

ANRIL Genetic Variants in Iranian Breast Cancer Patients

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DOI: 10.21859/mci-sup-70

Keywords:

ANRIL
Breast Cancer
Polymorphism

Abstract

Introduction: The genetic variants of the long non-coding RNA ANRIL (an antisense noncoding RNA in the INK4 locus) as well as its expression have been shown to be associated with several human diseases including cancers. The aim of this study was to examine the association of ANRIL variants with breast cancer susceptibility in Iranian patients.

Materials and Methods: In this case-control study, we genotyped rs1333045, rs4977574, rs1333048 and rs10757278 single nucleotide polymorphisms (SNPs) in 122 breast cancer patients as well as in 200 normal age-matched subjects by tetra-primer amplification refractory mutation system polymerase chain reaction (T-ARMS-PCR).

Results: The TT genotype at rs1333045 was significantly over-represented among patients (P=0.038) but did not remain significant after multiple-testing correction. In addition, among all observed haplotypes (with SNP order of rs1333045, rs1333048 rs4977574 and rs10757278), four haplotypes were shown to be associated with breast cancer risk. However, after multiple testing corrections, TCGA was the only haplotype which remained significant.

Conclusions: These results suggest that breast cancer risk is significantly associated with ANRIL variants. Future work analyzing the expression of different associated ANRIL haplotypes would further shed light on the role of ANRIL in this disease.