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Methylation Analysis of PHF20L1 and DACT2 Gene Promoters in Women with Breast Cancer

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Abstract : Breast cancer (BC) is the most common tumor in women over the world. DNA methylation is an epigenetic modification critical in CpG sites, aberrant methylation of CpG islands in promoters is a hallmark of cancer. So, gene expression can be regulated by alterations in DNA methylation. In cell lines DACT2 gene reduces the growth and migration of tumor cells by its participation in the suppression of TGFb/SMAD2/3. PHF20L1 is involved in histone acetylation therefore, it regulates transcription. Our aim was to analyze the methylation status of the DACT2 and PHF20L1 promoter regions in tumoral and healthy mammary tissue from women with BC in different progression states. The study included 77 patients from Centro Medico Nacional La Raza in Mexico City. After identifying a CpG island in DACT2 and PHF20L1 promoters, DNA methylation status was analyzed through sodium bisulfite with subsequent amplification using methylation-specific PCR. Results revealed no changes in methylation status of PHF20L1 and cancer stages (II y III) or in comparison to healthy tissues, it was demethylated. DACT2 promoter methylation was no significant between tumoral stages (II, P = 0.37; III, P = 0.17) or with healthy tissue. Previous data reported DACT2 methylated in nasopharyngeal carcinoma but in this study promoter methylation was not observed. PHF20L1 protein contains N-terminal Tudor and C-terminal plant homeodomain domains, it has been suggested that can stabilize DNMT1 regulating DNA methylation, therefore, was associated with poor prognostic in BC. We found no evidence of methylation in patients and controls in PHF20L1 promoter, so its association with BC may have no direct relation with promoter methylation. More studies including other methylation sites in these genes in BC are necessary.

Keywords : bisulfite conversion, breast cancer, DACT2, DNA methylation, PHF20L1, tumoral status
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