Analysis of peptidyl-propyl-cis/trans isomerase 1 (PIN1) gene -842(G > C) and -667(T > C) polymorphic variants in relation to breast cancer risk and clinico-pathological parameters.

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Abstract

BACKGROUND: The purpose of this study was to investigate the association between the peptidyl-propyl-cis/trans isomerase 1 (PIN1) -842(G > C) and -667(T > C) polymorphic variants and breast cancer risk among Malaysian ethnic groups namely the Malays, Chinese and Indians, as well as clinico-pathological characteristics of the patients.

PATIENTS AND METHODS: The polymerase chain reaction-restriction fragment length polymorphism was used to genotype 357 breast cancer patients and 252 normal and healthy women who had no history of any malignancy.

RESULTS: The distribution of -842(G > C) and -667(T > C) genotypes and alleles frequencies between breast cancer cases and normal individuals showed lack of statistical significance among the Malays (p > 0.05), Chinese (p > 0.05) and Indians (p > 0.05), respectively. Multivariate logistic regression analysis showed that the Malay, Chinese and Indian women who were -842CC homozygotes (p = 0.198, 0.089, 0.620), -842GC heterozygotes (p = 0.492, 0.176, 0.577) and -842C allele carriers (p = 0.226, 0.059, 0.669), respectively, were not associated with breast cancer risk. Furthermore Malay, Chinese and Indian women who were heterozygous (p = 0.777, 0.319, 0.710) and homozygous (p = 0.964, 0.956, 0.954) for -667C allele or carriers of -667C allele (p = 0.977, 0.915, 0.830), respectively, were not associated with an increased risk of breast cancer. None of the -842C and -667C allele genotypes were significantly associated with the clinico-pathological characteristics.

CONCLUSION: Our findings suggest that the polymorphic variants of -842(G > C) and -667(T > C) genes may not appear to have an influence on breast cancer risk among Malaysian Malay, Chinese and Indian women.

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