.05 P.M. – 12.25 P.M.: **Ms. Meenakshi Tanwar**, Dept. of Biochemistry

12.25 P.M. – 12.45 P.M.: **Mr. Rajeev Gupta,** Dept. of Biophysics

01.00 P.M.- 01.45 P.M. : Lunch

Session: 3

01.45 P.M.- 02.30 P.M. : **Poster session 2**

02.00 P.M. - 03.15 P.M.: **Idea Presentations**

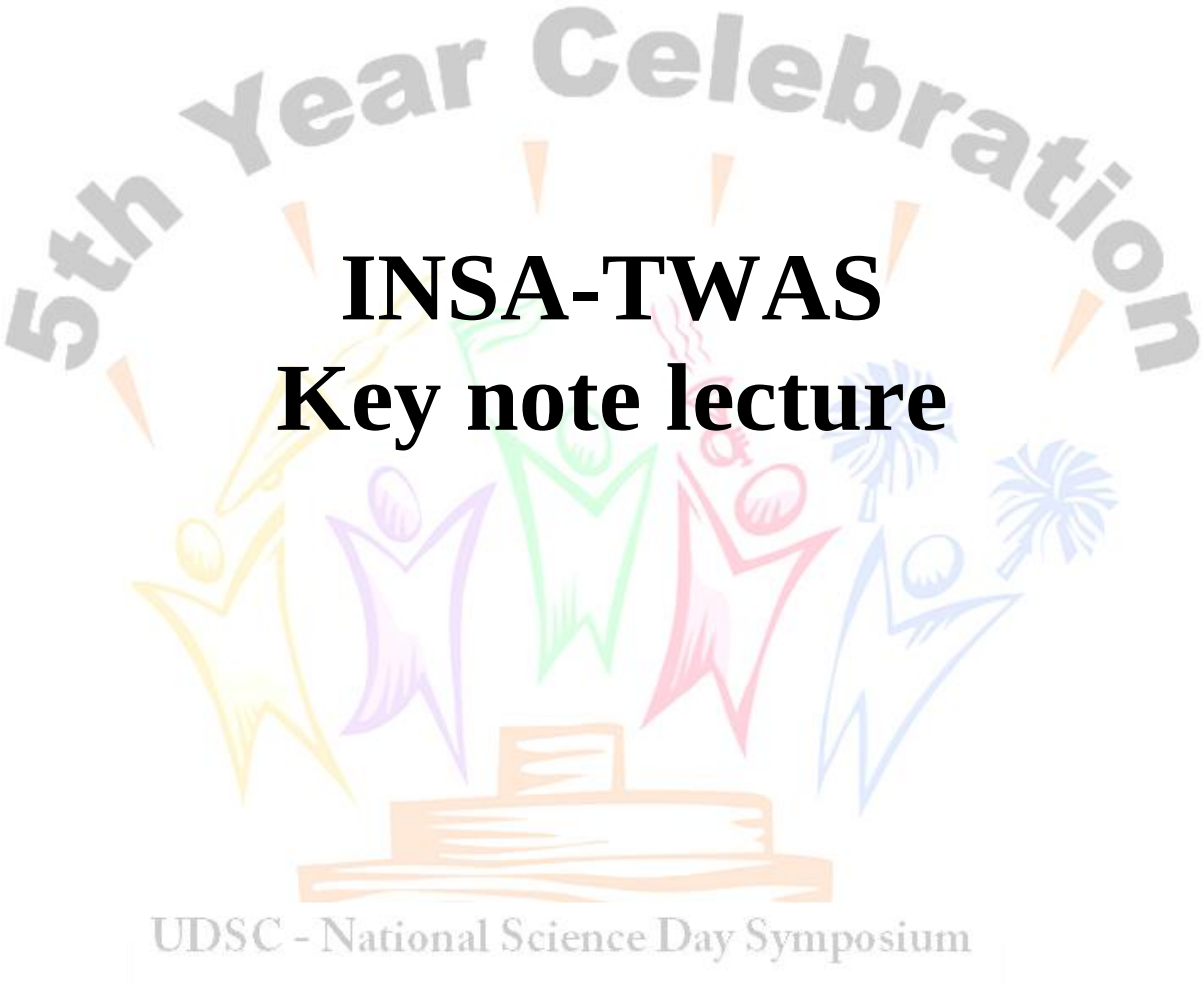
03.15 P.M. – 04.45 P.M.: **Quiz (Finals)**

04.45 P.M.- 05.00 P.M.: Tea

Session: 4

05.00 P.M. – 06.30 P.M.: **Cultural Program**

06.30 P.M. – 07.00 P.M.: **Valedictory & Prize Distribution Session**



INSA-TWAS
Key note lecture


5th Year Celebration
UDSC - National Science Day Symposium

Heart of the Liver

Prof. (Dr.) S.K. Sarin

MD, DM, DSc (Hony.), FNA, FIASc, FTWAS, FNASc

Institute of Liver and Biliary Science (ILBS), Vasant Kunj, New Delhi 110010

There is a rising trend of obesity and metabolic syndrome in the world, including India. Liver plays the central role in energy balance and metabolic homeostasis. Fatty liver is seen in about one in four Indians and fatty liver disease in about one in 20 Indians. There is therefore an epidemic kind of situation. The rising trend is attributed mainly to energy excess, sedentary lifestyle, dietary habits and importantly genetic predisposition.

There is a large spectrum of fatty liver disease, starting from benign fatty liver, non-alcoholic steatohepatitis (NASH), cirrhosis of the liver and liver cancer. The whole spectrum is called Non-alcoholic fatty liver disease (NAFLD) and is to differentiate it from alcoholic liver disease, which could have a similar spectrum. The risk of liver cirrhosis and cancer substantially increase in overweight and obese individuals. Men with BMI of 35–40 exhibited a staggering 4.52-fold increase in relative liver cancer risk. Insulin resistance among obese individuals possibly results in elevated circulating concentrations of insulin and insulin-like growth factor 1 (IGF-1), increased pro-inflammatory cytokines IL-6 and TNFα production, which cause liver inflammation and activation of the oncogenic transcription factor STAT3. Recent studies have pointed towards a role of gut microbiota as a causative factor influencing the liver functioning. High fat diet leads to increased intestinal translocation due to Small intestinal bacterial overgrowth, increased translocation through the enterocytes of LPS and toxin load to hepatocytes, the 'leaky gut'.

While obesity is often associated with NASH, nearly 15-20% of patients have lean NASH (BMI <25 in males and <23 in females), more often seen in the Indian subcontinent. The etiopathogenesis for development of NAFLD is proposed in the form of multiple hit hypothesis. The first hit being development of fatty liver (steatosis) and the second hit being progression to steatohepatitis and cirrhosis with its complications. NAFLD precedes the development of hypertension and can predict development of coronary artery disease and diabetes.

A rise in ALT, a stiff liver with increased fat content, an ultrasound of the liver and occasionally liver biopsy could help confirm the diagnosis.

The treatment of NAFLD is primarily energy balance and maintaining body weight. Regular exercise, careful choice of diet, weight reduction helps majority of the patients. In a proportion of patients, drugs like Pentoxifylline, vitamin E or s-adenosyl methionine are needed. Bariatric surgery is of great help in morbidly obsese patients.

Faculty Talks


5th Year Celebration
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World Leather Industry at Crossroads: Can Biotechnology Help?

Concept to Business, an Indian Achievement

Dr. R. K. Saxena

Department of Microbiology, University of Delhi South Campus, Benito Juarez Road, New Delhi-110021.

rksmicro@yahoo.co.in; rksmicro@hotmail.com

Leather and the leather industry is claimed to be the second oldest industry of the World. The leather industry produces about 18 billion square feet of leather per year, and the total value is estimated at about $ 40 billion. However on the other hand, this industry contributes to one of the major industrial pollution problems being faced globally. The major pollutants are chemicals like lime, sodium sulphide salt, solvents etc. used in the pre-tanning processes of leather manufacturing.

These chemical based processes are hazardous and toxic to the environment and to various flora and fauna. Therefore, there is an urgent need that the leather processing industries shift from chemical to bioprocessing. In this direction, enzymes can be a boon for the leather manufactures as they have very little impact on the environment and are more specific in their activity often working at milder conditions of temperature and pH. Earlier attempts were made and were partially successful for an enzyme assisted process for de-hairing. However, these procedures could not reduce the use of sulphides, oxides and other chemical substances in leather processing thereby could not help in the pollution check. Hence, there is still a great need to find out a process which is totally enzyme mediated rather than enzyme assisted.

In leather processing, the first step in the beam house is the removal of the hair & flesh from hides and skins. In this respect, our investigation have shown that we have produced enzymes which can efficiently carry out de-hairing, de-fleshing, de-greasing of animal skins and hides without using any chemicals. The results and the commercial importance of the process developed will be discussed during the presentation in the light of world's changing scenario of leather processing.

Understanding the cell differentiation in *Dictyosteliumdiscoideum*

Aruna Naorem

Department of Genetics, UDSC, New Delhi-110021

The main aim of our laboratory is to understand the regulatory mechanism underlying cell differentiation during starvation-induced development in *Dictyosteliumdiscoideum.* To achieve the aim, we follow different approaches - gene-specific transcription factors and genes regulated by them; a family of Peptidyl prolyl*cis/trans* isomerase (PPIase) in regulating the effector molecules such as transcription factors; cell cycle regulator as cell cycle influences cell differentiation; and finally integration of the molecular events in understanding how the action of these regulatory protein in concert to achieve a complex process of cell differentiation during multicellular development.

D. discoideum cells exist as unicellular haploid amoeba in moist soil under temperate conditions. The cells feed on soil microorganisms and divide by fission. Upon starvation, cells secrete cAMP and undergo a developmental program in which unicellular undifferentiated amoeba come together to form multicellular structure consisting of two terminally differentiated cell-types, spore cells and stalk cells. These homogenous cells respond to different signaling molecules, such as cAMP, DIF-1 etc. and differentiate into presumptive spore (prespore)/presumptive stalk (prestalk) cells. There is a clear and distinctive sorting of these cells and can be visualized in slug stage whereby anterior portion, $1/5^{th}$ is occupied by prestalk cells and the rest is occupied by prespore cells. These slugs are both phototacticandthermotactic. Once the condition is favorable, slugs culminate into fruiting body with live spores supported on dead stalk.

We have started characterizing two genes encoding a putative bZIP transcription factor, BzpG and a peptidyl prolyl cis/trans isomerase, PinA. Results from genetic and biochemical analyses of these two genes will be presented.

Mining Plant Viruses for Tools of Biotechnology

Indranil Dasgupta

Department of Plant Molecular Biology

University of Delhi South Campus

Plant viruses cause a number of diseases, which affect crop production worldwide, especially in tropical countries such as India. Some of these diseases, if not managed intelligently, can threaten food security and can seriously affect the wellbeing of farming communities. Hence, understanding plant viruses and their interactions with their hosts has been an important area of study. More recently, plant viruses, because of their unique intracellular lives, have been realized to be important sources for genes and control sequences, which have potential applications in plant science and biotechnology. In our group, we have worked with viruses impacting Indian agriculture and have shown that some of them can be used not only to control viruses, but also to develop useful tools for plant science. We used an RNA-interference-based approach with viral DNA to engineer resistance against virus infection in rice. Those plants have now been extensively back-crossed with several popular rice varieties and have shown to retain the resistance. Viral promoters have long been used to drive foreign gene expression in plants. We have also used plant viruses to obtain new promoters to drive foreign gene expression in rice but also in other dicot plants. Since viruses are intracellular pathogens, they trigger RNA-interference against themselves using the conserved RNA silencing machinery in plants. We have used a rice virus to derive a gene silencing system for rice, which has a potential to contribute towards revealing the functions of rice genes in a high throughput manner.

