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Title:	Aberrant Methylation in Promoters of GSTP1, p16, p14, and RASSF1A Genes in Smokers of North India
Authors:	Singh, Jagdeep (/jspui/browse?type=author&value=Singh%2C+Jagdeep) Chandel, Avinash (/jspui/browse?type=author&value=Chandel%2C+Avinash) Thapliyal, Shruti (/jspui/browse?type=author&value=Thapliyal%2C+Shruti)
Issue Date:	2012
Publisher:	International Scholarly Research Notices
Citation:	International Scholarly Research Notices, 2012:247631
Abstract:	<p>Promoter hypermethylation plays an important role in the inactivation of tumor suppressor/metabolic genes during tumorigenesis. The screening of high-risk population (smokers) for hypermethylation pattern in tumor suppressor/metabolic genes can be a good noninvasive biomarker tool, which should be included in prognosis so that therapeutic measures can be initiated at an early stage. The purpose of this study was to determine the prevalence of aberrant promoter methylation of GSTP1, p16, p14, and RASSF1A genes in smokers and nonsmokers of North India. Our study showed that compared with nonsmokers, smokers have an increased risk of hypermethylation in these genes. We found that 57.3% of the smokers samples showed methylation for GSTP1, 38% for p16, 18% for p14, and 32% for RASSF1A. Our population study allowed us to reveal the relationship between smoking and the subsequent appearance of an epigenetic change. Smoking speeds up the hypermethylation of these genes, which are thus unable to express, making the person more susceptible to the risk of lung and other solid carcinomas. Hypermethylation studies on DNA from two lung cancer cell lines (A549 and H460) were also done to compare the results, and the results are similar to samples of smokers.</p>
Description:	Only IISERM authors are available in the record.
URI:	https://www.hindawi.com/journals/isrn/2012/247631/ (https://www.hindawi.com/journals/isrn/2012/247631/) http://hdl.handle.net/123456789/3705 (http://hdl.handle.net/123456789/3705)
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