National Institute of Technology Rourkela

Departmental Seminar

Seminar Title	: KLF5/miRNA regulatory network modulates tumorigenesis by regulating EMT, DNA damage and apoptosis in TSCC
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Venue	: LS Seminar Hall
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Abstract	: Introduction Transcription factors (TFs) play pivotal role in regulation of gene expression and their altered expression leads to cancer development. Along with protein coding genes, TFs modulate expression of microRNAs (miRNAs). Dysregulations in these TFs/miRNAs regulatory network is crucial in understanding oncogenesis; however, it is poorly understood in tongue squamous cell carcinoma (TSCC). Objective Identification of key TFs/miRNAs regulating oncogenesis in TSCC. Investigating the role of TFs/miRNAs and their targets to decode their mechanisms of action in TSCC. Materials and methods We analyzed and obtained differentially expressed genes and miRNAs in TSCC. We selected TF, KLF5 based on its role in multiple cancer-related events. We validated the role of KLF5 in TSCC upon its overexpression by adopting different molecular assays, such as qRT-PCR, western blotting, confocal and fluorescence imaging. Results KLF5 expression is significantly downregulated in H357 and SCC9 TSCC cells. We predicted miRNAs regulated by KLF5, among which miR-203a is one of them, downregulated in TSCC. Further, overexpression of KLF5 reduces cell migration, and reduces the expression of mesenchymal markers like N-Cadherin, while increasing the expression of E-Cadherin in TSCC. Further, there was increased γH2AX, suggesting increased DNA damage upon KLF5 transfection. AO/EtBr staining, annexin V/PI apoptosis assay and western blot of apoptosis related genes- BAX and BCL2 confirmed KLF5 overexpression induces apoptosis in TSCC. Conclusion Upregulation of KLF5 inhibits cell migration and induces apoptosis. KLF5 induces expression of miR-203a, which in turn may exert its regulatory effects.