Human Papillomavirus, the Oncogenic SUMO Wrestler

Alo Nag

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

Oncogenic viruses are known to utilize cellular pathways to facilitate their survival and propagation. Emerging evidences suggest that SUMOylation pathways are hugely exploited to support viral replication, assembly and to evade host immune system. A detailed understanding of these processes will be extremely helpful in rational design of antiviral drugs that target viruses by preventing their successful hijacking of cellular pathways. Currently, we are investigating the mechanisms involved in manipulation of host SUMO system by high risk HPV. Recent findings from our lab show for the first time that the human coactivator protein hADA3 is posttranslationally modified by SUMOylation and HPV16E6 stimulates hADA3 degradation by enhancing its SUMOylation. Moreover, depletion of SUMOylating enzyme, Ubc9 elevated the level of hADA3 protein in cervical cancer cell that resulted in suppression of proliferation and migration abilities of SiHa cells.

In another study, we show that SUMOylation contributes to destabilization of the proliferation associated transcription factor, FoxM1. We present evidence that HPV16 E7 oncoprotein can modulate SUMOylation of FoxM1b by impairing its interaction with Ubc9. This suggests that d*ysregulation of SUMO pathway may be an underlying mechanism behind high levels of FoxM1 in HPV positive cervical cancers.*

Altogether, ourdata provide important mechanistic insight into the critical roles of SUMOylation in HPV mediated transformation of cervical cancer cells. Thus enzymes of SUMO pathway are likely to constitute promising targets for anticancer and antiviral therapies.

Dr. Manish Kumar

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

We the computational biology group of Department of Biophysics are working on three different research themes:

Annotation of Genomes/Proteomes: The rate at which sequencing technologies are generating sequence data is growing exponentially from last few years. But the rate of characterization/annotation of newly generated data is not in tune with the rate of their generation. We are constantly in endeavor of developing new tools/algorithms, which can reduce the time required for the annotation. In the last few years we have developed a number of algorithms that can predict different features of proteins for example nuclear and non-nuclear localization of proteins, palmitoylation sites.

Functional Characterization of Low Complexity of Proteins: Low complexity region (LCR) of proteins are considered as a floppy, non-structured and non-significant part of protein sequence. But recent studies have shown that LCRs are as important as the other regions of proteins. In this theme we are trying to discern different structural and functional properties of LCR regions of a protein sequence.

Evolution of Antibiotic Resistance in Pathogenic Microbes: Evolution of antibiotic resistance in the pathogenic microbes are becoming rapidly acquiring a global pandemic. There is not a single drug against which resistance is not known. The greatest worry is the fact that soon it will make non-pathogenic microbes pathogenic and render all drugs ineffective. We are trying to study the evolution of factors responsible for this and also search targets against which no resistance is reported till date.


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Platform Presentations


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OP 1

Insight into ACP-PPTase interaction essential for Fatty acid synthesis in *Leishmania major* with application in drug designing

Richa Arya[1], *Ambrish Kumar*[2], *Monica Sundd*[2], *Suman Kundu*[1]

1. Department of Biochemistry, University of Delhi South Campus, New Delhi-110021
2. Biomolecular NMR II Lab, National Institute of Immunology, New Delhi-110067

Leishmaniases impose devastating impacts on much of the world's population. The increasing prevalence of drug resistant parasites and the growing number of immuno-compromised individuals, particularly patients infected by HIV, are exacerbating the problem to the point that the need for novel, inexpensive drugs is greater now than ever.

The presence of **Type II fatty acid synthesis (FAS) pathway**in*Leishmania major* as suggested by genome sequencing, has provided a wealth of novel drug targets. Since this pathway is both essential and fundamentally different from the cytosolic Type I pathway of the human host, TypeII FAS has tremendous potential for the development of parasite-specific inhibitors.

Acyl carrier protein (**ACP**), a key player in this pathway, forms a thioester linkage to the growing fatty acyl group and shuttles this molecule between the other enzymes responsible for sequential fatty acid chain growth in the pathway. A detailed understanding of protein-protein interactions between ACP and other enzymes is crucial for exploiting FAS for drug designing as well as for biotechnological applications. However, little is known about how much of a particular ACP's surface participates in inter-protein interactions and whether different enzymes recognize separate regions of ACP. Here we report the investigation of a protein interaction surface on the LmjACP for phosphopantetheinyltransferases (PPTases), such as Sfp (*B.subtilis*) and LmjPPTase, by comparing LACP with other TypeII ACPs (*E.coli*, Pf, Mtb) involving combinatorial mutagenesis and enzyme kinetics. This protein interaction surface is highly localized in the helix II of ACP, and is distinct from the previously identified interface of other TypeII ACP characterized previously.

Therefore, this interaction and interface keeps the handle to design *Leishmania* specific drugs, not interfering with the Human TypeI FAS pathway.

OP 2

How to find loci governing quantitative traits? – A study of QTL analysis in *Brassica juncea.*

Namrata Dhaka *and Akshay Kumar Pradhan*

Department of Genetics, University of Delhi, South Campus

Brassica juncea (AABB) is a natural amphidiploid of *B. rapa* (AA) and *B. nigra* (BB). It is one of the major oilseed crops in India. Breeding objectives for *B. juncea* target yield traits, oil quality and resistance against biotic and abiotic stresses. This study focuses on elucidation of QTL involved in determination of seed size as well as other important yield traits in *B. juncea.* To dissect these traits,a bi-parental doubled haploid (DH) mapping population of 182 individuals was developed from F1 of the cross between EH2 and PusaJaikisan. A linkage map for EPJ population was constructed using a total of 860 microsatellite and intron polymorphic markers. The EPJ population was phenotyped in three locations – Delhi (2011-12), Alwar and Bharatpur (2012-13) over a span of two years. Trait values were measured for days to flowering, plant height, number of primary branches, main shoot length, number of siliqua per main shoot, silique length, number of seeds per silique, siliqua density, thousand seed weight and oil content. Various statistical analyses were done to calculate the mean trait values, range, frequency distribution and heritability of the traits and the coefficient of correlation between the trait values. QTL mapping was carried out resulting in discovery of 19 QTL for seed size and a total of 126 QTL for the other yield traits. Epsitatic and environmental interactions of these QTL were also studied. QTL data obtained from three previous studies in the laboratory using VH (Varuna-Heera), TD (TM-4-Donkaja IV) and DE (Donskaja IV-EH-2) populations was used to conduct a meta-analysis to identify consensus QTL. A total of 485 QTL from four populations yielded 134 meta-QTL. Identification of QTL and meta-QTL from this study shall be useful for carrying out marker assisted breeding for improvement of seed size and other agronomic traits in *B. juncea*. Also, this information can be used for further genetic dissection of these traits by using candidate genes and QTL information from related species.

OP 3

Functional Characterization of HY5 Homolog in Rice

Naini Burman, *Akanksha Bhatnagar and Jitender P. Khurana*

Interdisciplinary Centre for Plant Genomics and Department of Plant Molecular Biology, University of Delhi, South Campus, New Delhi, India

Light is one of these environmental cues and plays a very important role in plants life as they are sessile and photoautotrophic. Plants have developed an extensive array of network of light signal transduction, which integrates with almost all the important pathways. This pathway is highly hierarchical with photoreceptors like phytochromes and cryptochromes being at the top. They are followed by early signaling factors like HFR1 and central integrators like COP1. Then lies the downstream effectors like HY5. Most of the components of light signaling pathway have been characterized in *Arabidopsis*, a model dicot plant. In rice, *OsbZIP48*, one of the HY5 orthologwas functionally characterized using transgenic approach. Over-expression transgenics of *OsbZIP48* caused dwarf phenotype, more chlorophyll content and delayed senescence. There was a high degree of floret sterility, which severely affected the grain yield. RNAitransgenics of *OsbZIP48* showed tall phenotype in T1 stage but in the next generation (T2) they seggregated into two types of seedlings;one which resembled wild type and vector control in morpology and the other which showed lethal phenotype and died within 20 days. Microarray analysis of both the transgenics revealed that a number of hormonal pathways were affected. These data obtained by analysis of rice transgenics for *OsbZIP48* and the fact that it could functionally complement *Arabidopsis hy5* mutant provide evidence that rice ortholog of HY5, i.e. OsbZIP48, performs overlapping functions with HY5 as well as it plays some monocot specific roles in regulating plant development.

OP 4

Sustained production of L-theanine using γ-glutamyltranspeptidase

Shruti Bindal *and Rani Gupta*

Department of Microbiology, University of Delhi, South Campus

Γ-glutamyltranspeptidase (GGT) is a well known enzyme for the synthesis of various γ-glutmayl compounds and L-theanine (γ-glutamyl ethylamine) is one of the most important neutraceutical among them. Therefore, GGT from a laboratory isolated strain of *Bacillus licheniformis* was used to synthesis L-theanine and various parameters were optimized which affect the synthesis. Foremost, the enzyme production from *Bacillus licheniformis* (BLGGT) was optimized using one-variable at a time approach followed by statistical methods, viz., Plackett-Burman and response surface methodology (RSM) yielding a 3.3 fold increase. At the optimumconditions for enzyme production, a high level, 4000 U/L of GGT was obtained. For theanine synthesis, all the parameters viz. pH, donor to acceptor ratio, substrates and enzyme concentrations, time and temperature were optimized to be pH 9, 1:7.5, 80 mM L-glutamine, 600 mMethylamine, 1 U/ml and 2 h at 37^0C, respectively. A conversion rate of >80% was obtained in 2 h. L-theanine was detected and quantified with a retention time of 11.3 min on a reverse phase C_{18} column with 0.5% trifluoroacetic acid (TFA) in water as mobile phase using UV/Vis detector at 203 nm. Further, BLGGT was immobilized covalently on chitosan microspheres in order to make the process cost effective.A one liter reaction for L-theanine under optimized conditions was carried out using immobilized enzyme and same conversion rate was obtained. Immobilized enzyme was recycled upto 10 cycles with almost unaltered efficiency. L-theanine was purified by column chromatography using Dowex 50WX8 hydrogen form resin and >85% theanine was recovered by eluting it with ammonia water (pH 11.6) and the fractions containing L-theanine were lyophilized to obtained a white colored powder. The product thus obtained was identified to be L-theanine using H^1 NMR.

OP 5

The impact of epigenetic modulator drugs on *Cryptococcus neoformans* major virulence phenotypes

Marcio J Poças-Fonseca

Laboratory of Gene Regulation and Mutagenesis, Department of Genetics and Morphology, Institute of Biological Sciences, University of Brasilia.Brasilia– DF, Brazil.

Keywords: *Cryptococcusneoformans*, histone deacetylases inhibitors, sodium butyrate, Trichostatin A, chromatin structure, virulence factors.

Cryptococcus neoformans undergoes phenotypical changes during host infection in order to promote persistence and survival. Studies have demonstrated that such adaptations require alterations in gene transcription networks by distinct mechanisms. Drugs such as the histone deacetylases inhibitors (HDACi) Sodium Butyrate (NaBut) and TrichostatinA (TSA) can alter the chromatin conformation and have been used to modulate epigenetic states in the treatment of diseases such as cancer. In this work, we have studied the effect of NaBut and TSA on the expression of *C. neoformans* major virulence phenotypes and on the survival rate of an animal model infected with drugs-treated yeasts. Both drugs affected fungal growth at 37 ºC more intensely than at 30 ºC. HDACi also provoked the reduction of the fungal capsule expansion. Phospholipases enzyme activity decreased; mating process and melanin synthesis were also affected by both inhibitors. NaButled to an increase in the population of cells in G2/M. Treated yeast cells, which were washed in order to remove the drugs from the culture medium prior to the inoculation in the *Galleria mellonela* infection model, did not cause significant difference at the host survival curve when compared to non-treated cells. Overall, NaBut effects on the impairment of *C.neoformans* main virulence factors were more intense and stable than the TSA effects. We propose the employment of HDACi in combination to classical antifungal drugs in experimental treatment approaches for severe cryptococcosis animal models.

