Insight into Traf2 and Nck-interacting kinase role as a potential target in Colorectal Cancer Progression: Analysis of Expression Profiling and Epigenetic Analysis

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Abstract

Colorectal Cancer (CRC) remains a significant global health burden, needing a better knowledge of its molecular underpinnings to develop more effective therapeutic methods. TNIK (Traf2 and Nck-interacting Kinase) has emerged as a key regulator in a variety of malignancies, including CRC, but its exact role and regulatory mechanisms are unknown. The present study aimed to characterise the TNIK expression pattern across colorectal cancer by identifying its level of gene expression in normal vs CRC conditions. These shed light on the genes that are overexpressed and underexpressed in CRC conditions. This is achieved by performing the differential gene expression analysis (DEG) to elucidate TNIK-associated signalling pathways and molecular changes that promote CRC progression. This extensive revealing of the significant upregulation of TNIK would suggest it as a potential prognostic marker. Furthermore, the effective regulation of TNIK in colorectal conditions could be achieved by analysing its DNA methylation patterns. Hence, we conducted an epigenetic analysis focusing on colorectal cancer to identify the differentially methylated regions (DMRs). The identification of the DMR is pivotal for understanding the clinical implications and disease biology. Additionally, DMR analysis would offer insights into the disease pathogenesis by identifying the potential epigenetic changes that disrupt gene expression and cellular processes. This informs the development of specific therapeutic techniques aiming at reversing aberrant DNA methylation and normal cellular function, with far-reaching implications for extensive disease management. Our comprehensive study on the DEG and DMR aids in the identification of candidate genes and regulatory elements that are dysregulated at both epigenetic and transcriptional levels. Furthermore, linking the changes in DNA methylation patterns to the gene expression provides important mechanistic definitions of the impact of epigenetic modifications affecting gene regulation and its contribution to disease development and progression.

Keywords: Colorectal Cancer, TNIK (Traf2 and Nck-interacting Kinase), Differential Gene Expression, DNA Methylation, Differentially Methylated Regions (DMRs), Epigenetic Regulation