ABSTRACT - BOOK

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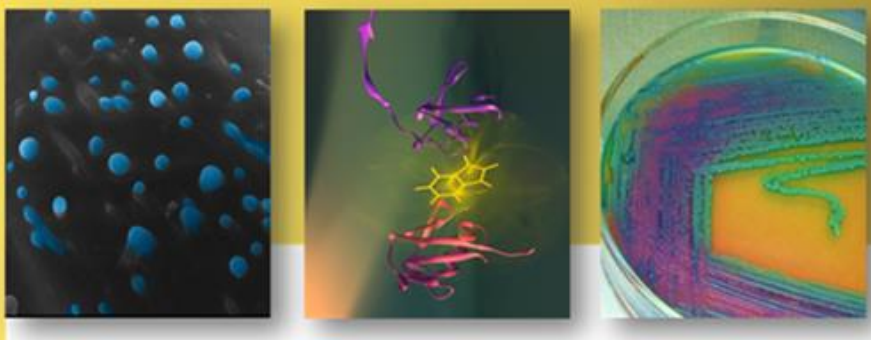

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SPONSORED NATIONAL LEVEL
VIRTUAL SYMPOSIUM ON

Recent Trends in Modern Biology

10-12 December, 2020

Special Focus on
Cell Biology & Genetics
Applied Microbiology & Biotechnology
Host-Microbe Interactions

Recent Trends in Modern Biology

SCHEDULE

DAY 1 (10/12/2020)		
Inaugural session		10:00 AM - 10:20 AM
Technical Time-out		10:20 AM - 10:30 AM
Session 1 Applied Microbiology and Biotechnology		
Session introduction		10:30 AM - 10:35 AM
Dr. Shashi Kumar Rhode ICGEB, New Delhi	Metabolic engineering of plant for antimalarial drug biosynthesis	10:35 AM - 11:35 AM
Prof. Yogesh Shouche NCCS, Pune	Human Microbiome and its implications on health and disease	11:40 PM - 12:40 PM
Lunch Break and poster display		12:40 PM -1:20 PM
Prof. Sunil Kumar Khare IIT, Delhi	Interaction of nanoparticles with non-halophilic and halophilic bacteria: evidence of nanotoxicity	1: 20 PM - 2:20 PM
Technical Time-out		2:20 PM - 2:25 PM
Flash talks by selected poster presenters *		2:25 PM onward
DAY 2 (11/12/2020) Session 2 Cell Biology and Genetics		
Session introduction		9:45 AM -9:50 AM
Prof. Bhudev C. Das AIMMSCR, Amity University, Noida	Targeting Cancer Stem Cells for effective treatment of Cervical Cancer	9:50 AM - 10:50 AM
Dr. Mahendra Seervi AIIMS, New Delhi	Anastasis, a mechanism of cell rescue from the brink of death and its impact on cancer disease and treatment	10:55 AM - 11:55 AM
Dr. Prakash Pillai The M S University of Baroda, Vadodara	Glial MeCP2 phosphorylation dynamics in normal development and glioma progression	12:00 noon - 1:00 PM
Lunch Break and Poster Display		1:00 PM - 1:30 PM
Flash talks by selected poster presenters *		1:30 PM onward
Day 3 (12/12/2020) Session 3 Host- Microbe Interaction		
Session introduction		9:50 AM - 9:55 AM
Dr. Anirban Dutta Tata Research Development & Design Centre, Pune	Deciphering host-microbiome cross-talk: Opportunities and Challenges	9:55 AM - 10:55 AM
Dr. Divya Chandran Regional Centre for Biotechnology, Faridabad	Effectoromics-based identification of molecular targets for pea powdery mildew disease control	11:00 AM - 12:00 Noon
Dr. Jagdis Gupta Kapuganti NIPGR, New Delhi	The role of nitrate and nitric oxide signalling in plant resistance against pathogen infection	12:05 PM - 1:05 PM
Lunch Break and Poster Display		1:05 PM- 1:45 PM
Flash talks by selected poster presenters*		1:45 PM - 3:00 PM
Valedictory function and Awards announcements		3:00 PM - 3.30 PM

Each expert talk is planned as around 45 minutes of presentation and 15 minutes of interaction

* A maximum of five flash talks shall be arranged. Each flash talk shall be a presentation for 5 minutes with 5 minutes of Q & A. Speakers of the flash talks are requested to be available while their talk is being featured

Contact: pdpiasevents.bio@charusat.ac.in; aditibuch.biochem@charusat.ac.in

Speaker's Abstracts

Metabolic engineering of plant for antimalarial drug biosynthesis

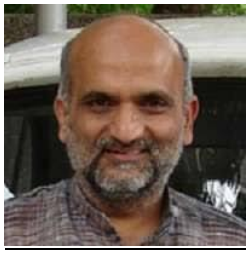
Dr. Shashi Kumar Rhode

International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi.

Email: skrhode@icgeb.res.in

Artemisinin, plant-derived sesquiterpenoids has a great potential to clears the malarial parasites from blood faster than any other drug present currently in the market. However, it is not affordable due to the high cost of extraction and purification process from the low yielding native plant (*Artemesiaannua*). Using the compartmentalized metabolic engineering approach, we have produced this drug in in an alternative plant like tobacco. The rationalized expression of the biosynthetic pathways in different compartment of plant has enabled us to reach the yield at clinically meaningful levels. Extracts from transgenic plants inhibited the progression of *Plasmodium falciparum*-infected red blood cells. Oral feeding of whole intact plant cells bioencapsulating the artemisinin has drastically reduced the parasitemia levels in challenged mice compared to the pure form of commercial artemisinin. Also, we are enhance the production of this drug into native *Artemisia annua* plant via metabolic engineering of the chloroplast genome as well producing this life-saving drug in an edible plant to make it affordable and coherent in treating malaria by delivering the drug through whole edible plant material.

Human Microbiome and its implications on health and disease



Prof. Yogesh Shouche

National Centre for Cell Sciences (NCCS) Pune.

Email : yogesh@nccs.res.in

There is a mounting evidence to indicate that the commensal microbiota is important for the general wellbeing and influences the upon host physiology locally and systemically. Perhaps the most important realization about the microbiota is that the human associated microbes are crucial component of host-microbe ecosystems that provides various benefits to the host. Interestingly, the studies on indigenous microbial communities has also changed clinicians' perceptions about microbes from the causative agents of diseases to largely beneficial microbial communities that occupies several human body parts. Thus, it seems that there are no areas of human health or for that matter human diseases that have not been linked with the gut microbiota in one or the other ways. There are growing evidences to support occurrence of distinct microbiota based on biogeographic location of the populations. Considering the geographic, ethnic and dietary diversity of Indian population, we hypothesize that the Indian population to be a perfect model to study the 'Genotype-Microbiome' association.

Initiation of many mega projects worldwide and the fact that human microbiota varies geographically, the commencement of nationwide Human Microbiome Initiative is a need of time. It will not only characterize population specific microbiota but also will establish a national microbiome repository which will help scientific community to integrate their data and perform comparative analysis to characterize functional role of human microbiota. Information on host genetics, microbial diversity from different body parts, and geographical locations will allow us to explore how the environment, diet, genetics are playing roles in health and disease which is still underexplored for Indian population.

Interaction of nanoparticles with non-halophilic and halophilic bacteria: evidence of nanotoxicity

Prof. Sunil K. Khare

Enzyme and Microbial Biochemistry Laboratory, Department of Chemistry,

Indian Institute of Technology, Delhi, (IIT-D) New Delhi.

E-mail: skkhare@chemistry.iitd.ac.in

There has been a quantum increase in the use of nanoparticles (NPs) in all spheres of life. Their increased presence in the environment necessitates a basic understanding of their potential impact on the environment and interactions with biological systems. Toxic effects of NPs, dubbed as "nanotoxicity," are being increasingly evidenced. Studies on animals and cell culture have amply demonstrated loss of cell viability, tissue damage, and inflammatory reactions. However, a more significant threat is perceived for the microbial community due to the accumulation of NPs. The study of nanotoxicity in microbial systems holds importance because (i) the discharge of NPs in water and soil might affect the microbial diversity, (ii) antimicrobial activity of NPs could be usefully exploited for application in medical science, (iii) their interactions with membrane proteins, DNA and various biomolecules inside the cells need to be understood. The toxicity of two commonly used nanoparticles, silver, and zinc oxide, on mesophilic and halophilic bacterial cells, has been investigated. *Enterobacter sp., Marinobacter sp., Bacillus subtilis, halophilic bacterium sp.* EMB4 were taken as model systems. The nanotoxicity was more pronounced on Gram-negative bacteria. The bacterium nanoparticle interactions were probed by electron microscopy and energy dispersive X-ray analysis. The results indicated electrostatic interactions between nanoparticles and cell surface as the primary step towards nanotoxicity, followed by cell morphological changes, increased membrane permeability, and accumulation in the cytoplasm. The differential interaction of nanoparticles and extracellularly secreted halophilic and non-halophilic enzymes has also been studied extensively. The differential interaction of two halophilic proteases and one non-halophilic protease with silver and zinc oxide nanoparticles served as

model systems—proteomic investigations on the interaction of silver nanoparticles with halophilic *Bacillus* sp. EMB9 revealed the differential expression patterns, which indicate adaptive strategies being employed by the bacteria for the functioning of the cellular machinery amidst nano-stress.