OP 6

Identification of two novel putative causal genes for Parkinson's disease

Sumedha Sudhaman[a], *MadhuriBehari*[b], *Uday B. Muthane*[c], *Ramesh C. Juyal*[d], *Thelma B.K.*[a]

[a]Dept of Genetics, University of Delhi South Campus; [b] All India Institute of Medical Sciences, New Delhi; [c] Parkinson's and Aging Research Foundation, Bangalore; [d]Regional Center for Biotechnology, Gurgaon

Parkinson's disease (PD), a dopamine deficiency disorder is the second most common neurodegenerative condition in humans and both sporadic as well as familial forms of the illness are well documented. While the genetic basis of the sporadic forms remains enigmatic, seven genes have been identified to date for familial PD. However, mutations therein explain <30% of all known familial cases, leaving considerable scope for new gene identification in PD. Next Generation Sequencing (NGS) technology has greatly facilitated this gene search. In this study, we sequenced two PD exomes each from two multi-member affected Indian PD families, shown to be negative for mutations in known genes. Using a combination of bioinformatic tools, we identified one novel homozygous and one novel heterozygous putative disease causing variantsin *PODXL* and *RIC3* genes, segregating with the disease in families 1 &2 respectively. On screening all exons of both genes in the lab PD cohort, we identified three heterozygous additional variants in *PODXL*, and one additional heterozygous variant in *RIC3*. Of note, mutations in *PODXL* and *RIC3* were absent in controls, PD and non-PD exomes from the lab and also in over 100,000 unrelated non PD exomes from EXAC database. However, both variants in *RIC3* are observed at a very rare frequency (<0.0001) in 12 exomes from a South Asian cohort of ~16,000 exomes. These findings suggest the possible pathogenic nature of the identified mutations. We then investigated the role of these variants in PC12 cells differentiated into neurons. Keeping in tune with known functions of these two genes, significant differences in neurite branching profiles in neurons with a *PODXL* mutant; and reduced chaperoning activity of *RIC3* mutants visualised by colocalisation experiments, as compared to their respective wild type alleles, were observed. Discovery of these two putative genes has provided leads for possible involvement of alternate pathways in PD etiopathology, validation of which warrants investigations in animal models.

OP 7

Development of Blue Light Photoreceptors as an Optogenetic Tools for Modulation of Cyclic Nucleotide Mediated Biological Functions

Meenakshi Tanwar[1]*, Nemneineng Haokip*[2]*, Lohit Khera*[3]*, Aruna Naorem*[2]*, Rajeev Kaul*[3]*, and Suneel Kateriya*[1]***

[1]Department of Biochemistry, [2]Department of Genetics, [3]Department of Microbiology, University of Delhi South Campus, Benito Juarez Road, New Delhi 110021

Light provides a signals/stimulus for many biological processes. Living organisms possess variety of photoreceptors to sense and respond to these light signals, which involved sensory transduction and for photoadaptive responses in many prokaryotes and in eukaryotes. The use of these genetically encoded natural photoreceptors as optogenetic tools has revolutionized the modern biology by allowing optically control of biological processes in spatiotemporal manner with several advantages over traditional methods.

BLUF (Blue light sensors using FAD) domain containing proteins are flavin-based blue light photoreceptors. BLUF domains are also present in multidomain architecture, where they fused with other effectors domain like GGDEF, EAL, CHD domain. BLUF domain linked to CHD (cyclase homology domain) domain is known as Photoactivated adenylyl cyclases (PAC). PACs have been reported in *Euglena gracilis*which mediates photobehavioral responses of the organism. These PACs were used as optogenetic tools for manipulating cAMP level simply by illumination in a controlled manner. Optical manipulation provides an opportunity to reversibly manipulate cAMP mediated signaling in living cells, which are difficult to achievable in control manner using traditional pharmacological or genetic approaches.

We are characterizing PACs from amoeboflagellate protozoa *Naegleriagruberi*(named NgPACs) which consist of cyclase homology domain (CHD) and BLUF domain. *In vitro*, these NgPACs exhibits light regulated cyclase activity. We have used NgPACs as an optogenetic tool to modulate the biological functions in HEK293T cells and *Dictyostelium. discoideum*. These NgPACs have also been engineered to develop photoactivatedguanylylcyclases (NgPGC). Biochemical characterization and optogentics potentials of the natural PACs and engineered PGCs will be presented in detail.

OP 8

Phosphorylation of Voltage-Dependent Anion Channel by c-Jun N- terminal Kinase-3: a Bilayer Electrophysiological Approach.

Rajeev Gupta *and Subhendu Ghosh*

Department of Biophysics, University of Delhi South Campus, New Delhi, India.

Stress activated c-Jun N-terminal Kinase-3 (JNK3) has been reported to act on mitochondrion to promote neuronal cell death. Phosphorylation of mitochondrial Voltage-Dependent Anion Channel (VDAC) plays an important role in mitochondria-mediated cell death. Keeping these in view phosphorylation of rat brain VDAC by JNK3 has been studied *in vitro*. Pro Q Diamond phospho-protein staining experiment demonstrates VDAC is phosphorylated by JNK3. Bilayer electrophysiological experiments show that single-channel conductance of VDAC phosphorylated by JNK3 is significantly lower than that of the native VDACat a membrane potential. The opening probability of VDAC undergoes massive reduction due to phosphorylation by JNK3.These indicate closure of VDAC due to phosphorylation byJNK3. Treatment of phosphorylated VDAC with alkaline phosphatase reversed the VDAC functional activity as shown by single-channel current and opening probability. The physiological consequence of closure of VDAC as a result of phosphorylation has been attributed to JNK3 dependent mitochondria-mediated apoptosis.

Poster Presentations


5th Year Celebration
UDSC - National Science Day Symposium

P 1

γ-glutamyltranspeptidase (GGT): Acceptor site characterization by functional divergence and molecular dynamics simulations for drug design.

VedVrat Verma[1], *Rani Gupta[2] and Manisha Goel[1*]*

1. Structural Biology Lab, Department of Biophysics, University of Delhi South Campus, New Delhi-110021, India
2. Department of Microbiology, University of Delhi South Campus, New Delhi-110021, India

γ-glutamyltranspeptidase (GGT: EC 2.3.2.2) is an N-terminal nucleophile hydrolase conserved in all three domains of life. GGT plays a key role in glutathione metabolism where it catalyzes the breakage of the γ-glutamyl bonds. GGTs from bacteria, archaea and eukaryotes are homologous proteins sharing >50% sequence similarity and a conserved four layered αββα sandwich like structure. These proteins though similar in sequence and structure are quite diverse in their enzyme activity. GGT is known to be involved in various diseases like asthma, parkinson, arthritis, and gastric cancer. It's inhibition prior to chemotherapy has been shown to sensitize tumours to the treatment. Microbial GGTs act as virulence factors, important for the colonization of bacteria in host. However, all known inhibitors (mimics of its native substrate, glutamate) are highly toxic. However, a few successful efforts have been reported previously in designing species specific inhibitors.

We aim to leverage the diversity seen in GGT family for designing specific inhibitors. In the present study we have identified type I and type II functional divergence sites. Molecular dynamics simulations were performed for homologous GGT proteins and the role of putative divergence sites has been delineated. On basis of this combined analysis, sites imparting specificity to GGT proteins have been highlighted and will be used for species-specific drug design against various organisms GGTs.

P 2

Diversity of chitinases in *Amycolatopsismediterranei*: Sequence comparison and phylogenetic analysis

Tanvi Kalra *and Rani Gupta*

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

Chitinases (EC 3.2.1.14) are glycoside hydrolases that catalyze the degradation of chitin, a natural polymer of β-1,4 linked N-acetylglucosamine units. Chitinases are ubiquitous in occurrence ranging from archae, bacteria, fungi, plants, humans. More than 10^{11} metric tons of chitin is annually produced in the aquatic biosphere worldwide, disposing this marine waste is still an issue that needs to be resolved [1]. In India, there exists a long coastal belt (7516.6 km), hence chitin waste management is important. Moreover, chitin and its derivatives are useful in various sectors such as biomedical, agricultural, biocontrol of insects and fungi by enhancing the innate resistance of plants [2].The complete genome of *Amycolatopsismediterranei* U32 was sequenced recently in 2010. The genome-wide survey of *A. mediterranei* reveals that it contains thirteengenes annotated as chitinases, out of which eleven are extracellular, that have yet not been explored (Table 1).Chitinase production was verified by colloidal chitin plate-assay. It produces an extracellular chitinase in a medium containing 0.3% shrimp chitin flakes, 0.2% yeast extract, 0.4% KH_2PO_4 and 0.1% K_2HPO_4 at 30˚C, 200 rpm. The shrimp chitin flakes were totally degraded in 250 ml Erlenmeyer flask in one week. All the chitinases belong to family 18 glycoside hydrolases. Phylogenetic analysis of chitinaseswas done using Clustal W2 and it suggests that their sequences vary amongst each other (Fig.1.1). The chitinases comprise mainly of three domains *viz.* chitin binding domain, catalytic domain and fibronectin type III domain. One of the chitinase of *A. mediterranei*(Chi 3)has all the three domains whereas the others have either two of them or a single catalytic domain. The isoelectric point of the chitinases vary from 4.6-8.9 with varying protein size between 316-737 amino acids.

P 3

CBMAR: A Comprehensive β-lactamase Molecular Annotation Resource

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

[1]Dept. of Biophysics, UDSC, New Delhi, [2]Dept. of Microbiology, UDSC, New Delhi

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

β-lactam antibiotics are among the most widely used antibiotics against microbial pathogens. However, enzymatic hydrolysis by bacterial β-lactamases is increasingly compromising their efficiency. β-lactamase enzymes encompass a large and diverse group of enzymes, which can be classified on the basis of primary structure-Ambler classification or on the basis of their functional characteristics-Bush classification. Ambler schema classifies β-lactamases into four classes, A, B, C and D. Class A, C and D is serine β-lactamases while class B were zinc-containing metallo-β-lactamases.

To tide over increasing β-lactamases mediated resistance newer generation β-lactam antibiotics were discovered, whichare more effective than their predecessors but have exerted a stronger selection pressure resulting in evolutionof newer variants of β-lactamases, denoted as extended spectrum β-lactamases (ESBL). The propagation of resistance in bacteria towards β-lactamase becomes a serious challenge and cannot be addressed until we gain a fair understanding of their sequence structure and functional relationship.Also analysis of individual mutations leading to expansion of hydrolytic profile can put a milestone in prediction of the future course of evolution of these β-lactamases. These detailed analyses are not possible until all relevant information is arranged systematically at one place.

Here, we describe a new database-CBMAR, which provides information about molecular and biochemical functionality of β-lactamases. The basic architecture of CBMAR is based on the Ambler classification. Each class is then divided into several families on the basis of their antibiotic hydrolytic profile and sequence similarity. Each family is annotated with (i) origin of the name of the family, (ii) genus/genera in which a particular family of β-lactamase was reported, (iii) genomic location (chromosomal/plasmid), (iv) antibiotic resistance profile, (v) inhibitor susceptibility, (vi) active-site, (vii) family-specific fingerprints, (viii) mutational profile, (ix) phylogenetic tree, (x) names of variants and various other features. The database also supports sequence similarity searches using BLAST and search for family-specific fingerprints using MAST. It is publicly accessible at http://14.139.227.92/mkumar/lactamasedb.

