iGEM IIT-Madras

Department of Biotechnology
Bhupat and Jyoti Mehta School of Biosciences

BIOTECH LAB DAY

SEPTEMBER 14TH, 2019

SCHEDULE

9-9.30AM	Inauguration	
9.30-9.50AM	Piyush Gupta	Prof. Rama S Verma
10-10.20AM	Prof. Athi N. Naganathan	Prof. Athi N. Naganathan
10.20-11AM	TEA BREAK	
11-11.20AM	Anisha Ashok	Prof. A Gopala Krishna
30-11.50AM	Muthu Dhanraj	Prof. Anju Chadha
12-1PM	LUNCH	
1-1.20PM	Meenakshi J	Prof. R Baskar
1.30-1.50PM	Samyukta	Prof. Smitha Srivatsava
2-2.20PM	Vignayanandam R. Muddapu	Prof. V Srinivasa Chakravarthy
2.30-2.50PM	Malavika	Prof. Karthik Raman
2.50-3.30	TEA BREAK	
3.30-3.50PM	Prof. Nirav Bhatt	Prof. Nirav Bhatt
4-4.20PM	Vinay Kumar	Prof. Anju Chadha
4.30-5PM	Ashley Xavier	Prof. Himanshu Sinha

PROF. RAMA S VERMA

Metal-Free Semi-Aromatic Polyester Nanomaterial: A Novel Tumor Targeting Drug Delivery Vehicle for Potential Clinical Applications

Polyester nano materials have played a significant role in drug delivery in recent years due to their broad applications. However, there are few concerns related to their toxicity. Polyesters are mostly synthesized by a ROCOP reaction using different monomers and organo-metallic catalysts. The use of metal compounds can be toxic to living systems, if not handled properly. This study for the first time reports the synthesis of metal-free semi-aromatic polyester (SAP) nano material for drug delivery and evaluates its *in vivo* acute and systemic toxicity for clinical applications. Our study suggest that this metal-free SAP nanomaterial can be used in clinical applications.

Presentation by Piyush Kumar Gupta

PROF.ATHI N. NAGANATHAN

Protein Folding and Dynamics: Working at the Interface of Physics, Chemistry and Biology

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Protein folding is the process by which an unstructured polypeptide chain attains a folded but functional conformation. Understanding protein folding, dynamics and mechanisms have a direct impact on predicting three-dimensional structures from sequences that is considered as one of the holy grails in Biochemistry. My research group employs a highly interdisciplinary approach involving experimental spectroscopic measurements, functional studies, simulations and theoretical modeling to understand and manipulate the basic energetic and entropic factors governing the folding of proteins, with implications in protein design and engineering.

Presentation by Athi N. Naganathan

PROF. A GOPALA KRISHNA

Molecular Mechanism of Signaling by Human APJ Receptorspace

An insight into the ligand-binding, mechanism of activation and downstream signaling of GPCRs is important as they are involved in various physiological processes. GPCRs form the targets of >50% of the currently available drugs in market. Due to their structural flexibility and large hydrophobic regions, GPCR crystallization has always persisted as a big challenge. Hence, mutational studies have been the only hope to scrutinize GPCRs. Here, we had chosen human APJ Receptor (APJR) as a model to understand GPCR ligand binding and activation mechanism.Like other GPCRs, APJR also exhibits signaling bias – G-protein dependent and β-arrestin dependent pathways.In our current study, conserved amino acids in the extracellular domains have been mutated and analyzed using functional assays for both G-protein and β-arrestin mediated signaling. Mutant receptors demonstrated receptor internalization, β-arrestin2 activation and Ca2+ release to varying extents. Hence, the importance of these residues in modulating receptor conformational changes on ligand interaction and thereby, aiding activation of different downstream effectors can be evidently understood.