These multiple investigative approaches at the cellular and proteome level provided significant insight into mechanistic interpretations of bacteria-nanoparticle interactions.

Targeting Cancer Stem Cells for effective treatment of Cervical Cancer

Prof. Bhudev C. Das

Stem Cell & Cancer Research Lab.

Amity Institute of Molecular Medicine & Stem Cell Research (AIMMSCR)

Amity University Uttar Pradesh Campus, Noida.

Email: bcdas@amity.edu

The principal etiologic agents that cause cancer of the uterine cervix in women is infection of Human Pappillomavirus(HPVs), but HPV alone is not sufficient to cause cancer. HPV E6/E7 is responsible for tumorigenic transformation and their expression depends on the availability of host cell transcription factor AP-1, which binds to the URR of high risk oncogenic HPVs and act as a signallingepicentre for cervical cancer. A small sub-population of cancer stem cells (CSCs) are responsible for tumor initiation, progression, metastasis, treatment resistance and disease relapse. We have, therefore, attempted to develop a novel triple conjugate drug for targeted delivery to cancer and cancer stem cells without affecting the normal cells which otherwise cause serious adverse/toxic side effects..Standard molecular biology methods and stem cell culture, sphere formation, immunobloting, Realtime PCR, mouse tumorigenicity testing, immunohistochemistry bandshift assay and synthesis of triple conjugate drug, clinical validation including stem cell targeting experiments and bioavailability assays were carried out.

HPV E6 is found to be differentially upregulated in CSCs and is responsible for stemness through upregulation of Hes1 and AP-1. AP-1 overexpression contributes to chemoradioresistance of CSCs which can be sensitized. A curcumin-folic acid -cancer drug (Doxorubicin) conjugate has been developed as a non-toxic, small molecular weight compound which will specifically be taken out by the cancer and cancer stem cells via receptor-mediated internalization due to over-expression of high-affinity folate receptor thereby improving the bioavailability and targeted delivery of the drug. While folic acid serves as a targeting ligant, curcumin chemoradiosensitizes the CSCs and reduces the toxicity thus making the cancer treatment most effective and relapse free. The novel Curcumin-Folate cancer drug conjugate potentially ensure targeting and sensitization of CSCs making the cancer treatment most effective.

Anastasis, a mechanism of cell rescue from the brink of death and its impact on cancer disease and treatment

Dr Mahendra Seervi

Department of Biotechnology, All India Institute of medical Sciences (AIIMS)

New Delhi

E-mail: mseervi12@gmail.com

Apoptosis, a form of programmed cell death, was considered as an irreversible and rapid biological phenomenon in which the cell fate is sealed upon crossing the final threshold of widespread cytochrome *c* release and caspase activation. However, recent studies from my lab as well as from other groups, demonstrated that apoptosis is intrinsically reversible even from the executioner stage provided the apoptotic stimulus is removed. This cellular process of recovery from late-stage apoptosis, *aka* "anastasis" has profound significance in cancer therapy and management strategies. Although anticancer therapies induce apoptosis in cancer cells, they also set a favourable milieu for anastasis due to their episodical delivery with drug-free intervals. Anastatic cancer cells acquire aggressive oncogenic characters such as invasiveness, migration and drug resistance while recovering from death. Hence anastasis has emerged as an important, unrecognized mechanism for cell rescue and mutagenesis that is presumed to significantly impact cancer drug-resistance and recurrence. Being a newly discovered phenomenon, gaining its mechanistic insight is paramount. By employing systematic integrative proteomic and transcriptomic approaches, our lab successfully delineated a repertoire of molecular determinants associated with cancer cells reverted from late-stage apoptosis. Targeting these anastasis-associated molecular factors may prove beneficial in overcoming drug resistance and recurrence challenges associated with cancer treatment.

Glial MeCP2 phosphorylation dynamics in normal development and glioma progression

Dr. Prakash P Pillai

Division of Neurobiology, Department of Zoology, Faculty of Science,

The Maharaja Sayajirao University of Baroda, Vadodara

E-mail: pillaippp@gmail.com

MeCP2 is a global transcriptional regulator of the CNS, which functions as a gene-specific transcriptional silencer by binding throughout the genome as well as transcriptional activator due to its involvement in the transcriptional modulation of active genes. Differential phosphorylation of MeCP2 is a key mechanism by which the methyl-binding protein modulates its affinity for its partners, gene expression and cellular adaptations to stimuli and neuronal plasticity. MeCP2 phosphorylation affects the dendritic arborization, spine maturation of the neurons. However, there are only few reports on the MeCP2 phosphorylation in the glial cells.Laminin (LN) differentially regulated the expression of pS80MeCP2 in immature and mature N19 OLGs indicating MeCP2 is phosphorylated in a stimulus-dependent manner during oligodendrocyte development. In astrocytes, BDNF increased the pS421MeCP2 expression levels in sub-nuclear localization and its association with the euchromatin region in CamKII signaling dependent manner. MeCP2 not only play a role in neurodevelopmental disorders but it has been a substantial epigenetic regulator in many cancers like prostrate, lung, liver, breast cancers etc. However, there are no reports on MeCP2 phosphorylation in this glial cell derived cancer. We demonstrated increased levels of pS80MeCP2 and pS421MeCP2 when C6 glioma was treated with BDNF and inhibition of TrkB receptor by K252a led to decrease in MeCP2 phosphorylation (S80 & S421). The chromatin association studies demonstrated that pS80MeCP2 to be associated with heterochromatin and on the contrary pS421MeCP2 associated with euchromatin suggesting particular type of association of phosphoMeCP2s to regions of the chromocenters. LPS stimulation leads to a large number of rapid post-translational and transcriptional changes in the astrocytes. Our study is the first to report that LPS stimulation leads to increase in

phosphorylation of the transcriptional regulator MeCP2 at S421 site in astrocytes and further the mechanism by which astrocyte plays a role in CNS immune modulation following a variety of infectious or inflammatory insults will be discussed. In conclusion, MeCP2 in glial cells is functionally regulated by stimuli-mediated phosphorylation and may provide regulatory specificity during CNS myelination and glioma progression.

Deciphering host-microbiome cross-talk: Opportunities and Challenges

Dr. Anirban Dutta

TCS-Research, Tata Research Development and Design Centre (TRDDC), Pune

E- mail: anirban.dutt@tcs.com

Recent advances in health-sciences have indicated that our body harbours trillions of microbes (the microbiome), which significantly outnumber our own cells. Quite evidently, these microbes are in constant interaction with our own cells and have been found to be deeply associated with our metabolism, physiology and immunity. While it is expected that deciphering these interaction patterns will unlock a treasure trove of health related information, studying millions of mirobial organisms in one go has its own share of challenges. The field of metagenomics deals with uncovering the genomes/DNA of these tiny inhabtants of our body, and allows a sneak-peak into the functional and metabolic potential of the microbes. While the next generatonseqeuncing technologies have provided a boost to this field in terms of generating high-throughput DNA sequencing data, the downstream analyses and interpretation keeps on gowing more and more complex. My talk will cover some of the aspects of modern metagenomic data analysis, the possibilities thereof, and some real use cases wherein the data has been churned into potential clinical solutions

Effectoromics-based identification of molecular targets for pea powdery mildew disease control

Dr Divya Chandran

Regional Centre for Biotechnology (RCB), NCR Biotech Science Cluster, Faridabad

E-mail: divya.chandran@rcb.res.in

Powdery mildews (PM) are significant fungal pathogens of legumes, which represent important food crops cultivated and consumed in India. The obligate biotrophic fungus *Erysiphepisi* (*Ep*) is the most commonly reported cause of PM disease in legumes. To facilitate successful host colonization, PM fungi deliver an arsenal of virulence proteins termed 'effectors' into plant cells, which primarily interfere with host metabolism and suppress immune signaling. Effectors (or effector functions), in turn, can be recognized by cognate plant resistance proteins leading to the activation of a robust form of plant immunity known as effector-triggered immunity. Thus, effectors have recently emerged as strategic tools to accelerate and improve the identification and characterization of plant resistance genes for crop improvement. A recent study in the lab identified 167 candidate secreted effector proteins (CSEPs) from *Ep*haustoria. *In planta* expression analysis of a subset of *EpCSEP*s revealed that they are predominately expressed in haustoria and at different stages of the infection process. We further examined the role of two *Ep*CSEPs using host induced gene silencing and found that both candidates are required for full virulence, indicating that they are *bona fide* effectors. Interestingly, homology modelling revealed that these proteins are analogous to fungal ribonucleases and may possess RNA cleavage activity. To obtain deeper insights into their role as pathogenicity determinants, future investigations will focus on the identification of their host targets.

The role of nitrate and nitric oxide signaling in plant resistance against pathogen infection

Dr. Jagadis Gupta Kapuganti

National Institute of Plant Genome Research (NIPGR), New Delhi.

