ABSTRACT

Numerous genes have been identified that act as oncogenes or tumor suppressor genes in the development of human breast cancer. *p21*, basically a tumor suppressor, is a cyclin-dependent kinase inhibitor and it is well known for its dual role in cell cycle based upon its subcellular localization and its relation with other transcription factors. It is activated in response to different stress stimuli where it could act as a cell cycle suppressor but this gene can also show anti-apoptotic or pro-apoptotic functions depending upon the conditions being involved either in tumorigenesis or in tumor suppression. Different transcript variants and isoforms of *p21* are said to be involved in breast cancer progression. In this study, we aimed to determine the differential expression of these variants in different breast cancer samples. MDA-MB-231 cancer cell line and breast cancer tissue samples were available for the analysis of *p21*'s isoforms. cDNA synthesis by reverse transcription was followed after the RNA extraction from the samples. Quantitative PCR was done to analyze the differential expression of its variants. It was observed that the expression of *p21B* was said to be the highest among all 5 transcript variants of *p21* followed by the expression of *p21A, p21D, p21C* and *p21E* in tissue samples and *p21C, p21D, p21A* and *p21E* in cell samples, respectively. These results imply that p21 and its isoforms may have an important role in breast carcinoma but its prognostic significance is yet to determine.