Presentation by Anisha Ashokan

PROF. ANJU CHADHA

A microbe from the coast of Tamil Nadu produces DHA can be used for global consumption: Studies from the lab to scaling up

Docosahexaenoic acid (DHA), an omega-3 fatty acid, is a high value nutraceutical extensively present in the nutrition supplements of feeding mothers and infants. It acts as an anti-inflammatory agent and is a potent therapeutic agent for Alzheimer's disease. In situ synthesis of DHA is minimal and does not meet the nutritional requirements in the human body. Hence, it is considered as an essential omega-3 fatty acid. Traditional source for DHA i.e. fish oil is currently being replaced by microbial sources in order to avoid unpleasant odour, reduced risk of chemical contamination, ease of production and purification of the product. These microbial sources are predominantly isolated from the decaying leaves and soil samples of Mangroves. The obtained results look promising for a commercial scale up.

Presentation by Muthu Dhanraj

PROF. R BASKAR

Developmental Genetics Laboratory

Our lab works on mechanism of caffeine action on Dictyostelium, thyroxine signalling in Dictyostelium, the roles of telomerase reverse transcriptase, Monoamine oxidase A and adenosine-associated growth factor during development and influence of protein kinase C during growth of Dictyostelium.

Our lab also works on the model flowering plant Arabidopsis thaliana, using which we try to understand if the seed storage age and parental age at reproduction could affect the somatic mutation and meiotic recombination rates in their transgenerational progenies. We use a combination of detector lines, which allows the quantitation of different kinds of spontaneous mutations and meiotic recombination (MR) rates.

Presentation by Meenakshi J

PROF. ANJU CHADHA

SpacA microbe from the coast of Tamil Nadu produces DHA can be used for global consumption: Studies from the lab to scaling upe

Docosahexaenoic acid (DHA), an omega-3 fatty acid, is a high value nutraceutical extensively present in the nutrition supplements of feeding mothers and infants. It acts as an anti-inflammatory agent and is a potent therapeutic agent for Alzheimer's disease. In situ synthesis of DHA is minimal and does not meet the nutritional requirements in the human body. Hence, it is considered as an essential omega-3 fatty acid. Traditional source for DHA i.e. fish oil is currently being replaced by microbial sources in order to avoid unpleasant odour, reduced risk of chemical contamination, ease of production and purification of the product. These microbial sources are predominantly isolated from the decaying leaves and soil samples of Mangroves. The obtained results look promising for a commercial scale up.

Presentation by Vinay Kumar

PROF. SRINIVASA CHAKRAVARTHY

A theory of Neurodegeneration – Energy crisis as a basis

Neurodegenerative diseases, including Alzheimer's (AD), Parkinson's (PD), Huntington's (HD) and Amyotrophic Lateral Sclerosis (ALS), are the prominent class of neurological diseases currently without a total cure. They are characterized by an inexorable loss of a specific type of neurons. Efforts to treat these diseases are often limited by the fact that they tend to address any one pathological change like protein aggregation, mitochondrial dysfunction, glutamate toxicity, calcium load, proteolytic stress, oxidative stress, or neuroinflammation while ignoring others. To search for an integrative theory of neurodegenerative pathology, we hypothesize that metabolic deficiency in certain vulnerable neuronal clusters is the common underlying thread that links many dimensions of the disease. The current work is about presenting an outline of such an integrative theory in case of PD and discuss how an energy crisis precipitates excitotoxic loss of particular type of cells in the brain which leads to PD. We present a new perspective of neuro-degenerative diseases as metabolic disorders at molecular, cellular, and systems levels and novel disease-modifying therapeutic interventions.

Presentation by Vignayanandam R. Muddapu

PROF. KARTHIK RAMAN

Ratio-metric features used to predict novel driver genes from pan-cancer mutational data

High throughput technologies such as NGS, has resulted in a large amount of data to be generated especially in the field of cancer biology. Understanding the mechanism of tumorigenesis and the interactions of proteins in cancer pathways can be studied only after identification of driver genes that confer a selective growth advantage to the cell. The underlying characteristics of driver genes are not well understood, and the current methods are not able to predict them based on the data available. These genes are functionally classified as Tumour suppressor genes (TSG) and oncogenes (OG). In this study, we define novel features to improve classification of genes as TSG and OG. The pan-cancer model was further used to predict and classify unlabelled genes and to identify genes specific for tissues. Overall, our approach illustrates the challenges faced during the classification of TSGs and OGs and a method to surmount them, predicting potential novel driver genes for further experimental screening.

Presentation by Malavika Sudhakar