Email: jgk@nipgr.ac.in

Nitric oxide is a free radical signal molecule. In recent years it emerged as an important signal molecule in plants regulating various processes including plant defense. We investigated the effects of N forms such as nitrite/ammonia on the hypersensitivity response (HR)-a pathogen-elicited cell death linked to resistance. Plants were grown either NO_3- or NH_4^+ were challenged with avirulent *Pseudomonas syringaepv. phaseolicola*. Nitrate nutrition accelerated cell death in NO_3^--fed in comparison to NH_4^+-fed plants, which correlated, respectively, with increased and decreased resistance. Nitric oxide (NO) was elevated in plants fed with nitrate and NO generation was reduced in NH_4^+-fed plants where N assimilation bypassed the NR step. PR1 expression and salicylic acid (SA), were elevated under nitrate nutrition .Conversely,total amino acid, cytosolic and apoplastic glucose/fructose and sucrose were elevated in ammonium treated plants. Under NO_3^- nutrition the polyamine biosynthesis was predominant, whilst after NH4+ nutrition, flux shifted towards the production of 4- aminobutyric acid. Suggesting that nitrate nutrition helps in increasing plant defense. Using tobacco RNAi lines with low nitrite reductase (NiRr) levels were also used to investigate the roles of nitrite and nitric oxide (NO) in this process we found that HR-associated changes in metabolism are often linked with primary nitrate assimilation hence influenced by nitrite and NO production. In another study we investigated the role of plant growth promoting *Trichoderma* in enhancing induced systemic resistance (ISR) via activation of high affinity transporters. Using various mutants and transgenic of nitric oxide biosynthetic pathway, we found that Trichoderma can induce short term NO production that can enhance disease resistance under the conditions low nitrogen.

Applied Microbiology and Biotechnology

Flash Talk

AMB-1: Purification and production of Novel Antioxidative peptides from fermented goat milk

Gauravkumar Panchal[1]*, JB Prajapati[2], Amar Sakure[2] and Subrota Hati[2]

[1]GCMMF Ltd., Anand [2]Dairy Microbiology Department, SMC College of Dairy Science, AAU, Anand-388110[1]

E-mail: panchal.gaurav4425@gmail.com

Goat milk differs from cow or human milk in context of higher digestibility, distinct alkalinity, higher buffering capacity and certain therapeutic in medicine and human nutrition (Park, 2009). Goat milk proteins may be digested more freely and their amino acids absorbed more efficiently than those of cow milk. Goat milk is considered to form a softer, more friable curd when acidified, which may be related to lower contents of αs1-casein in the milk (Zenebe *et al*., 2014). Goat milk fermented with different LAB increase the biologically active peptides from corresponding sequences of the precursor protein. Food-derived peptides have been demonstrated to be the natural antioxidants without marked adverse effects. An increasing number of food protein hydrolysates and antioxidant peptides have been found to exhibit antioxidant activity . Goat milk fermented with Lactobacillus fermentum (M2) exhibited notable antioxidant activities. The highest antioxidant activity (ABTS assay) (57.09%), hydroxyl free radical scavenging activity(57.30%) and superoxide free radical scavenging activity (51.40%) found after 48h at 37oC by M2 culture and proteolytic activity was maximum (8.13 mg/ml) at 2% inoculation rate after 48h of incubation. In SDS-PAGE and 2D-PAGE analysis, 10-51 kDa protein bands were observed from fermented goat milk. R**ALAPAG**APGR and **VYVEEL**KPTPEGNLEILLQK peptides sequence from 2D-PAGE were matched with antioxidant fraction of ALAPAG (β-lactoglobulin) and YVEEL (β-lactoglobulin) on BIOPEP databases, respectively. TIDMESTEVF**TKK** and FFIFTCLLAV**ALA**K peptide sequences from various HPLC fractions (3kDa permeate and 10 kDa permeate, respectively) were also matched with antioxidant fraction of EEEKNRL**TKK**TKLT (α-casein) and S**ALA**M (β-lactoglobulin) on BIOPEP databases, respectively. Further, in vivo study is required to validate the health claim, particularly antioxidant activity on small animal or human subjects.

Keywords: antioxidative, peptides, LAB

Flash Talk

AMB-2: Antihypertensive Peptides derived from fermented camel milk by proteolytic Lactobacilli (*in silico* & in vitro study)

D. Solanki, Subrota Hati*, Amar Sakure and Prajapati JB

Dairy Microbiology Department, SMC College of Dairy Science, Anand Agricultural University, Anand-388110, Gujarat

Email: subrota_dt@yahoo.com

Camel milk is known for many health attributes such as anti-inflammation associated with obesity, anti-carcinogenic, anti-diabetic and antihypertensive. Rising health problems, especially hypertension was reported to heal through eating habits. Angiotensin I-converting enzyme inhibitory peptides produced by fermentation of camel milk are reported to reduce hypertension without any side effects. 09 exhibited highest PepX activity (0.893) compared to control up to 12h of incubation at 37°C. Camel milk fermented with lactic culture showed significant increase in ACE-inhibitory activity with the time of incubation. 09 exhibited highest ACE-inhibitory activity (76.75%) compared to control up to 48h of incubation at 37°C. After 48h of incubation, 09 produced 2.487% lactic acid while it reduced pH of camel milk from 6.55 to 3.17 after 48h at 37°C in camel milk. It also showed 11.33 log cfu/ml of lactic counts during the incubation of 48h at 37°C. 09 exhibited maximum proteolytic activity at the rate of 2% and 12h of incubation at 37°C. So, 2% rate of inoculation and 12h of incubation was optimized for the peptide production. 09 showed higher peptide production (47.50%) compared to control under optimized growth conditions. In case of dipeptidase activity, 09 showed dipeptidase activity (0.080) in intracellular samples while in case of extracellular extract it showed 0.277 at the 2% rate of inoculation and 12h of incubation at 37°C. In case of tripeptidase activity, 09 showed tripeptidase activity (O.D. 0.077) in intracellular extract while in case of extracellular extract, it showed tripeptidase activity (O.D. 0.296) under optimized growth conditions. 3kDa permeate and 10 kDa permeate showed highest ACE-inhibitory activity compared to other 5 kDa permeate/retentate, 10 kDa retentate and 3 kDa retentate. Extensive homology search in NCBI (Uniprot/SwissProt database) and PIR revealed the peptide matched with camel milk protein, precursor and protein fragments. Peptides were found matched with many reported sources of ACE-inhibitory peptides with the similar type of sequences.

Keywords: Antihypersensitive peptides, ACE-inhibitory peptides, camel milk

Flash Talk

AMB-3: Comparison of antioxidant activities of various extracts of selected plants of Genus *Cucumis* L. and *Momordica* L. of family *Cucurbitaceae*.

Rupinderpal Kaur[1]*, Yumnam Devashree [1] and Vijay Singh[2] Renu Sharma[3]

[1] Department of Bioengineering and Biosciences, Lovely Professional University, Phagwara, Punjab India-144411

[2] Department of Botany, Mata Gujri College, Fatehgarh Sahib, Punjab, India-140406

[3] Department of Chemistry, Bhai Gurdas Institute of Engineering and Technology, Punjab,India-148001

E-mail :ripan151@gmail.com

Over the last decade, much research has focused on the potential health benefits of antioxidants and indeed many synthetic and natural compounds have been evaluated for their antioxidant profile. However, in several studies only a limited number of assays, often poorly validated, are used and the techniques available frequently lack specificity. These limitations may incorrectly influence the results. This review will therefore focus on several pitfalls that may emerge *in vitro* and *in vivo* antioxidant research. First, different *in vitro* techniques to determine antioxidant potential are discussed, including radical scavenging assays and fingerprinting methods. As a rule, a panel of different assays is indispensable to characterize and establish *in vitro* antioxidant activity. Furthermore, as problems of absorption, distribution, metabolism and excretion are only accounted for by *in vivo* studies, the need for *in vivo* antioxidant research is pointed out. Several methods to characterize the *in vivo* activity of antioxidants, including major drawbacks and pitfalls of some assays, have been discussed. The availability of both a representative "oxidative stress" animal model and a battery of well-validated assays to assess the broad diversity of oxidative damage and antioxidative defence parameters, are crucial for antioxidant research *in vivo*. From the present study it can be concluded that Cucumis melo L. and Momordica charantia L. have high antioxidant activity of gourd vegetable extracts could be attributed to their high levels of phenols and flavonoid compounds in particular. Methanol can be recommended as most appropriate solvent for the recovery of phytochemicals and hence increased antioxidant activity from these two genera.

Flash Talk

AMB-4: Influence of supplementation of *Lactobacillus* cultures on growth. performance, fecal microbiota, blood profile and cholesterol contents in broilers

[1]Subrota Hati, [2]B.K. Mishra, [2]Sujit Das*, [1]Maulik Patel, [1]Jashbhai B. Prajapati

[1]Dairy Microbiology Department, S.M.C. College of Dairy Science, AAU Anand-

[2]Department of Rural Development and Agricultural Production, North-Eastern Hill University, Tura campus, Tura-794 001, Meghalaya, India

E-mail: **sujitdas557@gmail.com**

The widespread use of antibiotics in poultry with the intent of encouraging growth rate, increasing feed conversion efficiency and for the reduction of intestinal diseases have resulted to an imbalance of the beneficial intestinal flora. The use of lactic acid bacteria as feed additives to substitute antibiotic-associated growth stimulator and their impact on the quality of the meat is one of the key research area. In this study, broilers were grouped into four different treatments: T1 (control): basal diet + antibiotic as growth promoter and immunomodulatory factor, T2: basal diet without having antibiotic as growth promoter and immunomodulatory factor + *L. plantarum* KGL3A, T3: basal diet without having antibiotic and immunomodulatory factor + *L. fermentum* KGL4, T4: basal diet without having antibiotic and immunomodulatory factor + combination of T3 and T4 bacterial strains. During the entire study, higher bodyweight was observed among the *Lactobacillus* fed broilers groups Lipid profile analysis further confirmed the significant decrease in low-density lipoprotein (LDL) content of T4 (19%) and T3 (16%) groups than the control group (T1) while more than 10% increase in high-density lipoprotein HDL content was observed in T4 and T3 groups than the control group (T1).The histopathological examinations of the fine macroscopically examined intestinal and liver tissues suggested well organized epithelial lining and villi structure in *Lactobacillus* fed broiler groups (T2, T3, T4) and control group (T1). Further, the decrease in fecal coliforms and enterococcus counts and an increase in *Lactobacillus* counts in treatment groups compared to the control group were found after 42 days of study. The supplementation of *Lactobacillus* isolates as feed supplements to the broilers had overall positive effects on broilers growth performance in this study without providing growth promoter as antibiotic.

