Research in Pharmaceutical Sciences, 2012;7(5)
School of Pharmacy and Pharmaceutical Sciences
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# Rapid quantitative determination of GSTP1 promoter methylation level using differential high resolution melting analysis (D-HRMA)

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**Background and Aims:** DNA methylation is one of the key regulators of gene expression. It also has an important role in carcinogenesis through epigenetic silencing of tumor suppressor and DNA repair genes. DNA hyper methylation in promoter region of glutathione S-transferase pi 1 (GSTP1) gene has been detected in a variety of cancers such as breast cancer. As studies show, GSTP1 promoter methylation status can be used as a prognostic and predictive factor in breast cancer. This study was designed to quantitatively determine the promoter methylation of GSTP1 gene in archival formalin fixed paraffin embedded (FFPE) tissues from breast cancer patients by differential high resolution melting analysis (D-HRMA) method.
**Methods:** Using D-HRMA technology, the methylation level of GSTP1 gene promoter was quantified in 98 breast cancer FFPE tissues and also 10 fresh frozen normal tissue samples.
**Results:** All the breast cancer samples were found to be methylated at the GSTP1 promoter region, with the average methylation level of 41.56% (range 3.93- 66.61%). The methylation level of normal samples was identified below 1%. Statistical analyses showed a significant correlation between the GSTP1 promoter methylation levels and cancer progression ($P< 0.001$). No significant correlation was observed between the methylation levels and patients' age and gender.
**Conclusions:** It is concluded that GSTP1 promoter methylation level can be used as a reliable and sensitive diagnostic and prognostic tool in breast cancer. Also D-HRMA is demonstrated as a robust, fast and cost effective method for quantitative evaluation of promoter methylation.

**Keywords:** Promoter methylation; GSTP1; High resolution melting