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Association of MIR146A rs2910164 Variation with a Predisposition to Sporadic Breast Cancer in a Pakistani Cohort

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Abstract : Single nucleotide polymorphisms (SNPs) in genes coding for microRNAs (miRNAs) play a pivotal role in the progression of breast cancer (BC). We investigated the association of miR-146a rs2910164 G/C polymorphism with the risk of BC in the Pakistani population. The miR-146a rs2910164 polymorphism was genotyped in 300 BC-cases and 300 age- and gender-matched healthy controls using T-ARMS-PCR. Genotype and allele frequencies were calculated, and the association between genotypes and the risk of BC was calculated by odds ratios (OR) and confidence intervals (95%). A significant difference in genotypic frequencies ($\chi 2=63.10$; $p \leq 0.0001$) and allelic frequencies (OR=0.3955 (0.3132-0.4993); $p \leq 0.0001$) was observed between cases and controls. Furthermore, we also found that miR-146 rs2910164 CC homozygote increased the risk of breast cancer in the dominant (OR=0.2397 (0.1629-0.3526); p=0.0001; GG vs GC+CC) and recessive (OR=2.803 (1.865-4.213); $P \leq 0.0001$; CC vs GC+GG) inheritance models. In summary, miR-146a rs2910164 G/C is significantly associated with BC in the Pakistani population. To our knowledge, this is the first study that assessed MIR146a rs2910164 G > C SNP in Pakistani population. By analyzing the secondary structure of MIR146A variant, a significant structural modification was noted. Study with a larger sample size is needed to further confirm these findings.

Keywords : breast cancer, MIR146A, microRNA, SNP
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