CIRCULAR RNA QUANTIFICATION IN PROSTATE CANCER CELL LINES WITH MODIFIED EXPRESSION OF SELECTED MICRORNAS

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Prostate cancer (PCa) remains a major global health burden, being the most frequently diagnosed malignancy among men in nearly two-thirds (118 of 185) of the countries worldwide [1]. Increasing attention has been directed toward noncoding circular RNAs (circRNAs), as their aberrant expression has been reported in various types of cancer and linked to tumor development or progression [2]. Some circRNAs can function as microRNA (miRNA) 'sponges' or interact with RNA-binding proteins, thereby influencing gene expression [3]. However, the regulatory interplay between various circRNAs and miRNAs in PCa cells remains poorly understood.

The aim of this study was to quantify selected circRNAs (circFOXO3, circFAT1, and others) in PCa cells with experimentally modified miR-155 and miR-137 expression. Firstly, a miRNA mimetic approach was used to induce the expression of selected miRNAs in PCa cells lacking endogenous expression. cDNA obtained from these cells was then analyzed using quantitative PCR (qPCR) to assess circRNA levels. Divergent primers were designed and applied to specifically amplify circular transcripts, allowing reliable discrimination between circular and linear RNA forms.

Our preliminary results confirm successful detection of circFOXO3, circFAT1 and circHIPK3 in both PC-3 and LNCaP cell samples. Differences in circRNA expression levels were observed between PCa cells transfected with miRNA mimetics and control cells lacking the selected miRNA expression. Notably, miRNA modulation appeared to be associated with circRNA-specific expression patterns, suggesting that individual circRNAs may respond differently to altered miRNA levels.

In conclusion, these preliminary findings indicate that experimental modulation of specific miRNA expression is associated with detectable changes in circRNA expression in PCa cell lines, indicating a potential regulatory interplay between circRNA and miRNAs that may be relevant to PCa biology.

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