Keywords: antibiotics, poultry, Lactobacillus, LDL, HDL.

AMB-5: Isolation and Screening of Potential Exopolysaccharide producing Bacteria from Marine Ecosystem of Gujarat

Mr. Vishal Patel, Dr. Falguni Patel

HVHP Institute of Post Graduate Studies and Research, SV Campus, Kadi (North Gujarat) Shree M. M Patel Institute of Science and Research, Gandhinagar

Kadi Sarva Vishwavidyalaya, Gandhinagar

E-mail : nirmascience@gmail.com

In recent studies many bacteria in the marine environment secrete Exopolysaccharides (EPSs), which comprise a substantial component of the extracellular polymers surrounding bacterial cells. In recent years, the increasing demand for natural polymers for pharmaceutical, food and other industrial applications has led to a remarkable interest in EPSs produced by marine bacteria. Gujarat contains 1600 km long costal area, which is very diverse in concern with bacterial diversity. Soil sampling was done from various coastal areas of Gujarat. Isolation and Screening of exopolysaccharide producing bacteria were carried out in Glucose Yeast Extract Broth with Glucose as a carbon source. Congo red Plate assay was carried out to check the nature of Exopolysaccharide. On the basis of Colonial and Morphological characteristics, total 57 different bacterial isolates were obtained in primary screening. Among these 10 good EPS producers were selected in Secondary screening and their EPS quantification was done by using Acetone as a solvent. In future, the EPS production will be optimized and their applications will be studied.

Keywords: Marine , EPS, Production

AMB-6*: Anoxybacillusrupiensis* TS-4 α-amylase: A thermostable amylase exhibiting prominent application in the detergent industry

Bhavtosh A. Kikani*, Susen Kurien

Department of Biological Sciences, P.D. Patel Institute of Applied Sciences, Charotar University of Science and Technology, Changa – 388 421 (Gujarat, India)

E-mail: bhavtoshkikani.bio@charusat.ac.in

The physicochemical conditions influencing α-amylase secretion by a thermophilic bacterium, *Anoxybacillusrupiensis* TS-4 (Genbank Number, KU360725) were optimized by the response surface methodology, using Plackett Burman design, followed by Box Behnken Design to enhance amylase production by 3 fold as compared to the one variable at a time approach. The trends revealed incubation temperature, medium pH and starch concentration as the most significant variables. The amylase was purified by ion exchange chromatography, followed by size exclusion chromatography with fold purification and yield of 17.85 and 34.72%, respectively. The molecular weight, K_m and V_{max} of the purified amylase were 48 kD, 0.58 $mgmL^{-1}$ and 3124 $\mu molmL^{-1}$ min^{-1}, respectively. It catalyzed starch over a broader range of temperature and pH, having optima as 80 ˚C and 8, respectively. The enzyme was stable at a broad range of temperatures and pH, displaying higher half-life and reduced deactivation rate constant. The feasibility of the starch catalysis reaction mediated by the studied amylase was substantiated by determining the thermodynamic parameters, such as alterations in the enthalpy, entropy, activation energy and Gibb's free energy. The attributes of the amylase such as calcium independence, alkalitolerance and stability in presence of various chelators and surfactants aid uniqueness, novelty and commercial promise.

Key words: Thermostable amylase; Box Behnken Design; Thermodynamics; Detergent application

AMB-7: Immobilization of fungal α-amylase on Graphene Oxide-Fe_3O_4 magnetite nanoparticles for yielding more production of high maltose containing syrup

Dave Dolly[1], Desai Rucha[2*] and Kikani Bhavtosh[1*]

[1]Department of Biological Sciences, P.D. Patel Institute of Applied Sciences, Charotar University of Science and Technology, Changa – 388 421, Gujarat, India,

[2] Department of Physics, P.D. Patel Institute of Applied Sciences, Charotar University of Science and Technology, Changa – 388 421, Gujarat, India

E- mail: davedolly709@gmail.com

Among hydrolytic enzymes, α-amylase (EC 3.2.1.1) shares almost 38% of global market. Being an endoamylase, it catalyses starch into maltose and glucose Amylases share range of industrial applications, a range of approaches is employed to meet the industrial demands. In the current study, we tried immobilize fungal α-amylase on Graphene Oxide-Fe_3O_4 magnetite nanoparticles with significant practical yield. Due to covalent binding, detachment of the amylase was greatly reduced. Therefore, the immobilized amylase was re-used for 9 subsequent cycles very efficiently. The temperature and pH range for amylase catalysis and stability was also be broadened upon immobilization. Alongside, the temperature and pH optima for catalysis shifted from 50˚C to 80˚C and pH 7 to pH 5, respectively. The immobilized amylase was also employed to produce high maltose containing syrup, consisting of three stages: gelatinization (90˚C for 2 h), liquefaction (75˚C for 6 h) and saccharification (50˚C for 24 h). Eventually, the structural stability of immobilized amylase was deduced and established using FTIR and TGA analysis. Overall, the attributes of immobilized amylase: better immobilization yield, higher thermostability, broad pH stability, better operational stability (re-useability) and efficient starch hydrolysis highlights its future commercial applications in the production of high maltose containing syrup.

Keywords: Fungal amylase, Graphene oxide, immobilization

AMB-8: Screening of amylase producing micro-organisms from the soil samples of house hold and municipal waste dump site

Prasanna R Kovath, Aswathy A K,Mariya Joy,Mariya K Saju, Sneha A P K, Tilda Mary

Department of Biotechnology,St. Mary's College Thrissur Kerala, India

E- mail: prasanna.r.kovath@smctsr.ac.in

The enzymes from microbial sources are more stable and obtained cheaply. Amylases are among the most important enzymes and are of great significance in present day industry. Starch degrading bacteria are most important for industries such as food, fermentation, textile and paper. The purpose of current investigation is to isolate Amylase producing microorganisms from two different soils from House Hold Waste dumping site and Municipal Waste Dumping site. Soil samples were collected from viyyur and shaktan stand of Thrissur district Kerala India. Morphological and Biochemical Identification were carried out, the species were screened for amylase production. The enzyme activity was studied. The species identification could be used as the auspicious source of Amylase in Industry.It can also enhances waste management processes.

Keywords: House Hold And Muncipal Solid Waste, Amylase Producing Micro Organisms, Enzyme Activity. Waste management.

Flash Talk

AMB- 9: Modification of a spectrophotometric method to screen hydroxycitric acid producing bacteria

Disha Patel, Aditi Buch*

Department of Biological Sciences, P D Patel Institute of Applied Sciences

Charotar University of Science and Technology (CHARUSAT), Changa, Gujarat.

E-mail: aditibuch.biochem@charusat.ac.in

Hydroxycitric acid (HCA), a natural phytochemical used for herbal therapeutic and dietary supplement; known for its anti-obesity and anti-diabetic properties by its biologically active stereoisomers (*2S, 3S*)-HCA and (*2S, 3R*)- HCA respectively. Due to geo-climatic cultivation of source plants, microbes are being considered as the only ecofriendly alternative and convenient source for bulk production of natural HCA. A convenient yet specific and accurate method for quantitative determination of HCA becomes essential to facilitate high-throughput screening of HCA producing bacteria. An existing spectrophotometric method so far reported to quantify HCA finds limited use owing to poor stability of HCA- metavanadate complex. The present work describes improvisations in this method to make it more suitable for use during screening of HCA producing bacteria. Modified assay system contain HCA standard, metavanadate reagent and 1 M NaOH to neutralize excess acidity. Resulting complex showed λmax at 485nm, obeying Beer- Lambert's law within concentration range of 33-677 µg/ml, enhanced stability of complex with retaining 70% absorbance even after 60 min of its formation. Also method was successfully scaled down up to 10 folds obeying Beer-Lambert's law between 67 and 542 µg/ ml. Of tested metabolites and media components only tartrate interfered with spectrophotometric estimation of HCA; a correction factor to eliminate which was established. Accordingly measured HCA level in the culture supernatant of a bacterial isolate IT 6 was comparable to that determined using standardized HPLC method.

Keywords: HCA, modified spectrophotometric method, phytochemical

AMB-10: Characterization and Production of Novel ACE-Inhibitory Bioactive Peptides derived from Fermented Goat Milk using potent *Lactobacillus* cultures

Heena Parmar*, Subrota Hati and JB Prajapati

Dept. Dairy Microbiology, Anand Agricultural University, Anand-388110, Gujarat, India

E-mail: heenaparmar18@gmail.com

Goat milk is popular for its beneficial attributes on the human beings. Lactic Acid Bacteria (LAB) is an important friendly bacteria exist in all the fermented milk products. Fermented goat milk has multiple therapeutic and nutritional effects. Goat milk has lot of health benefits like antihypertensive, antioxidant and antimicrobial activity. But there is scanty information on ACE-inhibitory activity of fermented Surti goat milk (Indian breed).

