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Title:	Methylation pattern of MGMT gene in relation to age, smoking, drinking and dietary habits as epigenetic biomarker in prostate cancer
Authors:	Singh, Jagdeep (/jspui/browse?type=author&value=Singh%2C+Jagdeep)
Keywords:	Biological marker Bisulfite Genomic DNA Methylated DNA
Issue Date:	2010
Citation:	Genetic Engineering and Biotechnology Journal, GEBJ-8 1
Abstract:	Epigenetic control of gene transcription is an important step for normal human development and cellular differentiation. Although altered methylation pattern is a well-defined epigenetic change linked to human cancers and other diseases, inter-individual epigenetic variation and cancer tissues due to ageing, smoking, drinking and meat-eating are poorly characterized. Population based studies are required understanding of epigenetic changes leading to progression of cancer. In this study, the methylation pattern of MGMT gene was studied in samples of prostate cancer patients along with 50 tissue samples of Benign Prostatic Hyperplasia cases and 100 blood samples from individuals as controls. The results establish that the methylation pattern increases with age in BPH and healthy individuals whereas the probability of developing prostate cancer is in the age group of 51-60 yrs. It is again proved in the study that smoking, drinking and no alcohol has a significant contribution in hypermethylation of MGMT gene, thus signifying that the methylation pattern can be designated as an epigenetic biomarker in prostate cancer patients where the diagnosis is not well defined in the early stages of tumorigenesis.
Description:	Only IISERM authors are available in the record.
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