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Accurate monitoring of promoter gene methylation with high-resolution melting polymerase chain reaction using the *ABCB1* gene as a model

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ABSTRACT. Multidrug resistance is the major cause of cancer chemotherapy failure. This phenotype is mainly due to the overexpression of the human *ABCB1* gene. Several studies have shown that the transcriptional regulation of this gene is complex. Yet, the impact of this transcriptional regulation has not been well studied in a clinical setting. The acquired expression of *ABCB1* is associated with the genomic instability of cancer cells. This includes the occurrence of mutational events that alter chromatin structures through epigenetic modifications such as promoter methylation. Therefore, it is important to introduce new clinical methods to monitor the methylation status of *ABCB1* and determine its association with gene expression in order to be able to predict response to therapies. The high-resolution melting (HRM) method has emerged as a highly accurate and sensitive

method to quantify methylation status at specific sites of DNA. Here, we established HRM parameters to evaluate the promoter methylation status of the *ABCB1* gene. Our study is the first to standardize the HRM dissociation curve to evaluate *ABCB1* gene methylation. The association between *ABCB1* methylation status and gene expression in established cancer cell lines shows that this method is accurate and reliable.

Key words: *ABCB1*; HRM-PCR; Methylation; Epigenetics