Fermented goat milks with two selected *Lactobacillus* cultures i.e. NK9 (*L. casei*) and LF (*L. fermentum*) with 2% rate of inoculation were used for production, purification and characterization of ACE-inhibitory peptides for 48 h at 37ºC. Various antihypertensive bioactive peptides were characterized and their similarity with different goat milk proteins were confirmed against goat milk protein databases of AHTPDB. From the study, it has been concluded that, fermented goat milk could be a best source of ACE-inhibitory peptides.

Keywords: ACE-inhibitors, bioactive, Lactic acid bacteria

Flash Talk

AMB-11: Fight/flight – The interaction between Population variants during motility in E. coli

Kavi Bharathi R, Sandeep Miryala, C.S. Srinandan

Biofilm Biology Lab, Anusandhan Kendra-2, School of Chemical

Biotechnology, Centre for Research in Infectious Diseases, SASTRA University,

Thanjavur 613401, Tamil Nadu, India

Email: srinandan@gmail.com; srinandan@scbt.sastra.edu

Urinary tract infection (UTI) is among the most common infectious diseases of humans and is the most common nosocomial infection in the developed world. UPEC is the major causative agent of the infection. Biofilm transform independent cells to specialised cell population. Biofilm is essential for establishment of the infection and increases the bacterial pathogenicity in the host. When Uropathogenic Escherichia coli were plated on the Congo red media, we observed heterogeneity which shows red (RCV), white (WCV) and heterogenic (HCV) colony variants. Sugar source in the media is one of the vital factors which determine the existence and survival of the population. When subjected with glucose in the media the ability of the variants to quench the glucose is analysed. Swarming motility is studied using fluorescence microscopy and image analysis using ImageJ and DAIME (Digital Image Analysis in microbial ecology) is done in order to study the interactions between variants.

Keywords: Population variants, motility

AMB-12: Production of L-Ribose from L-arabinose by co-expression of L-arabinose isomerase and D-lyxose isomerase in *E.Coli*.

Nidhi Patel, Darshan Patel, Kiran Patel

Department of Biological Sciences; Charotar University of Science and Technology, India

Email address: patel.nidhi1598@gmail.com

L-Ribose is an important pharmaceutical intermediate that is used in the synthesis of numerous antiviral and anticancer drugs. However, it is a non-natural and expensive rare sugar. Recently, the enzymatic synthesis of L-ribose has attracted considerable attention owing to its considerable advantages over chemical approaches. In this work, a new strategy was developed for the production of L-ribose from the inexpensive starting material L-arabinose. L-arabinose isomerase have been identified from *Shigella flexneri* **(**Patel et al., 2017). L-AI gene (1.5kb) amplified by gene specific primers and cloned in to pET21b cloning vector. The sequence confirmed constructed vector was transformed and over expressed in *E.coli* BL-21 strain and the soluble expression confirmed on 10% SDS-PAGE. The recombinant SF-AI and previously cloned D-LI from *Cohnella laevaribosii* in p-cold vector were purified to their apparent homogenicity by Nickle affinity chromatography. Purified proteins SF-AI and CL-LI showed homogenecity on SDS-PAGE.The L-arabinose isomerase (L-AIase) gene from *Shigella flexneri* and the D-lyxose isomerase(D-LIase) gene from *Cohnella laevaribosii* were cloned and co-expressed in *Escherichia coli*, resulting in recombinant cells harboring the vector p-Cold LAI/D-LI. Overall, this study provides an approach for producing L-ribose from L-arabinose using a co-expression system harboring L-AIase and D-LIase genes.

AMB-13: Nanofiber and metal organic framework based entrapment of an alpha amylase and its kinetic studies

[1]Patel, K., [2]Patel, V., [2]Dadhania, A. and [1]Patel, P.

[1] Department of Biological Sciences, Charotar University of Science and Technology

[2] Department of Chemical Sciences, Charotar University of Science and Technology

Email address: pankti5925@gmail.com

In yester years, immobilization of an enzyme has been presented as a tool for the enhancement of enzyme properties such as reusability and stability. On the other hand, type of material which is used, plays a vital role in the entire process of immobilization, because of powerful effect of support materials in the outcome of the catalytic system. For the purpose of entrapment of enzyme, two different methods are used, in which Nanofiber as well as metal organic framework are selected as support material. Nanofiber proved as a solid matrix for immobilization of enzymes because of their high surface area to volume ratio and less mass transfer resistance Whereas, Metal organic framework is crystalline, porous material composed of organic linker and metal nodes. This study provides the selection of appropriate background material for specific enzyme, and their kinetic properties

AMB-14: Characterization of the chirality of microbial hydroxycitric acid enantiomers

Disha Patel,Manali Chandnani, Aditi Buch*

Department of Biochemistry, P D Patel Institute of Applied Sciences

Charotar University of Science and Technology (CHARUSAT), Changa, Dist. Anand, Gujarat.

E-mail: aditibuch.biochem@charusat.ac.in

Hydroxycitric acid (1,2-dihydroxypropane-1,2,3-tricarboxylic acid, HCA) is a phytomolecule, naturally occuring in variety of plants including *Garcinia cambogia* and *Hibiscus subdariffa.* HCA availability is limited by the restricted habitat of plants and difficulty in organic stereoselective synthesis. HCA exists in 4 different isomers only two showing biologically active forms (*2S, 3S*) - HCA and (*2S, 3R*) – HCA Microbes are promising alternative sources for production of large scale stereospecific HCA. Till date only two microbial species are known to produce biologically active form of hydroxycitric acid .Extraction and characterization for its acid and lactone forms have been reported so far in both plants and bacteria.Both isomers are reported for inhibition of enzymes, (*2S, 3S*) - HCA for ATP citrate lyase and (*2S, 3R*) - HCA for pancreatic alpha amylase and alpha glucosidase enzymes. Subsequently both active isoforms have been reported for anti-obesity and anti-diabetic effects respectively. The present work focuses on characterisation of bacterial HCA by studying inhibition patterns with ATP citrate lyase and alpha amylase enzymes.Comparative analysis of inhibition patterns of ATP citrate lyase and alpha-amylase suggest that the microbial HCA produced was (2S-3R) which specifically inhibits alpha-amylase.

Cell Biology and Genetics

CBG-1: Effect of melatonin on alveolar type-2 cells in diabetic albino rats.

Krishna Yadav
Veer Bahadur Singh Purvanchal University Uttar Pradesh, India
Email: ky9256699@gmail.com

Melatonin is a hormone secreted by pineal organ of the body besides pineal organ there are other extrapineal organs from where melatonin secretion takes place. Lung is a main respiratory organ which contain large numbers of alveoli which are always filed with air.Alveolar type 2 cells secerete surfactant protein.Besides many other function of surfactant protein it also provide immunity to the lung.Diabetes is a metabolic processes which causes deleterious effect on multiple organ.In our experiment it was find out alveolar type -2 cells of lung which shows pathogenicity by diabetes get repaired by melatonin hormone.Melatonin hormone not only protect various organ but also help in providing immunity.

Keywords: Melatonin, surfactant protein, extrapineal organ, diabetes, immunity, respiratory organ.

Flash Talk

CBG-2: Cancer Stem Cells (CSCs) formation: Probable explanation for Cisplatin Resistance in Head and Neck Cancers

Humayara Khan, Ratika Srivastava

Department of Microbiology and Biotechnology Centre, Faculty of Science,

The MaharajaSayajirao University of Baroda, Vadodara, Gujarat.

E-mail srivastava.ratika@gmail.com

Head and neck cancer is the sixth most common cancer worldwide. In India, it comprises approximately 40% of total cancer sites. Cisplatin is one of the most extensively used effective chemodrug for treatment of head and neck cancers. Chronic usage of Cisplatin has irreversible side effects like ototoxicity (hearing loss), neurotoxicity, and nephrotoxicity along with increase risk of secondary malignancies like Leukemia. Also, about 50% patients at some point become non-responsive to it thus allowing reoccurrence or aggressive form of tumor. Hence, it is important to understand the mechanism of Cisplatin resistance. We hypothesize that Cisplatin exposure leads to formation of cancer stem cells which remain non responsive to chemodrug and proliferate. We tested the effect of Cisplatin on Proliferation potential and Cancer Stem Cells (CSCs) formation of HEp– 2 of laryngeal origin cancer cell line. Higher proportion of Ki-67+ (a nuclear proliferation antigen), CD44+ and Nanog+ (Cancer stem cell markers) cells were found upon treatment with suboptimal dose (IC25) of Cisplatin. This study indicates that Cisplatin resistance occurs due to formation of CSCs. Better understanding of the pathway involved in CSC generation can enable designing of novel therapeutic strategies for non responsive patients.

Keywords: Cancer stem cells, cisplatin resistance, therapeutic strategies

CBG-3: To check the effect of dietary supplementation of "*Murraya koenigii*" (Curry leaves) on Alzheimer's disease using *Drosophila melanogaster* as a model organism.