P 4

Identification of inhibitors against Iron Dependent Regulator (IdeR) by Structure Based High Throughput Virtual Screening

***Akshay Rohilla**, Garima Khare and Anil K. Tyagi*

Department of Biochemistry, University of Delhi South Campus, New Delhi

Objectives: According to 2014 report of WHO, there were 9.0 million new casesof TB in 2013 out of which 1.5 million people died worldwide. These staggering figures highlight the burden of tuberculosis worldwide and thus there is an urgent need to develop new therapeutics against *Mycobacterium tuberculosis*. The aim of this study was to identify inhibitors against Iron dependent regulator (IdeR), a transcription factor in *Mycobacterium tuberculosis*that regulates cellular levels of iron in the pathogen.

Methods: A customized NCI librarywas docked against the DNA binding site of IdeR by using Autodock 4. Electrophoretic mobility shift assay (EMSA) was developed and employed to screen 120top scoring molecules for their inhibitory potential against IdeR*in-vitro*. The most potent compounds were further employed for lead optimization studies. Two in-silico approaches, namely, pharmacophore screening followed by docking studies and similarity search based screening were carried out by using the ZINC and NCI database and shortlisted molecules were further procured and evaluated for their efficacy by EMSA.Subsequently, all the molecules exhibiting *in-vitro* protein inhibition were further evaluated forMIC_{99}studies against the growth of *Mycobacterium tuberculosis* (H37Rv) in broth culture and cytotoxicity studies against few mammalian cell lines.

Results: This study identified few potent IdeR inhibitors with IC_{50} values in low micromolar range by employing structure based virtual screening method. The lead optimization studies identified a pharmacophore model which included two rings and two hydrogen bond acceptors as critical features for binding to IdeR. One molecule obtained from the pharmacophore screening also exhibited *in-vitro*IdeR inhibition (at 25µg/ml) thereby validating the model obtained. The similarity search method identified the diazene-hydroxy phenyl series of compounds with IC_{50}ranging from 1 µg/ml to 100µg/ml out of which the most potent inhibitory molecule exhibited an IC_{50} of 1 µg/ml, $MIC_{99}$of 20 µg/ml and no cytotoxicity upto 200 µg/ml.

P 5

Isolation, screening and production of oil (fatty acids) from oleaginous yeast , "a potential source for biodiesel production"

***Garima Kudeshiya**, Anjali Garg, Saurabh Saran and R.K. Saxena*

Technology Based Incubator, University of Delhi South Campus, New Delhi -110021
Email id : garimakudeshiya@gmail.com,rksmicro@yahoo.co.in

Biofuels are among the most promising replacement for non-renewable fossils fuels. Biodiesel is the most common biofuel produced from oils or fats using transesterification. The microbial oils produced by oleaginous micro-organisms represents a potential alternative for Biodiesel production .In this present investigation , a total of 52 yeast isolates were screened for oil production from fruit pulp/residues. Out of these four isolates A_3, A_{16},A_{28}, A_{48}, were found to be oleaginous after qualitative screening and were found to stain with dies like Sudan Black B and Nile Red. Among these potential isolates A_{28} was found to be most potent as yeast oil producer and further identified as ***Rhodosporidiumtoruloides.*** on the basis of 18s rDNA analysis the isolate initially produce 3.096 gm/l of oil. Further process engineering was carried out to enhance the production of oil by using one variable at a time(OVAT) method and this results in 8.68 gm/l production. The present study aimed at improving yeast oil yield which resulted in 3.03 fold in yeast oil.

P 6

Spectroscopic Identification and Characterization of Hemoglobins with Single Amino Acid Mutations for Simpler Diagnosis of Hemoglobinopathies

Mamta, *Pushpanjali Dasauni and Suman Kundu**

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

Hemoglobinopathies affect the functioning of red blood cells and are the most common monogenic diseases worldwide. It has been estimated that about 7% of world population is affected with thesedisorders.The high frequency and clinical severity of the hemoglobinopathiesmake them a major public health problem. India is also burdened with hemoglobin disorders that pose several challenges. Probably the best strategy for the prevention and control of the disease is early diagnosis. Analytical and preparative procedures for the characterization of abnormal hemoglobin are complex and time-consuming. The current methods used for screening of hemoglobinopathies have their own strengths and weaknesses, sometimes failing to identify abnormal hemoglobin. Thus, fast, inexpensive, accurate and easier methods that could be successful independently or complement existing methods for screening are highly desirable. Spectroscopy could provide rapid identification of hemoglobin disorders since normal and abnormal hemoglobins and related biomolecules give rise to distinct spectral signatures. We aim to build on the minimal and preliminary information available in this direction and establish biomolecular spectroscopy (absorbance, FTIR) as the routine method for detection of hemoglobinopathies. Absorbance and FTIR spectra showed different pH induced local changes in normal v/s mutant hemoglobin. Spectral signatures associated with mutant hemoglobin could be used as a diagnostic marker for the detection of these variants for patients having hemoglobin disorders.In addition, methods/protocols for ligand binding kinetic to study single mutation in hemoglobin disorders was alsostandardized.

P 7

Targeting Cytochrome b5 Reductase3 to combat Cardiovascular Diseases

Gagandeep Kaur, *Sanjay Kumar Dey and Suman Kundu*

Department of Biochemistry, University of Delhi South Campus,Benito Juarez Road, New Delhi-110021

sumankundu7@gmail.com

Cytochrome B5 Reductase 3 (CYB5R3) converts ferric Hbα into its ferrous form in the myoendothelial junctions. Inhibiting this unique enzymatic function can increase the NO supply in blood-vessels and thus has been implicated as a side-effect-free novel-drug-target to combat cardiovascular diseases, especially hypertension. Unfortunately, only a limited set of inhibitors against CYB5R3 are reported till date and none of them seems to be very conclusive or effective. Such a lacunae presents immense scope for structure based drug design against CYB5R3, especially since the 3D structure of hCYB5R3 has recently been solved. Thus, small molecule chemical libraries from the National Cancer Institute, USA were virtually screened, scored and ranked against hCYB5R3. Top-hits were then tested *in vitro* against purified, recombinant hCYB5R3 using potassium-ferricyanide based high-throughput assay, takingmyricetin and PTU as positive controls. Four lead-compounds showed better efficacies (IC_{50}s calculated in µM range) than the controls. The leads were thus evaluated further using state-of-the-art biophysical and biochemical tools. The binding of the inhibitors to hCYB5R3 was validated using fluorescence, UV-Visible and CD spectroscopy as well as ITC, displayingK_d values in nano-molar range. The lead compounds also showed no toxicity against human RBCs.

Inhibition of Hb reduction by hCYB5R3 in presence of lead-compounds has re-confirmed their antagonistic efficacies. Pharmacokinetic properties of lead compounds were evaluated *in silico* and predicted to be safe drug-like molecules. These compounds are now being tested in *C. elegans* (survival assays) and are ready to be tested in appropriate rat models of hypertension. Leads have been optimized for their pharmaceutical improvements to develop them into likely drug to combat cardiovascular diseases.

P 8

Identification of Cell-type Specific Promoter in *Dictyostelium discoideum*

Bharti Pathak *and Aruna Naorem**

*Department of Genetics, University of Delhi South Campus, Benito Juarez Road, New Delhi-110021

Dictyostelium discoideum isahaploid eukaryotic micro-organism exhibiting unique life-style of motile unicellular and multicellularstages. In the slug stage of *D. discoideum* development, sorting of two major cell types: prestalk and presporecells could be observed. Genes such as*D-19, pspB*are specifically expressed in prespore region in the slug whereas genes such *ecmA, ecm B*are expressed in pres talk cells. Therefore, these genes are used for markers for prespore and prestalk respectively. These markers are limited in number, so in order to have more markers to facilitated the study of ectopic expression of genes we undertake our study to identify cell-type specific genes and characterize their promoter. Towards this objective, we selected two putative genes for promoter study i.e.DDB_G0279421 (P_{udpA}) and DDB_G0292710 (P_{mdcA}) by comparing their expressions profiles (available from Microarray data onwww.dictybase.org) in different cell types with already known cell-type specific marker genes.Spectrophotometry(ONPG test)and histochemicalassayswere used fortesting the activity of a particular promoter*lacZ*expression.Bothpromoterswere amplified usingPromoter region specific primers from Ax2 genomic DNA and the amplified productswerecloned in TA cloning vector. Further, these putative promoterfragments were sub-cloned in fusion with *lacZ* in *Dictyostelium* vector (promoterless). These constructs were electroporated into Ax2 cellswith P_{D-19} - *lacZ*as control and transformants were selected on G418 plates. Two independent transformants of each of the construct were put for development on non-nutrient agar plate. Growing cells as well asdifferentdevelopmental stages were collected and performed*β-galactosidase*assay from cell lysates following standard protocol. As expected, no activity was observed in vector transformed cells where asP_{D-19}-*lacZ* showed activity only in developmental structureswith increased activity from mound to fruiting body.Similarly, P_{udpA}-*lacZ*did not show any activity in vegetative cells, but showed activity in development as seen with P_{D-19}construct. However, P_{mdcA}showed activityonlyin vegetative cellsbut no activity indevelopment.Further, Histochemical staining ofdevelopmental structures are underway to observe the spatial expression of these promoter *lacZ*constructs.

P 9

Identification of Biotin biosynthesis inhibitors for inhibition of *Mycobacterium tuberculosis*

Swati Singh, *Garima Khare and Anil K. Tyagi*

Department of Biochemistry, University of Delhi South Campus, New Delhi

Drug resistance against currently available anti-mycobacterial drugs leads to the failure of control measures against tuberculosis. Hence, the identification of novel chemical entities exhibiting potent anti-mycobacterial activities is urgently needed. Biotin is an essential cofactor required for the synthesis of fatty acid component of *Mycobacterium tuberculosis* (Mtb) cell envelope making the enzymes of biotin biosynthesis important targets for the development of therapeutics against this pathogen. BioA, a PLP dependent DAPA synthase, is a crucial enzyme which catalyzes the second step of biotin synthesis involved in the transamination of 7-keto-8-aminopelargonic acid (KAPA) into 7,8-Diaminopelargonic acid (DAPA). Previous studies have shown an essential role of BioA in Mtb virulence as the Mtbmutant lacking BioA display an *in-vitro* growth defect as well as are unable to establish infection in mice. Moreover, humans lack the *de novo* biotin biosynthesis pathway, thus MtbBioA appears to be a promising target for anti-mycobacterial drug development. In this work, structure based virtual screening was carried out by employing a library of diverse compounds against the active site of BioA. Top ranking compounds were evaluated for their ability to inhibit BioA enzymatic activity. The compounds that exhibited greater than 20% inhibition (at a concentration of 100µg/ml) were further assessed for their ability to inhibit Mtb growth in broth culture. Subsequently, cytotoxic studies were carried out for the molecules that exhibited inhibition of Mtb growth. Our study has identified a few hit molecules against MtbBioA that can act as promising candidates for further development of potent anti-mycobacterials.

P 10

Isolation, screening and production of proteases enzyme from *bacillus*sps.

Samreen Fatima, *Mohd. Rizwan, VaishaliDhama, Raj Kumari, Saurabh Saran and Rajendra Kumar Saxena*

Technology Based Incubator, University of Delhi, South Campus New Delhi: 110021

Email ID: samreen.fatima444@gmail.com , Mohd.rizwan44@gmail.com; rksmicro@yahoo.co.in

Enzyme being biocatalyst is an important tool for various industries. Proteases are the largest group of enzyme that catalyze the hydrolytic reactions by cleaving peptide bonds in protein and plays important role in industrial biotechnology, viz food and feed industry, pulp and paper industry, detergent industry, oil industry and specially leather industry. In present study the proteases are produced from soil (Isolate bacteria). Proteases are very wide spread in the microbial world. Most of the microbial proteases are stable and highly active on alkali pH (6-11) and the temperature range 20-80^{o}C. The effect of temperature, pH on microbial proteases was studied. In the present the aim of this study was to screen the proteases producing microorganism and characterization of proteases enzyme.

