

ABSTRACT

miRNA are the molecules that are involved in regulating gene expression in the cells. The differential expression of various miRNAs is observed in cancer cases when compared to healthy controls hence, have the potential to act as biomarkers. Breast cancer is the most common cancer targeting the female population around the world and for early detection and efficient therapeutics; it is significant to identify potential biomarkers. The present study aimed to identify a set of differentially expressed miRNAs in breast cancer and their target genes. First of all, comprehensive bioinformatics analysis was performed on two GEO datasets “GSE121396” and “GSE20437”. DIANA Tool-mir path V.3, STRING, Cytoscape 3.6.0, Target Scan, Enricher, and Tarbase v8 were used for the identification of differentially expressed miRNA and their targets in breast cancer. Then the expression of these identified miRNA and their target genes were analyzed in breast cancer samples as compared to controls using quantitative PCR analysis. In the bioinformatics analysis, hsa-mir-205-5p was identified as differentially expressed miRNA in breast cancer which is shown to negatively regulate E2F1 expression in several cancers. mRNA expression analysis of hsa-mir-205-5p in breast cancer samples showed that it was significantly less expressed as compared to controls whereas E2F1 was over-expressed in breast cancer samples. This study concludes that hsa-mir-205-5p is a potentially significant target for regulating E2F1 expression in breast cancer.

Keywords: Breast cancer; miRNA; differential expression; E2F1; proliferation