A SINGLE NUCLEOTIDE POLYMORPHISM IN THE 5' UNTRANSLATED REGION OF RAD51 IN BREAST CANCER

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The breast cancer suppressor proteins BRCA1 and BRCA2 interact with RAD51, which plays a central role in homology-dependent recombinational repair of DNA double strand breaks, a process that is essential for maintaining genomic stability. Therefore, genetic variability in the RAD51 gene may contribute to the appearance and/or progression of breast cancer. Preliminary reports suggest that a single nucleotide polymorphism in the 5’ untranslated region of RAD51 (a G to C substitution at position 135, the G/C polymorphism) may modulate breast cancer risk. We investigated the distribution of genotypes and frequency of alleles of the G/C polymorphism in breast cancer. Tumor tissues were obtained from postmenopausal women with node-negative and node-positive ductal breast carcinoma with uniform tumor size. Blood samples from age-matched healthy women served as the control. The G/C polymorphism was determined by PCR-based MvaI restriction fragment length polymorphism. The distribution of the genotypes of the G/C polymorphism did not differ significantly (P>0.05) from those predicted by the Hardy-Weinberg distribution. There were no differences in the genotype distribution and allele frequencies between the node-positive and node-negative patients. There were no significant differences between the distributions of genotypes in subgroups assigned to histological grades according to Scarf-Bloom-Richardson criteria and the distribution predicted by Hardy-Weinberg equilibrium (P > 0.05). Our study implies that the G/C polymorphism of the RAD51 gene may not be directly involved in the development and/or progression of breast cancer.

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