Expression Analysis and Bioinformatics-Based Identification of miR-4534, miR-551a and miR-1294 in Breast Cancer

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ABSTRACT This study aimed to ascertain the potential role of specific microRNAs (miR-551a, miR-1238, miR-4534, and miR-1294) in breast cancer by analysing their expression levels and identifying the target genes and pathways they regulate. Expression levels in 82 samples from 41 patients were measured using quantitative Real-Time PCR. Bioinformatics tools were utilised to identify the potential target genes and pathways. Findings revealed that miR-1294 and miR-551a had significantly lower expression in tumour tissues compared to normal tissues, while miR-4534 was overexpressed in tumour tissues. No significant difference was observed in miR-1238 expression between the two. miR-1294, miR-551a, and miR-4534 were found to regulate genes associated with Mapk, ErbB, Hippo Wnt, EGFR, and P53 signalling pathways. The study concludes that miR-551a, miR-1294, and miR-4534 may play a role in the development of breast cancer.