

ABSTRACT

ERG is a transcription factor that regulates the proliferation of endothelial cells. The pathological role of *ERG* is associated with angiogenesis during metastasis of various cancers. It is hypothesized that angiogenesis can be prevented by down regulating *ERG* by using microRNAs (miRNAs). To validate this hypothesis, bioinformatics tools were used for finding microRNAs targeting 3'UTR of *ERG* and Venn diagram analysis was done to find out common target genes which were involved in angiogenesis. To study the expression of *ERG* and miR-361-5p and their target genes, breast adenocarcinoma cell line and breast cancer tissue samples were obtained and identified using H&E staining. Quantitative PCR (qPCR) was used for mRNA expression analysis. Results of bioinformatics analysis showed that miR-361-5p has its target site in 3'UTR of *ERG*, and Venn diagram analysis showed that they both regulate the angiogenic target genes. H&E staining results revealed three types of tissue samples; Normal Breast Tissue (NBT), Invasive Ductal Carcinoma (IDC) and Invasive Lobular Carcinoma (ILC). qPCR analysis showed elevated levels of *ERG* in all three cancer samples (breast cancer cell line, IDC, ILC) as compared to level of *ERG* in normal tissue sample, relative to levels of miR-361-5p. Whereas, miR-361-5p overexpression led to reduction in the expression levels of various genes of endothelial cell proliferation. From these results it is concluded that *ERG* can be targeted to stop cancer metastasis.