P 11

Liposomal delivery of antimalarial drugs under*in vitro* and *in vivo* conditions

Tania Banerjee, Shainan Hora, *Vinoth Rajendran, Mohsin Raza and Prahlad C. Ghosh*(pcghose@gmail.com)*

Dept. of Biochemistry, University of Delhi South Campus, New Delhi, India.

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

P 12

Targeted downregulation of dMyc(a homolog of human *c-myc* proto-oncogene) suppresses human Tauopathies in *Drosophila* disease models

Soram Idiyasan Chanu *and Surajit Sarkar**

Department of Genetics, University of Delhi, South Campus' Benito Juarez Road, New Delhi-110 021, India
(Correspondence: sarkar@south.du.ac.in)

Human Tauopathies, such as Alzhiemer's Disease (ADs), Frontemporal Dementia with Parkinsonism linked to chromosome 17 (FTDP-17), Parkinson's disease (PD) etc.,are a group of human neurodegenerative diseases which are characterized by accumulation of hyperphosphorylatedTau proteins in brain. Cytoplasmic accumulation of hyperphosphorylatedTau leads to formation of neurofibrillary tangles which subsequentlymark the affected neurons to undergo progressive degeneration and development ofassociated phenotypes. Recent advances have characterised the neuropathology of such disorders, however,the underlying molecular and cellular events of disease pathogenesis is still highly elusive. This is primarily because of the limitations associated with"Human"as a model system for such studies. Interestingly, *Drosophila*Tauopathy model recapitulates many of the prominent human degenerative features like early death, impairments of learning, memory and locomotorfunctions.In the present study we demonstrate for the first time that targeted downregulation of dMyc (a human homologue of *c-myc* proto-oncogene) significantly supresses the neurodegenerative phenotypes, cellular toxicity and behavioural defects ofhumanTauopathies (ADs and FTD-17 etc.) in *Drosophila*.We further demonstrate that dMycmediated suppression of neurodegenerative phenotypes is largely achieved by reducing the phosphorylation dynamic of Tau and promoting the clearance of protein aggregates.

Key words: Tauopathies; hyperphosphorylation; dMyc; *Drosophila.*

P 13

Low complexity and disordered regions of proteins have different structural and amino acid preferences

***Bandana Kumari*[1*], *Ravindra Kumar*[1] *and Manish Kumar*[1]**

[1]Department of Biophysics, University of Delhi South Campus, New Delhi, India-110021

*Email: bandana.kumari@south.du.ac.in

Low complexity regions (LCR) in a protein sequence are regions of biased compositionwhich are characterized either by the presence of homo-polymeric repeats of a single amino acid or by hetero-polymeric short repeats of amino acid residues, or by aperiodic mosaics of a few amino acids. Every amino acid has the potential to exist in LCRs, which are present in every domain of life viz. Eukaryotes, Archaea and Bacteria and have diverse function. Despite well-established importance and abundance, compositional and structural properties of LCRs are poorly understood and their structural status as ordered or disordered is at best ambiguous. Often, LCRs are considered as a part of disordered protein segments, which most likely do not form any secondary structure but exist as solvent-exposed, disordered coil. We have analyzed the secondary structure content and surface accessibility of a non-redundant dataset of Protein Data Bank (PDB) proteins and found that unlike popular belief, LCRs might have secondary structures (mostly helix) and they might not always exist as highly accessible disordered region. We also observed that in a LCR, all constituting amino acids might have same secondary structure or there may be combination of different secondary structures. We also observed that proteins whose structures was determined by X-ray crystallography were found to possess ordered LCRs while those whose structure was determined by NMR possessed disordered LCRs. Consensus disorder prediction by DISOPRED, IUPred, and IsUnstruct also supported our inference. Trans-membrane (TM) region of proteins are highly dominated by α-helices,which may be a possible reason for predominant occurrence of α-helices. But a very small fraction (<5%) of helices suggests that our observation was not biased due to presence of TM helices. Comparison of enrichment/depletion profile of disorder promoting amino acids for LCRs in ordered and disordered regions of proteins showed that they have different enrichment and depletion patterns of amino acids.

In brief, our analysis suggeststhat the structural state of LCR depends on the overall environment of the protein in which it is present. It is not the exclusive property of the LCRs.

P 14

Intrinsic plasticity: neuron's own way of modulating itself

Sandipan Talukdar[1]*, Rajan Shrivastava*[2]

1. Dept. of Bioengineering, Gauhati University

2. Dept. of Biophysics, University of Delhi South Campus

Aspects that fascinate Human cognitions are numerous. Probably that's why the most perplexing machine in this world is attracting a whole lot of people to dwell upon; that is, the human brain. Memory is one such aspect that overwhelms us. The more we practice the more we memorize, the more we do activity the more we learn. But how do the brain cells manage to do it? In the cellular level, there are Ion channels that conduct Ions to and from the cell, there are other proteins that are expressed or suppressed and active or inactive in times, there are conformational changes of Ion channels, temporary and persistent, cascades of Biochemical reactions, all of these processes collectively give rise to memory, learning or at large Human cognition. Studying the Memory and Learning phenomenon is studying the dynamics of all the processes. Until very recently, it has been thought that Synaptic Plasticity plays the sole role in learning and memory. But lately it has been realized that the plasticity can take place at the non-synaptic sites too, e.g. soma and dendrites, known as intrinsic plasticity. In other words, Intrinsic Plasticity is the mechanism by which the Neuron can modulate itself depending upon the activity; it can be in terms of modification in Ion channel numbers, its spatial geometry or the entire process of its activation/deactivation etc. Here, we present various aspects of Neuron's Intrinsic Plasticity related to memory.

*****Equal contributions by the authors***

P 15

NRfamPred: A proteome-scale two level method for prediction of nuclear receptor proteins and their sub-families

Ravindra Kumar*[*†‡], *Bandana Kumari*[†], *Abhishikha Srivastava and Manish Kumar

[†]These authors contributed equally to this work

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

[*]Email: banaudha@south.du.ac.in

Nuclear receptor proteins (NRP) are one of the most abundant type of transcription regulators, which are present exclusively in animals. Binding of cognate ligands with NRP enables interaction with a specific cofactors and cis-regulatory DNA sequences which alters the gene expression. Due to the vital importance of NRPs in many physiological and pathological aspects of metazoan life, they are considered as candidates of equal importance for drug development as are G-protein coupled receptors, ion channels and kinases. Another factor which makes NRPs a promising pharmacological target is the nature of ligands which are small lipophilic compounds such as steroids, thyroid hormone, vitamin D3, and retinoids, which regulate crucial biological functions like metabolism, homeostasis, development and disease. Since ligands are small molecules, they can be easily modified by drug designing, making NRPs a promising pharmacological target.

We have developed a SVM based two level prediction method for NRPs and their seven sub-families, named as NRfamPred, which uses dipeptide compositions as input vector. The 1st level screens NRPs, while the 2nd level identifies the sub-family to which it belongs. In summary the overall prediction works in following 3 steps: (a) The query protein is presented to the prediction algorithm. (b) If it is a non-NRP, the prediction stops after 1st level (c) If the query protein predicted as a NRP at the 1st level, it is forwarded to the 2nd level for sub-family prediction. Performance on independent dataset and the comparative study between NRfamPred and other available methods also proved NRfamPred as a better predictor. NRfamPred identified 14 novel NRPs, which have not been reported till date.

The prediction method is freely available to the scientific community as a web-server at http://14.139.227.92/mkumar/nrfampred.

P 16

A Comprehensive Genome-wide Analysis and Expression Profiling of Tetraspanin Gene Family in Rice

***M. Balaji*[1], *Manu Agarwal*[2] *and Surekha Katiyar-Agarwal*[1*]**
[1]Department of Plant Molecular Biology, UDSC, Benito Juarez Road, New Delhi-110021.
[2]Department of Botany, University of Delhi, Chattra Marg, New Delhi-110007.
[*]katiyars@south.du.ac.in, katiyarsurekha@gmail.com

Rice is a vital food crop for millions across the globe. However, worldwide rice production is not sufficient to meet the ever-increasing demand of burgeoning population and ensure food security. To a large extent abiotic and biotic stress factors are responsible for gradual decline in rice production. It is therefore important to understand the molecular mechanisms underlying plant responses to the environmental challenges, including high temperature, salinity, and drought. Molecular studies have shown that extensive reprogramming of genes occurs in rice plants when they are exposed to stressful conditions. It would be worthwhile to study these genes and elucidate their function in rice. Tetraspanins (TET)represents a large family of evolutionary conserved hydrophobic proteins with conserved structure (comprised of four transmembrane domains, two extracellular loops of unequal sizes, short cytoplasmic tails and highly conserved cysteines and 'GCCK' motif). TET proteins are known to function as 'facilitators' of protein interactions and are associated with diverse biological processes in different organisms. In Arabidopsisthese proteins are shown tobe involved in developmental process such as leaf morphogenesis, root development and floral organ formation. The present study was designed to gain an understanding on the biological role of tetraspanins in rice. *In silico*exploration of rice genome revealed the identification 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 tetraspanin genes 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. A number of tetraspanin genes exhibited significant differential expression in various tissues as well as under stress conditions tested in this study. We further performed transient subcellular localization of few tetraspanins in tobacco epidermal cells and found that most of these were localized to plasma membrane. On the basis of these studies it is proposed, that some of these tetraspanin genes might play an important role in abiotic stress tolerance in rice. It would be interesting to functionally characterize these stress-responsive tetraspanin genes in rice and extrapolate these results in other plants as well.

P 17

Cul4A: Moonlighting E3 Ligase in HPV driven Carcinogenesis

Bharti Nawalpuri*, Pradeep Singh Cheema, Deeptashree Nandi, Priyanka Gautam and Alo Nag*

Department of Biochemistry, University of Delhi, South Campus, New Delhi

High risk HPV is acclaimed to be the major causative agent of cervical cancer, a devastating disease with significant morbidity. Therefore, understanding the molecular pathway that contributes to HPV oncogenesis constitutes an important area of research. HPV oncoproteins E6 and E7 are known to exploit the host ubiquitin-proteasomal system to mediate cellular transformation.

The present study focuses on Cul4A, which is an essential part of cullin sub-family of E3 ubiquitin ligases, is involved in ubiquitination of prominent tumor suppressors, cell cycle regulators and is often upregulated in many human cancers. Previous reports have showed the functional modulation of Cul4A substrates such as p53, p27 and Cdt1 by HPV oncoproteins. This intrigued us to investigate the function of Cul4A ubiquitin ligase in HPV-mediated oncogenesis. Here, we report for the first time that HPV differentially regulates the functional determinants of Cul4A oncoprotein including stability, Neddylation status and its sub-cellular localization. Our results also demonstrated that high risk HPV 16 E6 and E7 stabilize p27 kip1. More importantly, we provide evidence for a role of HPV E7 in modulation of p27 activity by altering its cellular localization as well as by impairing interaction with its functional partner cyclin E.

Overall, this study has identified Cul4A as a significant target of HPV, thereby unraveling a novel molecular mechanism important for HPV pathogenesis. Interference with this pathway may block the growth and spread of cervical cancers.

