IISER TIRUPATI

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"Interdisciplinary Aspects of Disease Biology."

IISER Tirupati, January 3-5, 2026

SVICCAR

Conference Venue

Lecture Hall Complex

Jadavpur University

Indian Institute of Science Education and Research, Tirupati

Srinivasapuram, Yerpedu Mandal, Tirupati Dist, Andhra Pradesh, India – 517619

Session IV:	LH2	LH3
Chairpersons:	**Prof. Ganesh Nagaraju** IISc	**Prof. Rajesh Viswanathan** IISER Tirupati
4.45 - 5.05 PM	**Dr. R. Ilangovan,** University of Madras Hunt the WNT pathway to combat cervical cancer	**Dr. Pavithra Chavali** IISER Tirupati Building the cerebral cortex under stress
5.10 - 5.30 PM	**Dr. Biswarup Basu,** CNCI A Preclinical Study on Indian Phytopharmaceutical Mediated Mitigation Strategy for Taxol-Induced Peripheral Neuropathy and Diabetic Neuropathy	**Dr. Sudha Kumari** IISc Unusual contacts in unusual contexts: Cell biological mechanisms underlying
5.35 - 5.55 PM	**Dr. Arnab Ghosh** Rajiv Gandhi University Release of ERK-Inhibitor in the Hypoxic Zone by pH-Responsive Targeted Nanoparticle that Sensitize Gemcitabine in Pancreatic Cancer with Mutant K-Ras	**Dr. Sudipta Mondal** NIT Durgapur Enhancing the antimicrobial potency of antimicrobial peptides by small molecule adjuvants
6.00 - 6.20 PM	**Dr. Nilabja Sikdar,** NSF, Kolkata A multi-phase approach using supervised algorithms and clinical models to generate high-accuracy signatures for pancreatic cancer	**Dr. Vinod Kumar,** NIAB Placental Organoid Disease Model of Brucellosis
6.25 - 6.35 PM	**Tea Break**	
6.35 - 6.40 PM	**Revity Talk LH1**	
6.40 - 7.30 PM	**Cultural Programme LH1**	
7:30 - 9:30 PM	**Dinner**	

12. A multi-phase approach using supervised algorithms and clinical models to generate high-accuracy signatures for pancreatic cancer.

Akash Bararia[1], Agniswar Chakraborty[2], Gourav Ghosh[3], Debabrata Ghosh Dastidar[3], Sumit Mukherjee [4,5] and Nilabja Sikdar [1,6*]

[1]Human Genetics Unit, Indian Statistical Institute, Kolkata, India. [2] Department of Computer Science, Jadavpur University, Kolkata, India. [3] Guru Nanak Institute of Pharmaceutical Science & Technology, West Bengal, India. [4] National Cancer Institute, National Institutes of Health (NIH), Bethesda, Maryland, USA. [5]Department of Computer Science, Ben-Gurion University, Beer-Sheva, Israel. [6] Estuarine and Coastal Studies Foundation, Howrah, India.

Abstract:

Background: The in silico analyses provide evidence supporting the potential of methylation-driven differentially expressed genes as therapeutic targets across cancer types. This leads us to identify novel targets and their associated drug compounds for further progress towards pancreatic cancer treatment.

Objective: To identify targeted drugs based on methylation driven genes identified using bulk multi-omics data and single-cell level data to pinpoint important disease markers.

Methods: The workflow involves screening using the TCGA and ICGC databases, followed by validation with GEO datasets. The study employs supervised learning algorithms like kNN and random forests, and constructs a prediction model using adaptive LASSO-Cox regression. The process also includes pathway analysis, evaluation of survival status, and immune profile deconvolution, as well as multistage evaluation of the methylation driven genes. We conducted drug targeting and molecular dynamic simulations, taking into account genes of interest. Lastly, molecular docking and dynamics simulations were used to find out if the key MEDEGs could be utilized as drug targets.

Results: CD36, UGT1A1, TFF1, S100P, MUC13, CALHM3 and ANKRD44 were found to be top 7 methylation driven genes. The mutational profile was also documented along with pathway analysis, which showed concordance with our observation based on their significant enriched terms namely "Maintenance of Gastrointestinal Epithelium", and "Digestive System Homeostasis". CD36 had prognostic capabilities and was seen to significant in terms of survival and also showed significant immune dysregulation. Our novel findings suggest TFF1, S100P, and MUC13 were found to be associated with cell type specific expression as seen in single cell data and UGT1A1 was found to be suitable for probable drug targeting. CD36, UGT1A1, TFF1, S100P, and MUC13 showed concordance when observed at proteomics level and across other datasets. Apigenin-7-O-glucuronide emerged as the top binder for UDP-glucuronosyltransferase 1A1 (also known as UDP 1A1), forming stable complexes with favourable interactions. Catechin and epicatechin were identified as the best ligands for TFF1 and S100P, while rutin showed high-affinity binding to MUC13.