Title:	Study of Methylation Pattern of APC Gene as Epigenetic Biomarker in Lung Cancer Patients
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Abstract:	A malignant tumor results after a series of DNA alterations in a single cell4, or clones of that cell, which lead to loss of normal function genes, which are frequently lost or mutated, have been identified including those whose function is to induce cell proliferation under sp are programmed to halt proliferation in damaged cells (e.g. p53 and APC tumour suppressor genes6). Other mutations are also neces telomerase production. With the exception of rare familial cancers which are primarily caused by a germline inheritance of a specific m exposure to external or internal agents (such as tobacco, carcinogens, dietary factors, pollutants and sex hormones) and consequent subsequent clones may be heavily dependant on the efficiency with which potentially toxic exposures are metabolized and excreted a rectified13. This progress of carcinogenesis is likely to vary strongly between individuals because of the population variability in polym methylation1 have been associated with the altered expression of a number of genes involved in cell cycle control and apoptosis, inclu among many others in various carcinomas, including lung cancer. Silencing of tumor suppressor and tumor-related genes by hyperme tumorigenesis. In this study the methylation pattern of APCgene was studied in 25 lung cancer patients who included active, passive a methylation pattern can be designated as epigenetic biomarker14 in lung cancer patients5 where the diagnosis is not well defined in th
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