Samriddhi Choudhary[1], Dr. Anand K. Tiwari[2], Komal Panchal[3]

[1]Institute of Advanced Research, Gandinagar, Institutional Area, Koba, Gujarat 382426

[2]Department of Biological Science, P.D. Patel Institute of Applied Sciences,

Charotar University of Science and Technology, Changa- 388 421, Anand, Gujarat,

E-mail : samriddhichoudhary3@gmail.com

Murraya koenigii (curry leaves plant) is a medicinal plant that shows some neuroprotective properties. In this study, I have used Murraya koenigii in 1mg concentration to study the neuroprotective properties of Alzheimer's disease on Drosophila melanogaster as a good model organism. Two Drosophila flies' strains have been used that is Oregon R+ and GMRAβ42K52; GMRAβ42K53 and fed on Murraya koenigii supplemented food. Supplementation of Murraya koenigii in 1mg concentration increases the phototaxis and locomotor activity of AD Drosophila flies'. Therefore Murraya koenigii showed some therapeutic effect to rescue the symptoms of Alzheimer's in Drosophila melanogaster.

Keywords: Curry leaves, Alxheimer's disease, Drosophila melangoster

Flash Talk

CBG-4: Evaluation of the anti-cancer mechanism of berberine in human cervical cancer cells using mammalian cell culture and multiple spectroscopic approaches.

Darpan Raghav, Shabeeba M. Ashraf, Krishnan Rathinasamy
School of Biotechnology, National Institute of Technology Calicut, Kerala – 673601,

E-mail :darpan1991_raghav@yahoo.com

Berberine has shown to possess tremendous anti-cancer potential against different cancer types.One of the major echanisms behind the anti-proliferative effect of berberine is the induction of G2/M phase cell cycle arrest followed by apoptotic cell death. Several speculations have been made to explain the anti-cancer attributes of berberine; however, the exact cytotoxic mechanism and major cellular target of berberine remains elusive. In this study, we evaluated the anti- proliferative mechanism of berberine in human cervical cancer cells and characterized its interactions with the tubulin purified from goat brain using multiple spectroscopic approaches. The results from this study indicate that berberine inhibited the proliferation of HeLa cells with an IC 50 value of 18 µM and induced G2/M phase cell cycle arrest in a concentration dependent manner. At its IC 50 concentration, berberine depolymerized the cellular microtubules of HeLa cells. The in-vitro and in-silico experiments specify that berberine bound to purified tubulin at a novel site and inhibited its polymerization into microtubules. Data from FTIR study indicated that binding of berberine perturbed the secondary structure of tubulin. Collectively, our findings suggest that inhibition of tubulin polymerization could be the major molecular mechanism behind the G2/M phase arrest induced by berberine.

Keywords: Anticancer, berberine, IC50

CBG-5: Role of Synbiotic in Preventing the Progression of Alcoholic Liver Disease Targeting Gut-Liver-Adipose Tissue Axis

Dhara Patel , Farhin Patel , Kirti Parwani , Dixa Sharma ,Gita Chudasama and Palash Mandal*

Department of Biological Sciences, P. D. Patel Institute of Applied Sciences,

Charotar University of Science and Technology,

Changa-388421, Gujarat, India.

E- mail: palashmandal.bio@charusat.ac.in

Consumption of ethanol has been carried out since ages and it has been an important cause of death worldwide. Ethanol mediated liver injury is also known as Alcoholic liver disease (ALD) is caused due to surplus intake of alcohol. Several studies have proposed molecular pathways that may be leading to ALD. One of the factors that may affect the pathway is gut dysbiosis. The gut microbiota produces a various compound that play a crucial role in regulating distal organs such as adipose tissue and the liver. Dysbiosis causes bacteremia, hepatic encephalopathy, small intestinal bacteremia, increased intestinal permeability. Recent research has better understanding of the gut and liver axis and how it controls systemic metabolic modifications in liver cirrhosis. Reports of clinical and experimental studies demonstrates the association with gut-microbiota and fatty acid metabolism. Another factor that may affect the ALD pathway is dysfunction of adipose tissue metabolism. Excessive alcohol consumption disturbs lipid metabolism, by increasing lipolysis and decreasing or unchanged lipogenesis, impaired glucose tolerance of adipose tissue which results in ectopic fat deposition inside the liver. Adipokines are adversely modified upon chronic alcohol consumption including adiponectin, leptin, and resistin. When these two factors are combined develops a pro-inflammatory state within WAT. The futuristic therapeutic approach for treatments and prevention for liver cirrhosis patients must be focused on evaluation of the gut-liver-adipose tissue metabolic network and the modification of these interactions using probiotics, synbiotics, and prebiotics. This work focuses on the progression and metabolism of ALD, the effect of ethanol on gut and adipose tissue, the effect of Synbiotic (aged garlic extract and Lactobacillus rhamnosus) on adipokine secretion on 3T3-L1 cells and male Wistar rats in ethanol induced model.

Keywords: Synbiotic, adipokines, alcohol liver diseases, gut-liver adipose tissue

Host microbe interactions

Flash Talk

HMI-1: Metagenomic approaches to unravel Antimicrobial peptides from the zebrafish gut

Aishwarya S *, Gunasekaran K

[1]Department of Bioinformatics, Stella Maris College (Autonomous), Chennai-600086.

[2]CAS in Crystallography and Biophysics, University of Madras, Chennai- 600025.

E-mail: aishwaryasbioinfo@gmail.com

Recently efforts have been taken for unravelling mysteries between host-microbe interactions in gut microbiome studies of model organisms. Co-existence and the co-evolution of the microorganisms is the significant cause of the growing antimicrobial menace. Development of antimicrobials that act on the resistant microbes is favored by tapping them from the natural resources, preferably the gut of the most closely related animal model. In this study, we employed metagenomics approaches to identify the large taxonomic genomes of the zebrafish gut. About 256 antimicrobial peptides were identified using gene ontology predictions from Macrel and Pubseed servers. Upon the property predictions, the top 10 antimicrobial peptides were screened based on their action against many resistant bacterial species. Molecular modelling including docking and dynamics, were performed to estimate the antimicrobial peptides' binding against the target- putative nucleic acid binding lipoprotein. One specific antimicrobial peptide with the sequence "MPPYLHEIQPHTASNCQTELVIKL" showed promising results with 53% hydrophobic residues and a net charge +2.5, and docked against the target efficiently. The study is the first that unravels potential antimicrobial peptides from the zebrafish gut.

Key words: Antimicrobial peptides; Zebrafish; Metagenomics; Molecular docking; Peptide dynamics.

HMI-2: Phenotypic and genotypic identification of Phosphate solubilizing bacteria with PGPR activity and their efficiency on the growth of Banana

Chandni Shah, R. B. Subramanian *

Post Graduate Department of Biosciences, Sardar Patel University, Satellite Campus, Vadtal Road, Vallabh Vidyanagar, Bakrol-388 120

E- mail: promat103vans@gmail.com

Application of PSB along with PGPR activities as biofertilizer increase the availability of phosphate and other metabolites uptake for growth of plant without degrading the environment like chemical fertilizer. In the present study from the rhizospheric soil of banana, total seven PSBs were isolated based on Phosphate Solubilizing Index (PSI). Three isolates were selected and characterized for PGPR activities. According to the molecular identification, bacterial strains belonged to Bacillus stratosphericus, Bacillus haynesii, and Staphylococcus pasteuri as PSB01, PSB02, and PSB03 respectively. Out of them, B. stratosphericus and S. pasteuri were noted for the highest P solubilization activity in PVK broth 21.387±0.154-27.203±0.154 um/ml, with 35 carbohydrate utilization by Hi-carbohydrate TM Kit and other PGPR activities. Therefore, these two isolates were selected to study their effect on the Banana plant for pot experiment under natural (unsterile) soil condition. After the incubation period of 70days, Biochemical and morphological parameters were recorded. From the parameters, PSB03 (S. pasteuri) significantly enhances the growth of the plant in comparison to both PSB01 and uninoculated control. The biochemical parameter carbohydrate for T3 ranges 0.334±0.002mg/ml, protein 15.97±0.100mg/ml, Phosphate 58.50±0.11um/ml and Chlorophyll 103.32±0.35 in compare to control range C 0.246±0.003mg/ml, P 10.62±0.08mg/ml, phosphate 31.02±0.02um/ml and Chlorophyll 58.87±0.49.

Key words: Phosphate solubilizing bacteria; Plant growth-promoting microorganisms; Biofertilizers; Hi carbohydrate kit.

Flash Talk

HMI-3: Recombinant surface layer protein of *Lactobacillus helveticus* inhibits the binding of enterotoxigenic *E. coli* to human intestinal cell line

Ritu Choudhary [1, 2]* and Jai. K. Kaushik [1]

[1.]Animal Biotechnology Centre, ICAR-National Dairy Research Institute, Karnal

[2] School of Science, Indrashil University, Rajpur, Mehsana 382740 India.