P 18

Isolation, Screening, Production, Process Optimization and Characterisation for Maximum Lipase production

Amita, Namami*, Saurabh Saran and R.K. Saxena*

Technology Based Incubator, University of Delhi South Campus, Benito Juarez road, New Delhi 110021
Email id: amita.prasad321@gmail.com; rksmicro@yahoo.co.in

Lipases (triacylglycerol acylhydrolase, EC 3.1.1.3) are versatile biocatalysts that are used extensively in detergents, food industry, pulp and paper industry, leather and pharmaceutical formulations. Lipases have an immense potential for being employed as industrial catalysts for production of fine chemicals. Their superior values are mainly due to the specificity and efficacy, when compared to other chemical catalyst. However new lipase with properties that may be applicable to other industrial uses are being sought. The present investigation describes the attempt of obtaining potential lipase producing isolate from soil near canteen of University of Delhi South Campus. Screening of lipase producing bacteria was carried out using TBA plates in which tributyrin acts as a sole substrate. Lipase producers formed a clear zone of hydrolysis surrounding the culture. One of the strains, identified as *Bacillus* sp. N-15 through microscopic observation showed high lipase activity of 2.26IU/ml. Further optimization studies like media manipulation and optimization of environmental conditions resulted to about 10.33IU/ml at 50C, pH 8 after 48 hr of incubation period.

Keywords: Lipase, *Bacillu*s, TBA plates, media optimization

P 19

Viral oncoprotein HPV16 E7 perturbs SUMOylation of FoxM1 to induce Carcinogenesis

Neha Jaiswal, *Pradeep Singh Cheema, Rince John, Vaibhav Chand and Alo Nag**

*Department of Biochemistry, University of Delhi South Campus

Cervical cancer is the leading cause of death in women worldwide and is primarily associated with persistent infection of high-risk human papillomavirus (HPV). The oncogenic transcription factor, Forkhead box M1b (FoxM1b) is often overexpressed in many human tumors including cervical cancer, signifying its participation in tumorigenesis. Its proven role in carcinogenesis and its prospect as a promising therapeutic in cancer makes it a molecule of considerable clinical interest. It was therefore designated as "**Molecule of the year 2010"**. Interestingly, post-translational modifications of FoxM1 have been shown to modulate its activity in cell cycle control, genomic stability and tumorigenesis. A thorough understanding of FoxM1 will be extremely useful in the innovation of more rationalized strategies for treating and preventing cancer. Here, we report that FoxM1b interacts with SUMOylating enzymes Ubc9 and PIAS1 and subjected to SUMOylation. We also demonstrate that SUMOylation contributes to destabilization and nucleocytoplasmic shuttling of FoxM1b protein. More importantly, our work provides the first evidence regarding a role of E7 oncoprotein in HPV mediated upregulation of FoxM1b. The elevated expression of FoxM1 was determined to be posttranscriptional and was attributed to decreased SUMOylation of FoxM1b in the E7-expressing cells. Thus, our study provides valuable insights into SUMOylation dynamics of FoxM1b as well as identifies the biochemical mechanism that high risk HPV exploits to induce malignant transformation. Altogether, the investigation enriches our understanding of the mechanisms of HPV oncogenesis in development of cervical carcinoma which may facilitate in the discovery of new anticancer strategies.

P 20

Liposomes: Drug delivery system or possible doping agent???

***Nimker V*[1], *Jamal H*[2], *Ghosh P C*[1], *Jain S*[2], *Beotra A*[2]

[1] Department of Biochemistry, University of Delhi, South Campus
[2] National Dope Testing Laboratory, New Delhi

Liposomes being used as drug delivery vehicle for treatment of various diseases is well known in medical field but its possible role as a doping agent is not investigated thoroughly. Use of liposomes in sports doping came into light when Liposom Forte® was found stored together with banned and non-banned drugs during investigations carried out by Italian legal authorities and recent availability of IGF-1 Liposomal Spray on internet. It is postulate that these products could be used as masking agents to make detection of other forbidden drugs more difficult. Role of liposomes as masking agent for anabolic steroids in the field of doping has been investigated by Botre et al.[1]

The aim of the present work was to study the effect of different parameters like temperature, pH, charge, time, concentration etc. on the interaction of liposomes and doping agents and to identify a possible marker for detection of their abuse in sports. A broad range of doping agents were studied mainly threshold drugs, results showed that anabolic steroids have strong tendency to interact with the liposomes which result in the reduced concentration of compound in the sample. Results revealed that there was no significance effect of temperature and incubation time on interaction of liposome and doping agents while other parameters such as charge of liposome and concentration affect the interaction capacity.

Cholesterol, major component of liposomes, provides stability to the liposomes by fitting in between the lipid molecules, furthermore most of the steroids are derivative of cholesterol thus similar in structure, this study hypothesized that when liposomes were mixed with anabolic steroids, anabolic steroids fit into the lipid molecule which release the free cholesterol into the samples, and reducing the amount of steroids present in the urine matrix thus acting as a masking agent for anabolic steroids. Being endogenous compound cholesterol is present in routine dope testing samples; reference concentration of cholesterol was monitored in routine samples and found to be increased 5 to 10 folds when liposomes were spiked, thus detection of cholesterol can act as marker for abuse of liposome as masking agent

P 21

MTG3, a putative GTPase that regulates mitochondrial ribosome function in *Saccharomyces cerevisiae*

***Upasana Mehra**, Yash Verma and Kaustuv Datta*
Department of Genetics, University of Delhi South Campus, New Delhi 110 021 India

Mitochondria are made up of proteins encoded by the nuclear genome as well as its own genome, thus requiring both cytosolic as well as its own translation apparatus for its biogenesis.Importance of mitochondrial translation apparatus can be estimated with the fact thatapproximately 25% of the mitochondrial proteome is involved in the establishment and the maintenance of the mitochondrial protein synthesis apparatus and mitochondrial DNA.During evolution, the RNA content of the mitochondrial ribosome has reducedand the protein mass have increased giving rise to numerous mitochondrial specific proteins conserved from lower eukaryotes to humans.Ribosome biogenesis (bacterial/ cytosolic/ mitochondrial) is a complex process which requires ordered association of several ribosomal proteins and rRNAs, aided by a number of assembly factors including GTPases.A number of non-exclusive models have been proposed to account for utilization of energy released upon GTP hydrolysis in (1) recruitment/ removal of individual ribosomal proteins from precursor molecules, (2) alteration of the rRNA structure or (3) conformational changes within the precursor molecule to expose ribosomal protein binding surfaces.Mtg3p, is a nuclear encoded mitochondrial protein that is conserved from yeast to humans and is a member of YawG/YlqF family of circularly permuted GTPases.Members of this family in yeast include Lsg1p, Nog2p and Mtg1p that influence large subunit biogenesis either in cytosol or mitochondria. Deletion of *MTG3* lead to defect in utilization of glycerol as a sole carbon source and aberrant 15S rRNA processing, indicating arole in small subunit biogenesis.My focus is to identify the molecular complex that Mtg3p is associated with, domains of Mtg3p that are essential for its *in vivo* function and the downstream partners/processes that it likely controls.We have shown Mtg3pto be associated with the 37S small subunit of the mitochondrial ribosome in a salt dependent manner. In addition, we have isolated spontaneous suppressors for *Δyor205cρ*$^{+}$and have determined them to be due to second-site mutations in the mitochondrial genome. We are in the process of determining the site of suppressor mutation on the mitochondrial genome. We will also be presenting our studies to determine the site of interaction of Mtg3p on the ribosome and the energy requirements for it.

P 22

Deciphering the biological implications of *Hemoglobin1 (glob1)* in *Drosophila*

Renu Yadav *and Surajit Sarkar**

Department of Genetics, University of Delhi, South Campus, Benito Juarez Road, New Delhi-110 021

(*Correspondence: sarkar.surajit@gmail.com)

The prominence of globin gene family can be anticipated by its unanimous conservation in all the genera of life. Universally, Globin protein(s) have been known to be involved in transportation and metabolism of oxygen in higher organisms. However, it is gradually substantiated now that many globins are also involved in regulating several aspects of cellular functions and development.*Drosophila*genomepossesses three *globin* genes i.e. *glob1*, *glob2* and *glob3*, located at different cytogenetic positions. Incidence of multiple *globins* in *Drosophila*seems to be surprising as it has a well-developed and self-sufficient tracheal network for transportation of gaseous oxygen. Hence, a comprehensive study has been performed to examine the functional significance of *glob1*in *Drosophila.* We report that *glob1* expresses dynamically during different stages of *Drosophila* development. Interestingly, tissue specific cytoplasmic as well as nuclear expression of Glob1was detected in several tissues such as nervous system, muscles, tracheal cells, gut and fat bodies. Reduced expression of *glob1* results in lethality at various stages of development and a few escapers emerge as adults. Such escapers exhibit developmental delay, defects in tracheal and cytoskeletal arrangement, compromised fitness, short life span and reduced fecundity. Intriguingly, reduced expression of *glob1* leads to increased levels of cellular Reactive Oxygen Species (ROS). FRT/FLP mediated somatic clonal analysis further establishes an active role of *glob1* in maintenance of cytoskeletal integrity. In view of above, we propose for the first time that *glob1* is essential for maintenance of cellular homeostasis and various aspects of *Drosophila* development.

Key words:*glob1*, *Drosophila*, Reactive Oxygen Species

P 23

Sustained production of Lip11 from *Yarrowialipolytica* in *Pichia pastoris* X-33 using methyl oleate as slow release methanol source to induce AOX1 promoter

Arti Kumari, *Yogesh Singh, Poonam Syal and Rani Gupta*

Department of Microbiology, Delhi University South Campus, New Delhi

A gene encoding *lip* 11 from *Yarrowialipolytica* MSR80 was cloned in pPICZαA and functionally expressed in methylotrophic yeast *Pichia pastoris* X-33 under methanol inducible *AOX*1 promoter. For which methanol induction is necessary at regular intervals. However, repeated methanol induction after every 24.0 h is tedious, also it increases the risk of contamination. In addition to this, methanol rapidly evaporates under small scale culture conditions, that is why it is hard to maintain constant methanol concentration. Hence, a process is needed which allows slow and constant release of methanol. So, a strategy was developed where 0.5 % methanol was used as a first inducer followed by induction with methyl esters. It was hypothesized that induction with 0.5 % methanol in early hours induced the *AOX*1 promoter to release lipase, subsequently methyl esters will be hydrolysed to methanol and fatty acids, where methanol can lead to sustained production of lipase by inducing*AOX*1 promoter constantly. Further, process parameters i.e, initial inoculum density, methanol concentration and time of production were optimised in BMMY medium. The result showed that optimum lipase yield 1945.0 U/L/x^{-1}, was obtained after 120 h at initial inoculum OD_{600} = 4.0 and 2.0 % methanol induction after every 24 h. Alternatively among various methyl esters used, maximum lipase yield 2701.0U/L/x^{-1} was recovered in 0.5% methyl oleate after 120 h. Later on fed batch strategy was developed which further enhanced the lipase yield to 3147.0U/L/x^{-1}. Lip11 was purified By Ni^{+2}affinity chromatography and was a 52 kDa glycosylated protein.

