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Investigation of Methylenetetrahydrofolate Reductase C677T Polymorphism and Human Papilloma Virus Genotypes in Iranian Breast Cancer.

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Abstract

Breast cancer (BC) is the leading cause of death among Iranian women. Development of BC is a multistep process, arising from genetic changes such as methylenetetrahydrofolate reductase (MTHFR) polymorphism and infection with human papillomavirus (HPV). In this study, we investigated HPV genotypes associated with BCs and its relation with MTHFR C677T polymorphism for early detection of familial BCs. A total of 84 archival BC samples from Iran were collected. Verification of each cancer reported in a relative was sought through the pathology reports of the hospital records. Then, DNA was extracted from all samples by standard methods and HPV genotypes and MTHFR C677T polymorphism genotypes were analyzed using multiplex polymerase chain reaction (PCR) and amplification-refractory mutation system (ARMS)-PCR. Finally, data analysis was performed using version 7 of the Epi Info™ 2012 software and test chi-square (x2) for trend. The frequencies of the CC, TC, and TT genotypes of MTHFR (C677T) were 0.53, 0.38, and 0.09 in familial BC patients, and 0.46, 0.51, and 0.03, respectively, in nonfamilial BC patients. Furthermore, HPV DNA typing identified 29 infections and C677T TT genotype was significantly associated with an increased risk of familial BC in the study population. Our results demonstrate that infection with HPV was prevalent among Iranian women with familial BC. Finally, the testing of C677T GG genotype in combination with HPV genotyping as molecular markers can be helpful in the early diagnosis of Iranian familial BCs by PCR.

KEYWORDS: C677T polymorphism; MTHFR gene; breast cancer; human papilloma virus

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