



Association between Selected microRNA SNPs and Breast Cancer Risk in a Vietnamese Population

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KEYWORDS rs11614913. rs6505162. rs2910164. Association Analysis. Breast Cancer Risk. Vietnamese

ABSTRACT MicroRNAs play a central role in the regulation and management of gene expression. miR-196a2, miR-423, and miR-146a were shown to regulate the protein expression in breast cancer signaling pathways. Known SNPs in these miRNAs (rs11614913, rs6505162, and rs2910164) have demonstrated their relationship with breast cancer risk in some populations. This study aimed to identify the association between three selected SNPs and breast cancer risk among Vietnamese women. The HRM and TAPMA genotyping methods were performed in 300 cases and 300 healthy controls, supporting the case/control analysis method. Statistical analysis showed two of three selected SNPs were associated with breast cancer risk in Vietnamese. CC genotype of rs11614913 (OR (95% CI) = 1.64 (1.15 – 2.35), P = 0.006) and CG genotype of rs2910164 (OR (95% CI) = 1.44(1.04 – 1.98), P = 0.027) significantly increase breast cancer risk. Haplotype analysis indicated that two haplotypes ((rs11614913T-rs2910164G-rs6505162A) and (rs11614913T-rs2910164C- rs6505162C)) strongly reduce the risk of the disease.