National Institute of Technology Rourkela

Registration Seminar

Seminar Title	: The role of m6A Epitranscriptomic markers of glioma in oncogenesis and clinical outcome
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Venue	: Life Science office room
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Abstract	: In recent years, m6A RNA methylation has been considered an important epitranscriptomic modification in various pathological processes, including cancers. The m6A is dynamic and modified by a set of readers, writers and erasers. More than 140 RNA modifications have been discovered, and the most common one is N6- methyladenosine (m6-A). The m6A is enriched in the 3&rsquo UTR of RNA, which decides the RNA fate, localisation, splicing, nuclear export, and stability. Glioblastoma is an aggressive and deadly central nervous system tumour. The RNA modifiers are reported to regulate oncogenic properties and resistance phenotypes in various tumor models, including glioma. The downregulation of writers and erasers of m6A modifiers inhibits glioma growth. The present study will highlight the role of different RNA m6A modifiers and their role in glioma oncogenesis. This study empirically evaluates different RNA modifiers' roles in different glioma grades stratified by molecular subtyping. First we propose to evaluate the m6A modifier levels in different types and molecular subtypes of glioma, followed by whole transcriptome level differential m6A mRNA modifications and understanding the functional significance of such differential m6A modifications in glioma cell lines through functional assays. To date, 190 glioma tissue samples have been collected. As per the sample selection criteria, 85 glioma and 2 normal brain tissues were subjected to gene expression analysis of m6A writers (n=7), m6A erasers (n=2) and m6A readers (n=5). All m6A modifiers except METTL16 helped significantly distinguish WHO 2021 classification glioma subtypes, types, molecular and histological features, and glioma tissue types. The correlation, regression, and functional enrichment analysis provided the importance of these m6A modifiers based on the relative expression data. The clustering and dimensionality reduction of relative expression of m6A modifiers (2 clusters) and glioma samples (3 clusters) helped distinguish glioma subtypes and their clinical features. The western blot analysis of m6A writers (METTL3, METTL14 and WTAP) was performed for a few glioma samples and normal brain tissue samples. The global m6A level was performed for representative glioma and brain tissue samples. Further work in progress.