E-mail rituchoudhary8nov@gmail.com

Probiotic bacteria adhere to host gastro-intestinal tract and inhibit the pathogen binding by acting as a physical barrier. Preliminary studies suggest that probiotics interact with host GIT through their surface proteins. So we hypothesized that purified recombinant surface layer proteins might be interacting with intestinal cell line and would inhibit the adhesion of enteric pathogens to epithelial cells as probiotics do.. 1.2 kb surface layer protein gene (slp) of Lactobacillus helveticus was cloned in E. coli. The 45 kDa recombinant protein was expressed and purified. Immunofluorescence assays were used to analyse the binding of the protein with human intestinal cell line, Caco-2. Inhibition of enterotoxigenic E. coli (ETEC) binding to Caco-2 cells by Slp was investigated. slp gene was successfully cloned, expressed and purified to homogeneity. Slp showed good binding with human intestinal cell line, Caco-2. Slp was found to inhibit the adhesion of enterotoxigenic E. coli (ETEC) binding to Caco-2 cells by approximately 78%. Recombinant slp of Lactobacillus helveticus could be used as nutraceutical as well as for developing into alternative molecules to fight gastrointestinal tract infections as it is found to inhibit the binding of enteric pathogen to the human intestinal cell line.

Keywords: Lactobacillus helveticus, enterotoxigenic, Caco-2

HMI-4: Role of Probiotics and Anti-glycative Compound in Prevention of Diabetic Nephropathy

Kirti Parwani, Farhin Patel, Dhara Patel , Dhruvi Patel Mehul Solanki and Palash Mandal*

Department of Biological Sciences, P. D. Patel Institute of Applied Sciences, Charotar University of Science and Technology, Changa-388421, Gujarat, India.

E-mail palashmandal.bio@charusat.ac.in

Hyperglycaemia has an important role in the pathogenesis of diabetic complications by increasing protein glycation and further accumulation of advanced glycation end products (AGEs) in body. AGEs are accompanied by increased free radical activity that contributes to bimolecular damage in diabetes. It is evidenced that interaction of AGEs with RAGE alters, gene expression, by increase in various pro-inflammatory cytokines and free radicals that contribute towards the pathobiology of diabetic complications. There is considerable role of anti-glycation compounds (AGC) because of their therapeutic potential. There is also evidence that AGEs can promote gut microbial growth which leads to gut dysbiosis which results into gut permeability. Studies have shown that probiotics can repair gut barrier and hence it may increase insulin sensitivity and helps in controlling glycemic index in body. Consequently, we hypothesize that probiotics and AGC help in maintaining blood glucose level and hence may prevent AGEs formation, which can further prevent the diabetic nephropathy (DN).

Keywords: Hyperglycaemia, anti-glycation compounds, diabetic nephropathy

HMI-5: Copper induces pleomorphic structures in *Sinorhizobium meliloti* 1021 altering *ctr*A gene expression

Murali Sharaff*, Jigisha V Vivadiya, Aakash K Varma

Department of Biological Sciences, P. D. Patel Institute of Applied Sciences, Charotar University of Science and Technology, Changa-388421, Gujarat, India.

E-mail: muralisharaff.bio@charusat.ac.in

Sinorhizobium meliloti 1021 (sm1021) is a gram-negative soil bacterium known to infect the Medicago species to induce symbiotic rhizobium legume associations for fixing atmospheric nitrogen. During these symbiotic interactions several signalling genes and transcriptional regulators were orchestrated for successful rhizobium invasion and nodule formation. Copper (Cu) is an essential micronutrient for plant growth and acts as cofactor for microbial enzymes at optimum concentration but it becomes toxic to when it exceeds its limit. Cu is an oxidizing agent which causes oxidative damage to the cell by the production of reactive oxygen species. Copper is known to inhibit the growth of soil microflora affecting the crop yield, due to its exceeding concentration by urbanisation and industrialisation. Our earlier studies have shown that Cu affects the growth of *Medicago truncatula* and sm1021 growth. In the current study Cu has induced certain morphological changes in sm1021 exhibiting pleomorphism mimicking to the bacteroid like structure present in legume root nodules. In sm1021, although bacteroid like structures are formed they were found to be non-functional (no change in BacA expression). In fact Cu stress has altered the master cell cycle regulator ctrA to induce pleomorphism. Additionally oxidative stress responsive genes (sodC, kat A) andRNA chaperon hfq were induced positively in sm1021 cells to confer resistance against Cu stress.

Keywords: Sinorhizobium meliloti, Copper, Medicago truncatula

Flash Talk

HMI-6: Potential of a marine *Pseudomonas aeruginosa* strain OG101 to combat *Fusarium oxysporum* associated wilt in legume crops

Keyur Patel[1], Ujawala Makwana [1] , Kinjal Parmar [1], Jinal Badrakia[1] , Pinakin Dhandhukia[2] and Janki N. Thakker [1]*

[1.]Department of Biotechnology, PD Patel Institute of Applied Sciences, CHARUSAT University, Changa-388421, Gujarat, India.

[2.]Department of Microbiology, Sheth P T Mahila College of Arts and Home Science, Veer Narmad South Gujarat University, Athwa Gate, Surat, Gujarat 395001.

E-mail: jankithakker.bt@charusat.ac.in

The continuous and overwhelming activity of humans releasing greenhouse gas (GHG) into the atmosphere causes additional warming and long term changes in climatic components that lead to a direct or indirect effect on the ecosystem. Changes in climate matters during crop season and it tractcan decrease the mean value of crop production. The present study focuses on the use of bacterial fertilizer and biocontrol agent for the better growth of pulseslike chickpea (Cicer arietinum) and cowpea (Vigna unguiculata) plant which helps to improve physical, chemical and biological health of the soil by fixing the nitrogen and reducing the addition of chemical fertilizers. Pseudomonas strain OG101 controls mycelial growth of Fusarium oxysporum f.sp. ciceris and F. oxysporum f.sp. pallidoroseum up to 24.4% and 20.5%, respectively. In addition, OG101 showed a significant improvement in the germination index of 93.3% and 98.3% with disease index of 1.6% and 3.3% in chickpea plant and cowpea plant, respectively. Pot experiments of chickpea and cowpea plants refer to use it as a seed bacterization for the best effect for growth promotion and its biocontrol activity against F. oxysporum f.sp. ciceris and F.oxysporum f.sp. pallidoroseum respectively.

Keywords: Biocontrol; Biofertilizer; Pulses; wilt; disease index; germination index; Chickpea; Cowpea.

HMI-7: Potential of *Brivibacillus* Strain as Plant Growth Promoting Bacteria in Rice (*Oryza sativa L.)* Crop

Pavan K. J [1] , Naveen Kumar M [2] and Prakash K.K [1]

[1].Dept. of Biotechnology and Microbiology, GM Institute of Technology, Davanagere,

[2].Dept. of Biotechnology and Genetics, Ramaiah College of Arts, Science and Commerce, Bengaluru

E-mail : prakashkk@gmit.ac.in

Rice crop yield is affected by ecological and heritable factors. The use of chemical fertilizers has commanded lot of environmental destruction and has been toxic to many living things. The chemical fertilizer leads to soil erosion and this in turn leads to ecological imbalance. The use of natural or bio fertilizer is one of the best methods to prevent the degradation of soil and reduce the level of soil pollution. The plant growth and its tolerance to various biotic and abiotic factors can be improved by the bio fertilizers. The bio-fertilizer is the use of live microorganisms which help in proper growth of the plants. The bacteria used are called Plant Growth Promoting Bacteria. The bio fertilizer in turn is available at low cost and is very convenient for the environment. Present study reveals that the efficacy of Brivibacillus sp. Biofertilizer showed significant difference in performance and plant vigour compared to untreated plants.

Keywords: Brivibacillus, Bio fertilizer, Yield, carrier material

HMI-8: Allelochemical mediated protection and growth stimulation of Vigna radiata plants during Podosphaera xanthii attack

Nidhi Patel and Anamika Jha *

Department of Biological Sciences, P. D. Patel Institute of Applied Sciences, Charotar University of Science and Technology, Changa-388421, Gujarat, India.

E-mail: anamikajha.bt@charusat.ac.in

Allelochemicals are the secondary metabolites produced by living organisms such as plants, animals or microbes that are not necessary for their primary metabolic functions. Asafoetida (hing), an aromatic gum-resin is a kind of allelochemical from the genus Ferula that has been widely used as flavors in the household cooking. Vigna radiata (Mung bean) is the most susceptible plant for infection with the fungus, Podosphaera xanthii that cause powdery mildew disease in these plants reducing yields by more than 40% in conducive seasons, when established well before flowering. Plants can be infected at any stage of growth, when air-borne spores land on the plant surface and germinate. The fungus then extends its haustoria into the leaf epidermis, developing chains of spores from fungal strands, resulting in the white, powdery growth on infected tissues. Most of the research work mentions the medical applications of Asafoetida on human beings like anti-spasmodic, anti-inflammatory, anti-viral and antibiotic effects, but limited plant applications have been explored. Thus, the study focused on evaluating the possibilities of hing application in controlling Podosphaera xanthii attack and eventually stimulating the growth of Mungbean plants in a better way. The Mungbean plants were challenged with a range of hing solutions alongwith standard reference of Neem oil. Asafoetida demonstrated its ability in protecting mungbean plant growth when tested in vitro and in planta. 1500-3000ppm was found to be the optimum concentration range of Hing which reduced the Podosphaera xanthii infestation and increased mungbean growth. Plant growth was recorded in terms of plant height, plant weight and chlorophyll content. The present study results may open a new avenue to use the plant based allelochemicals for effective control of Podosphaera xanthii and stimulate Mungbean productivity.

Keywords: Allelocehmical, stimulation, Mungbean

HMI-9: Isolation and characterization of root associated bacteria from *Curcuma longa* plant and its antibacterial activity

Divyesh K Patel[1] , Dr. Anoop Markande[2]

C.G. Bhakta Institute of Biotechnology, Malibacampus, UkaTarsadiaUniversity, GopalVidyanagar, Bardoli- MahuvaRoad, Tarsadi, Surat(Dist) 394350, Gujarat, India.

