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Dynamic changes in the genome lead to uncontrolled cell growth and make them able to metastasize and invade other regions and cause cancer. Experimental carcinogenesis studies in animals have shown that cancer involves an initiation process that is irreversible. All cancers arise by accumulating structural and/or functional alterations in cellular DNA involving mutations in proto-onco, tumour suppressor and DNA repair genes.

In 2001-2002, lung cancer remained a major health problem: according to WHO, it accounts for more than 1,002,000 deaths worldwide. This number continues to increase. Before the diagnosis of lung cancer, a series of morphologically distinct pre-neoplastic changes may help us to identify molecular markers that may be useful in the early detection of lung cancer and also in deciding and designing specific treatments. Currently, there is no marker that has major clinical prognostic value, but with the help of recent molecular techniques, new insights are being provided into how the tumour cells by altering oncogenes and tumour suppressor genes achieve growth advantage, uncontrolled proliferation and metastatic behaviour via disruption of key cell cycle regulation and signal transduction cascades. Moreover, new knowledge is being accumulated in terms of molecular definition of individual susceptibility to various carcinogens and the ability to detoxify them before they cause structural alterations in DNA, leading to cancer. This area of molecular epidemiology also explores gene-environment interactions such as carcinogen-metabolic activation, DNA repair, endogenous mutation rates and inheritance of tumour suppressor genes. It is, thus, feasible that the future advances will allow molecular epidemiologists to develop cancer risk profile for an individual that includes the assessment of a number of exposures and other environmental factors. This will help to focus on preventive strategies and strength quantitative risk assessments.
Though quite a bit of work in this direction has been carried out to find out an association of host susceptibility markers for lung cancer development but no conclusions have been made so far. Moreover, main problem is that the data in one population cannot be extrapolated to the other as there is not only inter population differences but even an inter individual differences in this regard and all these make the things complex. This field particularly with respect to lung cancer in India is still virgin as no work on this aspect is available on population of India which is multi-ethnic. It is because of this, the present work was undertaken at the Department of Biotechnology, Panjab University, Chandigarh.

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