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Epigenetic effects on gene expression in lymphoma

DNA methylation is an epigenetic (modulation of chromatin organization without affecting the DNA sequence) modification with an important role in the control of gene expression in mammalian cells. Treatment of tumor cells with 5-aza-2-deoxycytidine (demethylating agent) and/or trichostatin A (deacetylase inhibitor) is known to restore expression of some genes in tumor cells. Control of expression is particularly important in genes that regulate the cell cycle, because some of these genes prevent the development and growth of tumors. For example, if a gene's purpose is to suppress tumors, it is essential for that gene to be expressed. This study examines gene expression in Non-Hodgkin's Lymphoma (NHL) cell lines before and after treatment with 5-aza-2-deoxycytidine and trichostatin A using the polymerase chain reaction (PCR). PCR allows amplification of a specific nucleic acid segment; in this case genes of interest are amplified for the purpose of quantification of expression. Quantitative Real-time reverse transcription PCR is used to quantify mRNA expression in a series of lymphoma cell lines. The *GAPDH* gene is used as an internal control to give a point of reference for the amount of total RNA in each cell line. The control for each gene is the untreated cell line. Gene expression in the control is compared with expression in cells treated with 5-aza-2-deoxycytidine and trichostatin A. 14 genes were studied in 4 cell lines. In genes known to be methylated and silenced in Non-Hodgkin's Lymphoma, there is a clear correlation between drug treatment and gene expression. Induction of expression is observed following treatment with 5-aza-deoxycytidine and trichostatin A.