P 24

Alleviation of poly (Q) mediated neurotoxicity by modulating insulin signaling in *Drosophila* disease models

Kritika Raj *and Surajit Sarkar**

Department of Genetics, University of Delhi, South Campus
Benito Juarez Road, New Delhi-110 021, India
(*Correspondence: sarkar@south.du.ac.in)

Polyglutamine or Poly(Q) disorders are a class of dominantly inherited neurodegenerative disorders that are caused as a result of an expanded stretch of glutamine (Q) repeats in the coding region of the affected gene. Prominent examples of poly(Q) disorders includeSpinocerebellar ataxia(s) (SCAs), Huntington's disease (HD), Spinal and Bulbar Muscular Atrophy (SBMA) and Dentatorubralpallidoluysian syndrome (DRPLA) etc. Most of thepoly(Q) disorders are age onset and exhibit progressive degeneration of vulnerable neurons in brain. Interestingly, group of neurons that are majorly affected are those residing in the cerebellum, basal ganglia and cortex of the adult human brain. One of the most important reasons among many that have been postulated to be responsible for disease pathogenesis and neurodegeneration is protein misfoldingandaggregation.The superfluous poly(Q) stretch obstructs native protein folding and instigates aggregate formation. Subsequently, poly(Q) mediated protein aggregates sequester other essential cellular proteins to form inclusion bodies which could be found in both nuclear and cytoplasmic domains. However, in spite of several pointers, precise molecular and cellular mechanism of poly(Q) disease pathogenicity and their suitable therapeutic approaches remains elusive. We report for the first time, that targeted modulation of insulin signalingcould significantly mitigates poly(Q)-induced cellular toxicity and neurodegeneration in SCA3 and HD models of *Drosophila.* Moreover, cellular abundance of inclusion bodies is also reduced in such cases. We propose that modulation of insulin signaling could have a major impact on the pathogenesis of poly(Q) disorders.

P 25

Boosting BCG vaccinated guinea pigs with recombinant MVA expressing α-crystallin gene of *M.tuberculosis* augments the protection imparted by BCG against tuberculosis.

***Prachi Nangpal**, Ritika Kar and Anil K. Tyagi*

Department of Biochemistry, University of Delhi South Campus, New Delhi

Tuberculosis (TB),known to devastate mankind throughout the history, still haunts the world claiming 1.3 million deaths worldwide annually. The only preventive measure available against TB is *Mycobacterium bovis* BacilleCalmette- Guerin (BCG) which has fared extremely well in providing protection against the childhood form of TB. However, its efficacy in adults and older people remains inconsistent which underlines the urgency for innovative research to develop more effective vaccines for the eliminationof this resilient human pathogen. One of the approaches to develop new TB vaccines involves strategies to boost BCG vaccination by employing an immunodominant antigen of *M.tuberculosis* along with an appropriate delivery vehicle in order to increase its efficacy against the disease. In this study, we have constructed and characterized a marker free recombinant Modified Vaccinia Ankara virus expressing α-crystallin gene (rMVA.acr)of *M.tuberculosis*. The rMVA.acr thus generated was then evaluated for its ability to boost the protective efficacy of BCG by using two different routes of immunization (intramuscular and intranasal).Our results suggest that this boosting regimen with rMVA.acr provides a significantly higher protection than BCG vaccination alone in guinea pigs (0.89 $\log_{10}$ and 1.34 $\log_{10}$ fewer bacilli in lungs and spleen respectively; p,0.05). We believe that this strategy would help in prolonging the protection imparted by BCG.In addition, further research on discerning immune mechanisms underlying this protection would help in identifying the biomarkers of protective immunity which would aid in the development of efficient booster vaccines for BCG vaccinated individuals.

P 26

Molecular characterization of modular microbial flavin binding photoreceptors and their optogenetic potential

Yama Atri[1], *Madhu Baghel*[1], *Lobzang Tsering*[1], *SuneelKateriya**[1]

yama108atri@gmail.com, *skateriya@south.du.ac.in

[1]Department of Biochemistry, UDSC, Benito Juarez Road, New Delhi-110021

Nature has provided an array of light sensing proteins called photoreceptors that consist of a protein moiety and a chromophore group. They are broadly divided into six classes based on their chromophore structure, among which are UV-A/blue light sensing modules, LOV (Light, Oxygen and Voltage), BLUF (Blue Light Utilizing FAD) proteins and cryptochromes. These proteins get activated upon UV-A/blue light illumination and return to their ground state with dark incubation. LOV domain containing proteins and BLUF proteins exhibit modularity wherein; at one terminus is a light sensor which is coupled to an effector domain like, Ser/Thr kinases, histidine kinases, DNA binding domain, phosphodiesterases, cyclases, DNA binding motifs and oxygen sensing motifs. Cryptochromes are structurally similar to DNA photolyases that repair UV damage induced DNA breaks but lack photolyase activity.

Optogenetics, an emerging field of science, combines optics and genetics to control and regulate cellular events with spatio-temporal precision by illumination. LOV and BLUF proteins make an attractive component of the optogenetic toolkit by virtue of having small size (~ 100-140 amino acids), higher solubility, diverse photophysical properties, and ubiquitous flavin cofactor and by being light switchable. Their modularity only adds to this repertoire for biotechnological and biomedical applications. Moreover, engineering of photosensors with altered photocycle lifetimes and coupling to novel modular domains increases targeted studying of cellular and biological events. Here, we study and analyze some of these blue light sensing proteins from a variety of organisms using bioinformatic, biophysical, biochemical approaches and discuss their optogenetic potential.

P 27

Process optimization for production of 2, 3 butanediol: fuels for future-the microbial route.

Sheeba Zarin, *Saurabh Saran & R.K.Saxena*.

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

Technology Based Incubator, University of Delhi South Campus, New Delhi-110021

2,3 Butanediol is a promising bulk chemical due to its extensive industrial applications. It is a highly valuable fuel with the burning value of 27198 J/g which is comparable to other liquid fuels as ethanol (29055 J/g) and methanol (22081 J/g).

Besides its use in production of high grade aviation fuel, it finds applications in polymers, cosmetics, food, adhesives, lubricants, laminates, solvent, antifreeze and pharmaceutical industries.

Isolation and Screening for 2,3 Butanediol was performed using Gas Chromatography and a high producer *Klebsiella* strain was obtained from sewage sample. The present study aimed at improving the production of 2,3 Butanediol by optimizing the nutritional and physiological parameters using "one variable at a time" , "plackett-burman statistical design" and "response surface methodology". The production of2,3 Butanediol was found to increase to 9.32g/L after two level PB design as compared to initial 0.8g/L. 5 significant factors including the initial concentration of of glycerol, tryptone, peptone, inoculum size and incubation time were then optimized by response surface methodologyandtheproduction of2,3 Butanediol was enhanced upto 13.96g/L. This resulted in 17.45 fold increase in 2,3 Butanediol production.

P 28

Characterization of the MCM homohexamer from the thermoacidophilic euryarchaeon *Picrophilustorridus*

Kasturi Goswami*, *Jasmine Arora* & Swati Saha*[#]

Department of Microbiology, University of Delhi South Campus

The typical archaeal MCM exhibits helicase activity independently *invitro*. This study characterizes MCM from the euryarchaeon *Picrophilustorridus.* While PtMCM hydrolyzes ATP in DNA-independent manner, it displays very poor ability to unwind DNA independently, and then too only under acidic conditions. The protein exists stably in complex with PtGINS in whole cell lysates, interacting directly with PtGINS under neutral and acidic conditions. GINS strongly activates MCM helicase activity, but only at low pH. In consonance with this, PtGINS activates PtMCM-mediated ATP hydrolysis only at low pH, with the amount of ATP hydrolyzed during the helicase reaction increasing more than fifty-fold in the presence of GINS. While the stimulation of MCM-mediated helicase activity by GINS has been reported in MCMs from *P.furiosus, T.kodakarensis,* and very recently, *T.acidophilum*, to the best of our knowledge, this is the first report of an MCM helicase demonstrating DNA unwinding activity only at such acidic pH, across all archaea and eukaryotes. PtGINS may induce/stabilize a conducive conformation of PtMCM under acidic conditions, favouringPtMCM-mediated DNA unwinding coupled to ATP hydrolysis. Our findings underscore the existence of divergent modes of replication regulation among archaea and the importance of investigating replication events in more archaeal organisms.

P 29

Characterization of a modular rhodopsin from *Chlamydomonasreinhardtii* and its optogenetic potential for drug discovery

***Komal Sharma**, Mayanka Awasthi, Peeyush Ranja and Suneel Kateriya**

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

*skateriya@south.du.ac.in

Chlamydomonas reinhardtii, a unicellular, motile green alga, comprises of eight rhodopsins named as chlamyopsins 1-8 (Cop1-8). Cop1 and Cop2 function is not identified till now.Phototaxis and photophobic movements in *C.reinhardtii* are mediated by chlamyopsin 3 and chlamyopsin 4. Cop3 (channelrhodopsin 1) and Cop4 (channelrhodopsin 2) are functioning as direct light-gated cation channels. These channelrhodopsins are currently widely used as an optogenetic tool for non-invasive control of neuronal cells or live animals to study neuronal network. Cop5 to Cop8 belongs to histidine kinase rhodopsin family.

Chlamyopsin 5, known as modular rhodopsin, consists of HK and RR with an effector cyclase domain at the C-terminus. The proposed signaling may be like rhodopsin captures light causing autophosphorylation of HK which further phosphorylates RR. Phosphorylated RR will activate cyclase which further carries forward the signal cascade in the form of cAMP. All these modules are encoded in a single protein making cop5 a two component system just like bacterial two component system. Computational analysis of cop5 sequence showed phosphorylation sites conserved for HK and RR domain. In vivo presence and cellular localization of cop5 has been checked using its RR and Rh specific antibodies. Interestingly, bioinformatic protein-protein interaction analysis of cop5 reveals the presence of phototropin and ChR1 as interacting partners. This photoreceptors interaction might be useful in deciphering the physiological relevance of one photoreceptor for another.

Animal eukaryotes usually lack two component system due to which many bacteria utilize their TCS as virulence factor to infect their host. These proteins and their associated signaling proteins can serve as a new target for antibiotic development. Cop5 can be potentially used as a model protein for the search of targeted drugs.

P 30

Identification of Novel Microbial Consortia for Rapid Degradation of Synthetic Polymers

Siddharth Srivastava[1*], *Anusha Chaudhary[1*], Deepali Vaid[1*], Deepika Rana[1] Lakshmi Rana[1], Nishant Jain[2], Monika Yadav[1], Akanksha Agarwal[2], Ravinder Singh[2], Anu Anmol[1], Krishna Dutt[2], Siddharth Sirohi[2], Divya Bajaj[3,] Yogender Pal Khasa[4#], Vijay Kumar Nalla[#]*

* Authors contributed equally.

[1]Department of Microbiology, Bhaskaracharya College of Applied Sciences (University of Delhi), Dwarka, New Delhi-110075

[2]Department of Polymer Sciences, Bhaskaracharya College of Applied Sciences (University of Delhi), Dwarka, New Delhi-110075

[3]Bhagini Nivedita College (University of Delhi), Najafgarh, Delhi - 110043

[4]Department of Microbiology, University of Delhi (South Campus), New Delhi
Corresponding Authors

The worldwide production of non-biodegradable plastics is estimated to be 280 million tonnes, according to first rough estimates published by Plastics Europe in 2011 and amount of mismanaged plastic waste per year is 0.6 million tonnes. A study in 2014 called *Valuing Plastic* by the Plastic Disclosure Project and Trucost, estimated plastic caused about $13 billion in damages to marine ecosystems each year—and noted that estimate was probably low, given what we don't know yet. The indiscriminate use of non-biodegradable plastics is detrimental to the environment and there are very few technologies that address the problem of plastic waste in a sustainable manner. In our present work, we have exploited the action of microbial communities to overcome the issue of the non-recyclability of PVC, Nylon 6, PVA and Polyethylene. The possible role of microbes likes*Klebseilla spp.*, certain bacilliform and cocci bacterial species, various oil microorganisms (including actinomycetes and fungi) among others were tested. A five month controlled experiment has shown an adverse effect on polymer quality. Notable differences in the surface properties were observed in the selective microbial treated samples in comparison to the control samples, as revealed by the Scanning Electron Microscopy (**SEM**). Among set of conditions used, temperature and pH played a major role in influencing polymer degradation. Although the role of several microbial communities was investigated, bacilliform bacteria were found to promote degradation process by a fold of 30±5% in comparison to others. We postulate that microbial communities could be fostered to target polymer degradation by creating them as a consortium. Our research findings suggest that polymers can be degraded with naturally occurring and non-pathogenic microbes in a sustainable manner.

