Summary

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Around 1.35 million people of worldwide suffer from breast cancer each year, whereas in India, it has been seen that 1 in every 17 women is suffering from breast cancer. Mutation in Breast Cancer 1 (*BRCA1*) gene is accounted for the majority of breast/ovarian cancer families. The purpose of study is to provide prevalence of *BRCA1* germline mutations in North-East Indian population. The cytological and immunohistochemical reactions of the study were very helpful to design the molecular screening of the breast cancer patients. In relation to the personal history and family history with the breast cancer, the study has found mutations of 6.25% and 12.5% respectively. The three different types of mutations 185DelAG, 1014DelGT and 3889DelAG are found in North-East Indian population in exon 2 and exon 11 respectively, which results in protein truncation of *BRCA1* protein by forming stop codons individually at 39, 303 and 1265 position of amino acid. This also exaggerates medical researcher to do extensive mutation screening study of high risk breast cancer cases in North-East Indian population. It will provide better decisive medical and surgical preventive options for breast cancer patients.

To detect specific mutation in *BRCA1* without sequencing, critical denaturation (Tc) concept was applied with reference to sequenced data. The concept of Tc was elaborated from the COLD PCR technique. Based on sequenced data, we categorized the samples in to wild and mutant types. We determined appropriate critical denaturation temperature for each of both the categories through gradient PCR using single primer pair. We tested the amplification using determined Tc. We detect the mutant types in parity with the sequencing results. We propose that a strategic use of Tc, that we prefer to call Clever-Tc, can be applied to detect mutations in *BRCA1* cutting down the diagnostic cost.

In addition to mutations of Breast cancer 1 gene, tumor cell survival by toxification of numerous carcinogenic products is highly influential to breast

cancer. Metabolism and detoxification of environmental carcinogens are mostly carried out by *Glutathione S-transferase Theta1 and Mu1 gene (GSTT1 and GSTM1*). Female individuals lacking each of these enzymes have more chances to develop breast cancer due to reduction in removal of secondary organic oxidation products. The purpose of this study is to correlate the susceptibility of breast cancer 1 gene mutation by the polymorphism of *GSTT1* and *GSTM1* gene. We compared the sequenced data of breast cancer patients with the variation of the *GSTT1* and *GSTM1* gene. We used the Multiplex-PCR to investigate the variation of the *GSTT1* and *GSTM1* genes in fifty nine breast cancer patients and one hundred seven healthy control subjects. A significant contribution was found in between mutations of BRCA1 and polymorphism *GSTT1* and *GSTM1* in the risk of breast carcinoma (OR=1.60, P=0.02). The lack of the *GSTM1* gene was significantly associated with the poorer mutation rate (OR=2.29, P=0.03). This contribution was significantly higher in patients carrying both null-*GSTT1* and *GSTM1* genotypes. The gene polymorphism of GSTs may predict not only in the proliferation of breast cancer patients but also influence to the mutations in breast cancer 1 gene in breast cancer patients.