Openventio PUBLISHERS

PULMONARY RESEARCH AND RESPIRATORY MEDICINE

ISSN 2377-1658 Open Journal http://dx.doi.org/10.17140/PRRMOJ-2-119

Short Communication

*Corresponding author
Zhaolin Xu, MD, FRCPC, FCAP
Professor
Department of Pathology
Dalhousie University;
Pulmonary Pathologist and Cytopathologist
QE II Health Sciences Centre;
Senior Scientist
Beatrice Hunter Cancer Research Institute;
5788 University Ave
Halifax NS B3H 1V8, Canada
Tel. 902-473-7287
Fax: 902-473-3897
E-mail: zxu3@dal.ca

Volume 2 : Issue 3
Article Ref. #: 1000PRRMOJ2119

Article History
Received: October 2nd, 2015
Accepted: October 19th, 2015
Published: October 19th, 2015

Citation
Xu Z. Significance of molecular genotyping for lung cancer in modern oncology. *Pulm Res Respir Med Open J*. 2015; 2(3): 120-121. doi: 10.17140/PRRMOJ-2-119

Significance of Molecular Genotyping for Lung Cancer in Modern Oncology

Zhaolin Xu*

Professor, Department of Pathology, Dalhousie University; Pulmonary Pathologist and Cytopathologist, QE II Health Sciences Centre; Senior Scientist, Beatrice Hunter Cancer Research Institute, 5788 University Ave, Halifax NS B3H 1V8, Canada

Lung cancer is one of the most prevalent life-threatening diseases and remains the leading cause of cancer-related death worldwide. Although surgical resection of the tumor is considered as one of the most effective treatments, most lung cancer patients present with locally advanced or metastatic disease at the time of the diagnosis and are not candidates for surgical treatment. For these patients palliative chemotherapy and radiation therapy, alone or in combination, become the main treatment of choice. The prognosis for lung cancer in general is poor and an overall 5-year survival rate for all stages of lung cancer, regardless of subtypes, is about 18%, which has not been significantly improved in the past several decades. For those in an advanced stage of the disease the prognosis is even worse. About half of all lung cancer patients have metastatic disease at the time of diagnosis with a 5-year survival rate of less than 5%. There is no doubt that the conventional treatment of lung cancer would not significantly change the outcome for lung cancer patients.

In order to conquer the deadly disease, it is important to understand the pathogenesis of lung cancer that involves alteration and accumulation of molecular abnormalities over time. The abnormalities can occur in different levels including DNA sequence, gene transcripts, protein expression and cell signaling involved in cell proliferation, differentiation, apoptosis, and angiogenesis. These changes are related to alterations in normal genes due to gene mutations, gene silencing, and gene amplification or deletion. Most of cancers are likely to be caused by or related to these driving genes that function as oncogene and make cancer cell develop and grow. Characterization of the gene mutations in lung cancer would provide valuable information for better understanding the clinical significance of the mutations and for developing effective targeted treatment. Recent development in understanding of molecular pathogenesis in lung cancer has led to new strategies for early detection, molecular profiling, and personalized targeted therapy, which provide additional options for lung cancer treatment in modern oncology. Most of the driving genes identified in lung cancer patient such as KRAS, EFGR, ALK, BRAF, PIK3CA, ROS1, HER2, etc. are mainly in lung adenocarcinoma. These mutant genes are often mutually exclusive and identified collectively in about a half of the lung adenocarcinomas. Tyrosine kinase inhibitors to treat lung cancer patients with EGFR gene mutations and ALK gene rearrangement are already in clinical practice and targeting these genes would achieve a better clinical outcome.

Although achievements have been made in molecular based targeted therapy to treat subsets of lung cancer cases, our knowledge in the understanding of pathogenesis for lung cancer is still limited. The driving genes have not been identified in approximatelly half of lung adenocarcinomas and little is known in other subtypes of lung cancer such as squamous cell carcinoma, large cell carcinoma, and neuroendocrine carcinomas including small cell carcinoma, etc. It is important to search new driving genes in lung cancer as tumor markers in order to further improve clinical outcome through molecular based targeted therapy. Analysis of various histologic types of lung cancer using high-throughput methods such as next generation sequcncing in cancer cell DNA sequence, gene transcription and protein expression levels has made it possible to identify new tumor biomarkers as potential targets to develop personalized

ISSN 2377-1658 Open Journal http://dx.doi.org/10.17140/PRRMOJ-2-119

targeted therapy. Detailed analysis of lung cancer at the molecular level would provides the basis for a totally new direction of treatment which would result in much higher response rates, longer progression free survival and improved quality of life. Therefore, molecular genotyping of lung cancer is critical and the treatment options in modern oncology have included tumor marker based targeted therapy in addition to conventional methods that may bring the new hope for lung cancer patients if more driving genes can be identified in lung cancer.