P 31

Functional characterization of *YDR332w* a putative DEAD box helicase essential for mitochondrial functioning in *Sacchromyces cerevisiae*

Jaswinder Kaur and Kaustuv Datta
Department of Genetics, University of Delhi South Campus, New Delhi 110 021

Mitochondrial gene expression requires dedicated translation machinery, distinct from its cytosolic counterpart as well as its bacterial ancestor. Mitochondrial ribosomes are made up of proteins encoded nuclear genes and rRNA molecules encoded by the mitochondrial DNA. Mutation in either genome can lead to either mitochondrial dysfunction or it's an inability to assemble a functional organelle. Ribosome biogenesis is aided by a number of assembly factors including RNA helicases. Yeast contains four nuclear encoded RNA helicases targeted to the mitochondria belonging to DExH/D super family of NTP dependent RNA remodeling enzymes including *YDR332w*. *YDR332w* orthologous are present in prokaryotes and lower eukaryotes but absent in higher eukaryotes so far sequenced. Yeast cells deleted for *YDR332w* gave rise to two set of colonies that can be differentiated on size on media containing fermentable carbon source glucose. When *Δydr332w* cells were plated on non-fermentable carbon source glycerol, there were fewer number of colonies in comparison to wild type cells. Sub-culturing *Δydr332w* cells in glucose resulted in changes in the colony size and ability to utilize glycerol as the sole carbon source. The percentage glycerol$^+$ cells among the total viable cells in cultures grown in glucose were found to rapidly decrease. Interestingly the number of *Δydr332wρ*$^+$ cells also decreased when sub-cultured in glucose albeit at a slower rate, indicating that *YDR332w* is essential for mitochondrial function. We have shown that Ydr332wp associates partially with both the small and large subunit of the mitochondrial ribosome in a salt-independent manner consistent with Ydr332p's role in mitochondrial gene expression. Our current studies are aimed at understanding the molecular complex that Ydr332wp binds to and whether mitochondrial translation or mito-ribosome assembly is the primary function for Ydr332wp.

P 32

Identification and Characterization of Calcineurin-B like Proteins (CBL) in *Chlamydomonas Reinhardtii*

Madhu Baghel[1], Akhilesh Yadav[2], Komal Sharma[1], Suneel Kateriya[2], Girdhar K. Pandey[2]

[1]Department of Biochemistry, University of Delhi, South Campus

[2]Department of Plant and Molecular Biology, University of Delhi, South Campus

All organisms in environment encounter multiple abiotic and biotic stresses. Thus, have evolved multitude of signaling mechanisms to cope up with these stress conditions. In plants, calcium mediated activation of signaling pathways had been shown to be involved in large number of stress responses. Calcium in such cases is hypothesized to act as secondary messenger whose molecular sensors, although partially known are different calcium binding protein. Many plant species possess multiple intracellular calcium sensing proteins known as Calcineurin-B like (CBL) proteins which gets activated under different abiotic stress condition and recruits their effector partners, CIPKs (CBL Interacting Protein Kinases), which transduce signal downstream in signaling pathway. Ten CBLs and twenty five CIPKs have been reported in *Arabidodpsis thaliana*. Similarly, these plant's unique calcium sensors (CBL) have been also reported in the genome of unicellular green algae,*Chlamydomonas reindarditi*. In this report we identified two putative CBLs in *C. reinhardtii* named CrCBL1 and CrCBL2 respectively via bioinformatics analysis. Out of two putative CBLs, CrCBL1 was found to be more conserved based on calcium binding EF-hand analysis. Calcium binding ability of CrCBL1 and CrCBL2 was checked using gel shift assay, which showed difference in mobility of CrCBL1 with and without calcium. Western blotting of *C. reinhardtii* total cell lysate with anti-CrCBL1 primary antibody confirmed the presence of a similar protein of 17kD in *C. reinhardtii*. Confocal microscopy showed cellular localization of CrCBL1 in basal-bodies of the organism. Further research is going on to strengthen our hypothesis for presence of CBL-CIPK system in algae to mediate stress response.

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Development of fungal resistant tomato plants by host-mediated gene silencing

Manish Pareek and M. V. Rajam*

Department of Genetics, University of Delhi South Campus, Benito Juarez Marg,
New Delhi-110021
(* rajam.mv@gmail.com)

Plants are subjected to various kinds of stresses like biotic and abiotic stresses which ultimately lead to the decreased plant productivity. Biotic stresses due to the insect attack, nematode infection and fungal pathogen causes a colossal loss of yield in crop plants. Among the biotic stresses, fungal pathogens cause devastating crop yield loss and need urgent attention to increase the crop production worldwide. Tomato is an important vegetable crop and it is severely affected by a fungal pathogen, *Fusarium oxysporum* which causes wilt disease. Fusarium wilt symptoms include fungal root colonization, stunting, progressive wilting and death of the plant. While, conventional control measures like use of fungicides, soil sterilization and crop rotation met with certain limitations, there is an urgent need of alternative method. Recently, RNA interference (RNAi) has proven to be potent and promising tool for the control of fungal pathogens. In the present work, we are targeting the *Fusarium* MAP kinase (*Fmk1*) gene by expressing the hair-pin RNAi construct in tomato plants. For the functional analysis of the Fmk1 gene, we have developed *Fmk* RNAi fungal transformants, which showed decreased pathogenesis. Further, the fungal resistant tomato lines are being developed by expression of dsRNA specific to the *Fmk1* gene for its silencing. The host-mediated gene silencing approach may prove to be efficient way to control the fungal pathogens.

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Artificial microRNA (amiRNA) mediated gene silencing for insect resistance in tomato

Sneha Yogindran, Sunil K. Mukherjee and M. V. Rajam*

Department of Genetics, University of Delhi South Campus, New Delhi-110021
(*Email: rajam.mv@gmail.com)

Tomato (*Solanum lycopersicum*) is one of the important vegetable crops and is consumed in diverse ways. It contains the carotene lycopene, one of the most powerful natural antioxidants. Besides lycopene, tomato is a rich source of vitamin C and other important nutrients. However, tomato is affected by biotic stresses like pathogen and pest attacks. *Helicoverpa armigera*, is one of the notorious pests which feeds upon tomato and is a great threat to the farmers due to its abundance, high mobility and non-specific eating habits. The gradual diminishing effects of pesticides, unavailability of insecticides in covered and deeper parts of plants, development of resistance due to detoxification mechanism in the insects are some of the reasons contributing for the huge crop losses. Conventional breeding is one of the effective ways to raise resistant plants but this process is time consuming and laborious. Recently, RNA interference (RNAi) mechanism is demonstrated as a potential alternative tool and many reports of transgenic plants that are resistant to viruses, fungal pathogens and insects are known. RNAi pathway mainly comprises small-interfering RNAs (siRNAs) and micro RNAs (miRNAs), both of which bind to their complementary bases on the target mRNA and lead to the silencing of latter RNA. Artificial miRNA (amiRNA) technology employs endogenous pri-miRNAs, in which the miRNA and miRNA* sequences have been replaced with desired amiRNA/amiRNA* sequences that direct highly efficient silencing of the target gene. The present study focuses on the use of amiRNA to target *Ecdysone Receptor (EcR)* gene of *H. armigera*. The insect steroid hormone Ecdysone and its receptor play important roles during development and metamorphosis and regulate adult physiology and life span. In this context, we have carried out bioassays using an insect feeding vector expressing amiRNA. We have also developed plant transformation construct to generate tomato transgenics which will be further analyzed for insect resistance.

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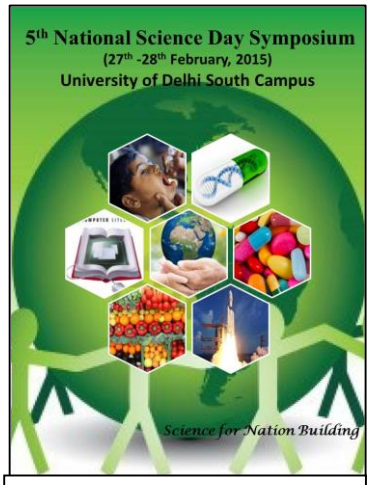

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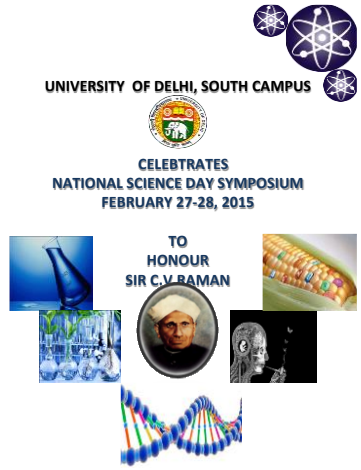

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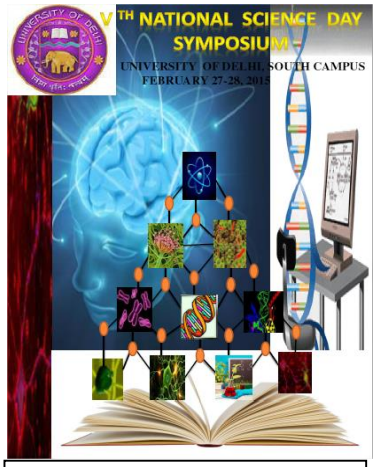

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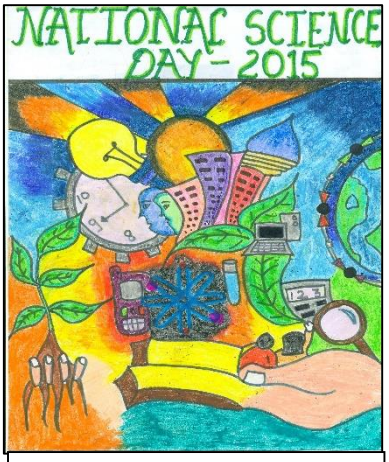

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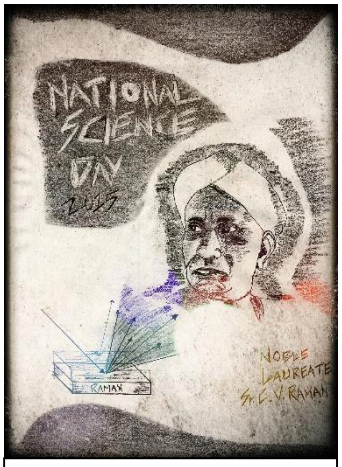

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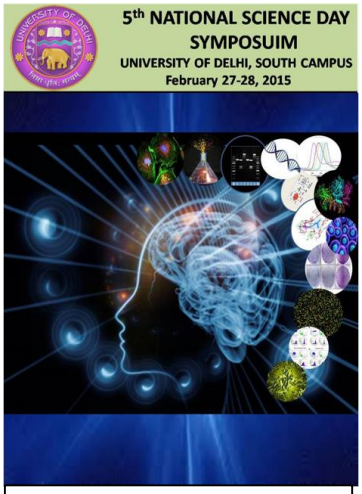

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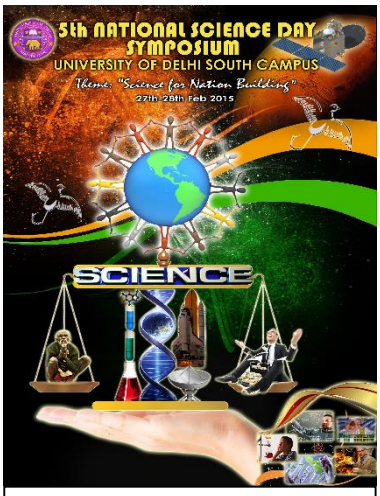

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