Regulatory role of miR-9-5p disturbed in nucleoli-enriched fractions in protein expression and oncogenic pathways in clear cell renal cell carcinoma

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The prevailing type of kidney cancer, clear cell renal cell carcinoma (ccRCC), exhibits a noteworthy association between changes in nucleolar morphology and the advancement of the tumour. In contrast to healthy renal proximal tubule epithelial cells (RPTEC), aberrant expression of miR-9-5p in the nuclei of ccRCC-derived cell lines (786-0, Caki-1) has been identified in our prior research. This finding underscores the potential role of miR-9-5p in the pathogenesis of ccRCC. Employing synthetic miR-9-5p miRNA mimic transfection in Caki-1 cells, we conducted a proteomic analysis to observe changes in protein levels. Additionally, we assessed cell proliferation using the BrdU assay, viability through the MTT assay, and adhesion in both Caki-1 and 786-0 cell lines after miR-9-5p transfection. The results revealed that this miRNA stimulated proliferation in both cell lines and enhanced the viability of Caki-1 cells, with an increased proportion of cells entering early apoptosis following transfection. Proteomic analysis after transfection of Caki-1 cells with miR-9-5p showed an upregulation of 69 proteins and downregulation of 71 proteins, engaged in key oncogenic pathways such as ferroptosis, adherens junction, ErbB signalling pathway, and HIF-1 signalling pathways as demonstrated by KEEG analysis. These findings suggest that miR-9-5p plays a significant regulatory role in ccRCC tumorigenesis, affecting cancer cells proliferation, viability, and apoptosis probably through its impact on key oncogenic pathways, underscoring the potential of miR-9-5p as a therapeutic target in ccRCC treatment strategies.

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