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THE PRE-MIR 27A VARIANT RS895819 MAY CONTRIBUTE TO BREAST CANCER RISK IN PAKISTANI COHORT

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MicroRNAs (miRNAs) are recently discovered major class of regulatory molecules that control gene activity by base pairing with target messenger RNA at the 3'-untranslated regions leading to their cleavage or translational repression. Matured miRNA sequences of the cluster (MIR23A: hsa-miR-23a-5p, hsa-miR-23a-3p), (MIR24-2: hsa-miR-24-2-5p, hsa-miR-24-3p) and (MIR27A: hsa-miR-27a-5p, hsa-miR-27a-3p) are involved in breast cancer (BC). In the present study, genes codding for miR-23a/24-2/27a cluster was screened for genetic mutation. Heterozygous (A/G allele) as well as homozygous (G/G allele) mutants were found in MIR27A in all screened BC patients samples. The detected SNP affects the size of the terminal loop of the precursor miRNA. The altered (C allele) hairpin structure resulted to be two bases longer than the wild-type (T allele) hairpin. The minimum free energies (MFE) were calculated to be the same for both the mutant and reference microRNA genes (-37.10 Kcal/mol). The free energy of the thermodynamic ensemble was -38.24 kcal/mol for reference and -38.40 kcal/mol for mutant microRNA. The frequency of the MFE structure in the ensemble was 15.62 % for reference and 12.20 % for mutant miRNA. The ensemble diversity was 4.41 for reference and 4.80 for mutant miRNA. The centroid secondary structure with a minimum free energy was -34.40 kcal/mol for reference and -34.10 kcal/mol for mutant miRNA. Genetic polymorphism rs895819 (A/G, G/G) exists in *mir-27a* gene and may be associated with breast cancer in Pakistani population.

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