

## GSTPI Promoter Methylation in Breast Cancer

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*Breast carcinogenesis is a multistep process, involving both genetic and epigenetic modification process of genes, ranging from DNA repair to metabolic processes. This study was undertaken to assess the role of promoter methylation of GSTP1 gene, a member of GST family of enzymes, in relation to breast cancer in Kashmir population. Further this promoter methylation of status of GSTP1 was checked in relation to polymorphism of gene and clinicopathological parameters of patient population. Tissue samples were taken from breast cancer patients and paired with their normal adjacent tissues. A total of 51 subjects were studied, in which the frequency of promoter methylation in cancerous tissue was 62.7% as against 11% in the normal tissues ( $p = <0.001$ ). Further, when compared with the clinical parameters the significant association was found between the promoter hypermethylation and lymph node metastasis, ( $p < 0.001$ ), tumor stage ( $p = 0.039$ ), tumor grade ( $p = 0.028$ ), Estrogen receptor status ( $p = 0.018$ ) and Progesterone receptor status ( $p = 0.046$ ). Our study is the first of its kind in kashmiri population, that indicates GSTP1 shows aberrant methylation pattern in the breast cancer. Further it also shows that the gene polymorphism (Ile105Val) at codon 105 is not related to the promoter methylation and the two occur independently in breast cancer.*