E-mail: anoopmarkande@gmail.com

Those microorganisms which grow in, on or around plant root and influence healthy plant growth and yield are known as plant growth promoting Rhizobacteria (PGPR). These microorganisms can act and parasitize on other harmful condition or microorganisms' populations by antagonistic behavior. Curcumin, the active ingredient of turmeric, is known for its antioxidant, anti-inflammatory, anti-fatigue, antiparasitic, antiallergic, anti-microbial, anti- mutagenic and anticancer properties. It exhibits wide therapeutic potential due to the multi targeting nature against variety of different cancers. Microbes are also associated with medicinal plant roots which have antimicrobial activity. This study involves isolation and characterizations of root associated bacteria with their applications in therapeutics and used of this potential novel isolate for potential PGPR activities. After bacterial isolation, screening was done by observing inhibition against four different well known pathogens (*E. coli*, *S. aureus*, *B. cereus*, and *P. aeruginosa*).

Keywords: Curcuma longa, antibacterial activity, PGPR

Flash Talk

HMI-10: Amelioration of obesity by probiotic fermented milk in high-fat-diet induced obese rat model

Shrushti Makwana*, J.B.Prajapati and Subrota Hati

Dairy Microbiology Department, SMC College of Dairy Science, AAU, Anand-388110.

E-mail: shrushti.makwana.sm@gmail.com

The present study was planned to test the hypothesis that probiotic bacteria have a significant role to play in modulation of obesity using Wistar rats. Obesity was induced through feeding High Fat Diet (HFD). The rats were divided into four group's viz., normal pellet diet fed (NC), HFD fed (DC), HFD fed rats treated with probiotic fermented milk with Whey protein concentrate (WPC) and Soy protein isolate (SPI) (T1), HFD fed rats treated with probiotic fermented milk without WPC and SPI (T2). Daily administration of the probiotic fermented milk products @ 2 ml/day for 4 consecutive weeks caused a significant ($p<0.05$) decrease in body weight, liver, abdominal fat weight, as well as serum Alanine aminotransferase and Alkaline phosphatase level. Whereas, Aspartate aminotransferase and C-reactive protein levels were not altered at significant extent. The histology of liver from the disease model group showed widespread lipid vacuoles deposited inside the parenchyma cells. Product T2 showed lesser micro vesicular fatty changes and the appearance of T2 was better than T1. Overall, the in vivo study results indicated that the test product exerted better anti-obesity activity.

Keywords: Obesity, Probiotic, fermented milk

Flash Talk

HMI-11: Uncover the role of *Osmium tenuiflorum* (Tulsi) for virus induced influenza using network pharmacology

Komal Tilwani, Gayatri Dave *

Department of Biological Sciences, P. D. Patel Institute of Applied Sciences, Charotar University of Science and Technology, Changa-388421, Gujarat, India.

E-mail: gayatridave@charusat.ac.in

Ocimum sanctum (Tulsi) is perennial herb that has culinary and medicinal applications. Ayurveda has narrated its application in treating various ailments. The present study investigates the chemical interaction of Tulsi components with cellular targets. To achieve that, the network pharmacology approach was adopted. The network pharmacology studies facilitate the structural diversity of the traditional herbs to explore the mechanism action. To elucidate the impact of tulsi extract on common and virus induced influenza network-based screening was used. The targets were selected through literature survey and were further investigated for their interaction with virus induced influenza targets. The targets are associated to the various cellular functions such are cell growth and apoptosis. The study shows the scope of *Osmium tenuiflorum* (Tulsi) as a treatment option for Virus-induced Influenza. Our preliminary In-silico network-based screening approach shows that Apigenin (Tulsi component) can exert the anti-viral activities through regulating the targets like CFTR and Akt.

Keywords: Tulsi; Influenza; Apigenin.

HMI-12*: Pseudomonas aeruginosa* Predominates as Multifaceted Rhizospheric Bacteria with Combined Abilities of P-solubilization and Biocontrol

Vaishnawi Gupta, Aditi Buch*

Department of Biochemistry, P D Patel Institute of Applied Sciences

Charotar University of Science and Technology (CHARUSAT), Changa, Gujarat.

E-mail: aditibuch.biochem@charusat.ac.in

Use of multifunctional plant growth promoting rhizobacteria (PGPR) for managing plant growth and health could not only facilitate higher positive effects on plants but also enable their predominant rhizospheric prevalence. While multi-functional PGPR are common, those harbouring both direct and indirect traits of growth promotion are relatively fewer. The present work aimed at isolating and characterizing the otherwise unusual multipotential PGPR with P-solubilizing ability in combination with broad-spectrum biocontrol abilities from diverse soils and analysing their relative prevalence. Primary screening yielded 50 isolates with varying P-solubilizing potential; of which only 8 showed *In vitro* antibiosis of *E. coli*. Selected 14 isolates with varying degree of P-solubilizing and antibacterial potential were evaluated for siderophore, HCN and indole-3-acetic acid (IAA) production. While all selected isolates produced HCN, 13 of them produced IAA and 10 showed siderophore production, at varying levels. Biochemical characterization of these isolates indicated that siderophore production was maximum with fluorescent *Pseudomonas* isolates while isolates of *Enterobacteriaceae* family were best IAA producers. However, molecular characterization of isolates capable of efficient P-solubilisation along with strong ability to exhibit all the three biocontrol traits, identified them as *Pseudomonas* spp., typically *P. aeruginosa*. Overall, these results indicate that categorically *P. aeruginosa* species are likely to predominate as rhizobacteria with co-existence of discrete abilities to solubilize P as well as produce IAA, siderophore and HCN. The study also implies relatively higher metabolic versatility of *P. aeruginosa* species as compared to other members of fluorescent *Pseudomonas* family; thus, accounting for their rhizospheric abundance.

Keywords: Indole acetic acid, Siderophores, Pseudomonas aeruginosa

HMI-13: Social Interactions between the variants in a biofilm during antibiotic stress

Veena G Nair, Sandeep Miryala, C.S. Srinandan

Biofilm Biology Lab, Anusandhan Kendra-2, School of Chemical & Biotechnology,

Centre for Research in Infectious Diseases, SASTRA Deemed to be University,

Thanjavur 613401, Tamil Nadu, India

E-mail: srinandan@gmail.com; srinandan@scbt.sastra.edu

Uropathogenic Escherichia coli (UPEC) is the major cause of urinary tract infections (UTI) inboth community and health care settings. UPEC strains possess a superfluity of both structural and secreted virulence factors that contribute to their capacity to cause infection. Biofilm formation in UPEC are the major cause of chronic and recurrent urinary tract infections (rUTI). Bacterial subpopulations within biofilms have competing interests and needs. Deciphering the mechanisms of interactions within these microbial communities shows how bacteria can cooperate with each other to sort out a form of social conflict. The mechanism of biofilm to stress does not evolve from a specific gene or from a first-rated cell type, it emerges from the zestful of the community. In this poster, we will discuss the social behaviour between the biofilm variants of UPEC with response to the antibiotic stresses

Keywords: UPEC, rUTI, antibiotic stresses

HMI-14: A Study on Community Acquired Bacterial Pneumonia (CAP): Characterization of Bacterial Pathogen and Antimicrobial Resistance Patterns

Jignisha S Patel*, Dr. Jignaben P Naik

Department of Microbiology & Medical Laboratory Technology,

Shri J S Bhakta & Shri K M Bhakta Arts, Shri A N Shah Science and Shri N F Shah Commerce College (Veer Narmad South Gujarat University), Surat, Gujarat, India

E-mail:: jignisha.r@gmail.com;

Globally, pneumonia is a serious public health concern and a major cause of mortality and morbidity and development of antibiotic resistance becomes a great concern for all. Total 134 sputum samples and 16 throat / nasopharengial swabs were collected from the patients having pneumonia or lower respiratory tract infection from August 2019 to November 2020. Bacterial pathogens were isolated and identified and their antimicrobial resistance patterns were studied from the clinical samples. At least one organism was detected from 115 cases (77%). 27 samples (18%) showed the polymicrobial growth. 8 samples (5%) showed no bacterial growth on culture media. *Klebsiella* spp. was the commonest organism (22%) identified, followed by *E.coli* (11 %), *Pseudomonas* spp. (9%) and *Citrobacter* spp. (9%). Majority of the organisms were resistant to Amoxyclave (Amoxicillin/ Clavulanic acid). >50% resistance against all the major antibiotics was seen for *Acinetobacter* spp. Isolated in this study. Cefuroxime and cotrimoxazole resistance were found in almost 50% of the organisms isolated. Majority of isolated Klebsiella spp. were resistant to 3rd generation cephalosporins. *Pseudomonas* were resistant to Aztreonam and Cefotaxime (Cephotaxime) (50%). *E.coli* were resistant to 3rd generation cephalosporins and to some extent, to ciprofloxacin (79%) also.

Klebsiella spp. was the commonest organism in community acquired pneumonia followed by *E.coli*, *Pseudomonas* spp. and *Citrobacter* spp. Penicillin, cotrimoxazole and even third generation cephalosporins, ciprofloxacin resistance was found in patients suffering from pneumonia in this part of country.

Key words: Community acquired pneumonia, bacteriological profile, resistance pattern