National Institute of Technology Rourkela

Departmental Seminar

Seminar Title	: Single nucleotide polymorphism- a genetic mutation influencing the structural configuration and function of long noncoding RNAs
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Venue	: LS Seminar Hall
Date and Time	: 17 Mar 2025 (16:00 hrs)
Abstract	: Background: Recent studies have reported that long noncoding RNAs (lncRNAs) are inevitable for the functioning of cellular transcriptome. They are classified as the regulatory noncoding RNAs spanning throughout the genome. They take part most of the cellular functions through interacting with RNA Binding Proteins (RBPs). As the Genome wide association studies (GWAS) report suggested, most of the single nucleotide polymorphisms (SNPs) reside within the noncoding region of the genome, from where myriads of lncRNAs are emerged. SNP is a genetic mutation in which single nucleotide substitution occurs at specific genomic position. These SNPs are also associated with multiple diseases. So, transcription of lncRNA habouring SNP may lead to various pernicious diseases. This makes the SNP a pivotal element in determining the plausible mechanism of interconnection among SNP, lncRNA, and RBP. Materials and Methods: GWAS tagged SNPs were obtained from lncRNASNP2 database and sequences of lncRNAs were collected from Ensembl genome browser. Softwares like RNA Structure, CentroidFold and RNAFold were employed for structural prediction of lncRNAs with or without SNP. RBPs, binding to the SNP containing region of lncRNA, were obtained by analyzing the published data of Encyclopedia of RNA Elements (ENCORE). Through molecular docking, the interconnection of lncRNA and RBP was studied. Result: The in silico structural analysis have shown the SNP-induced structural alterations in the lncRNA obtained from above mentioned softwares. Analysis of published data, acquired from the ENCORE, have provided the RBPs binding to the SNP containing region of the lncRNA. From molecular docking, the SNPs have been found to exert influence on the RNA-RBP interaction. Conclusion: Impact of SNP on the structure of lncRNA ultimately affects the function executed by lncRNAs. Therefore, the interconnection among SNP, lncRNA and RBP is prerequisite to decipher the underlying molecular mechanism of disease pathogenesis. Keywords: LncRNA, RNA structure, SNP, RBP, ENCORE