National Institute of Technology Rourkela

Departmental Seminar

Seminar Title	: Search for ovarian cancer biomarkers: An integrated bioinformatics and coordinated network analysis reveals clusters of differentially expressed genes and key hub gene
Speaker	: Prof. Samir Kumar Patra
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Venue	: LS Seminar Hall
Date and Time	: 21 Feb 2025 (17:00)
Abstract	: The progress in high-throughput genomic data and the emerging improvements in bioinformatics tools are useful for the discovery of potential biomarkers. Utilizing insights from bioinformatic analyses of genomic data, one can apply systems biology methods to improve the precision of diagnosis and prognosis of various cancers, including ovarian cancer (OvCa). Comparative analysis was performed on normal versus tumor samples utilizing advanced bioinformatics software and tools. Differential expression analysis was based on fold-change statistics, with Gene Ontology (GO) enrichment analysis and KEGG pathway enrichment analyses carried out using DAVID 6.8 software. The construction of the Protein-Protein Interaction (PPI) network for Differentially Expressed Genes (DEGs) employed the STRING database, while Cytoscape 3.9.1, along with the MCODE and CytoHubba plugins, facilitated network visualization, analysis, and module identification. Hub gene expression and overall survival were assessed using the KM plotter, and tumor staging for Ovarian Cancer (OvCa) patients was analyzed using GEPIA2. Additionally, the expression of hub gene proteins was investigated through immunostaining results in the Human Protein Atlas (HPA) database., hub genes were examined for single nucleotide variations, methylation status, and pathway activity. Validation of mRNA expression levels of hub genes was conducted through qRT-PCR analysis. A total of 607 Differentially Expressed Genes (DEGs) were identified, comprising 248 upregulated and 359 downregulated genes. Through Protein-Protein Interaction (PPI) network analysis, the top 20 candidate genes were selected. Notably, the genes BUB1B, CCNA2, MAD2L1, PRC1, TRIP13, and ZWINT demonstrated significant relevance in the prognosis of ovarian cancer. Six genes, namely BUB1B, CCNA2, MAD2L1, PRC1, TRIP13, and ZWINT—identified as functional hub genes, are likely involved in promoting tumorigenesis. With the exception of TRIP13, the protein products of these genes are functionally associated with the cell cycle. Targeting these genes may offer promising therapeutic strategies for the treatment of OvCa.