

## ABSTRACT

Prostate cancer is the second-leading cause of cancer-related deaths in males. Age, race, family history, smoking, lifestyle choices, and genetic and epigenetic factors are the major risk factors involved. MicroRNAs (miRNA) are short, naturally occurring non-coding RNAs that suppress translational expression of protein-coding genes. They have been found in diverse tumor types, demonstrating that various sets of miRNAs are typically dysregulated in various malignancies. The aim of the present study was to investigate the miRNA biomarkers in prostate cancer. miRNAs were selected using bioinformatics tools. 25 prostate carcinoma samples and 20 prostate healthy control samples were recruited from Shaukat Khanum Cancer Hospital Lahore. RNA was extracted using TRIzol method and cDNA was made. The miRNA expression profiling of selected miRNAs was done by quantitative real-time PCR. Malignant and non-malignant tissue samples did not significantly differ in the expression of miRNA-6756 and miRNA-3190, while non-malignant tissue expressed significantly higher miRNA-4482 and miRNA-3192 than the prostate cancer patients. miRNA-4482 and miRNA-3192 can be investigated further to be used as prostate cancer biomarkers.