

A prospective evaluation of sputum examination to predict lung disease

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Lung cancer, the most common cause of cancer-related death in men and women, accounts for over 1 million deaths worldwide annually. The vast majority of primary lung cancers are carcinomas of the lung, derived from epithelial cells. There are many types of lung cancers and each type of lung cancer grows and spreads in different ways and it is treated differently. Treatment also depends on the stage and may require chemotherapy, radiation and/or surgery. The most common lung cancer symptoms are shortness of breath, coughing and weight loss.

Smoking is the main contributor to lung cancer. In countries that have seen a high prevalence of smoking, around 90% of diagnoses of lung cancer are attributable to cigarette smoking.

Chronic obstructive pulmonary disease (COPD) refers to chronic bronchitis and emphysema, a pair of two commonly co-existing diseases of the lungs in which the airways become narrowed. This leads to a limitation of the flow of air to and from the lungs causing shortness of breath. In contrast to asthma, the limitation of airflow is poorly reversible and usually gets progressively worse over time.

Because the first symptoms appear in late stages, the main treatment is surgery. For this reason, it is important to explore novel methods for an early diagnosis of lung cancer.

The less invasive method of obtaining airways cells is the collection of induced sputum. This represents a valid and responsive method for sampling airways safely, reproducibly and serially in clinical investigation. It has been suggested that the method can be used to monitor airway inflammation and to provide information used to identify the best treatment [1].

The objective of our study is to identify specific genetic alterations from early stage in patients with COPD, through the use of molecular and microscopic techniques. Lung carcinoma is the consequence of molecular changes in the cell, resulting in deregulation of pathways controlling

normal cellular growth, differentiation, and apoptosis. In the last decade, several studies have focused on the role of cell-cycle control in lung carcinogenesis. A precise regulation of the cell-cycle is a fundamental requirement for the homeostasis of a eukaryotic cell [2].

Therefore, we focused our work on the analysis of DNA content and on the expressions of same genes that are responsible of the standard cellular mechanism of proliferations.

Image cytometry will be used to identify ploidy of sample through microscopic quantification of DNA content according to standardizations of the European Society for Analytical Cellular Pathology (ESACP)'s Task Force [3, 4]. Real Time-PCR will be used to detect genetic expression of specific "sensible genes" which are frequently altered in various types of lung cancer.

Taking into account the extensive functional network constituted by the cell-cycle regulator proteins, it appears evident that the knowledge of the expression levels of these factors, and their co-regulation, may be critical in predicting patient clinical response to therapy.

References

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