National Institute of Technology Rourkela

Departmental Seminar

Seminar Title	: Structural and Functional modification of Long Noncoding RNAs induced by Single Nucleotide Polymorphism
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Venue	: LS Seminar Hall
Date and Time	: 31 Jan 2025 (15:00 hrs)
Abstract	: Background: Long noncoding RNAs (lncRNAs) are the category of regulatory noncoding which are widespread throughout the genome. From recent research, they are found to be the key element for the functioning of cellular transcriptome. They execute most of the function by interacting with RNA Binding Proteins (RBPs). Genome wide association studies (GWAS) has reported that noncoding region of the genome includes a large number of the single nucleotide polymorphism (SNP), a mutational phenomenon where a single nucleotide is replaced by another nucleotide at specific genomic position. The noncoding RNAs are also emerged from the noncoding region of the genome. So, transcription of lncRNA containing SNP may lead to various detrimental diseases. This makes the SNP study crucial to decipher the possible mechanism behind the association among SNP, lncRNA, and RBP. Objective: In our study, the impact of SNP was investigated on the lncRNA configuration. Apart from that, SNP-induced RNA-RBP remodelling was also studied. Materials and Methods: For structural prediction of lncRNAs with or without SNP, softwares like RNA Structure, RNAFold and CentroidFold were employed. RBPs interacted with lncRNAs were obtained from Encyclopedia of RNA Elements (ENCORE) data analysis. MPRDock molecular docking was implemented to study RNA-RBP binding. Result and Conclusion: From in silico work, SNP-induced structural alterations are found in the lncRNA, which are validated by above mentioned RNA structure prediction softwares. RBPs interacting with lncRNAs were obtained by analyzing the published data acquired from the ENCORE. From molecular docking, the SNPs are found to be associated with the remodelling of RNA-RBP interaction. This ultimately affects the functions performed by lncRNAs. Therefore, the interconnection among SNP, lncRNA and RBP is essential to understand the underlying cellular mechanism of disease pathogenesis. Keywords: ENCORE, GWAS, lncRNA, RBP, RNA structure, SNP