

Omic Technologies and Lung Cancer

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Editorial

Lung cancer is the most common cause of cancer death in the world. According to results it's nearly one in five (1.59 million deaths, 19.4% of the total) [1]. Studies show that smoking is the principal cause of the lung cancer. Among the multiple components of tobacco smoke such as polycyclic aromatic hydrocarbons, inorganic compounds, the tobacco specific nitrosamines are likely to play major roles in lung cancer induction [2]. Smoking carcinogens causes lung cancer with their induction of multiple mutations in critical genes [3].

Omic technologies are providing remarkable opportunities for a better understanding of exposure and prediction of potential adverse health effects. Recent years, there is an impressive improvement in omic technologies as transcriptomics, epigenomics, proteomics, and genomics. Omic technologies are increasingly important for the understanding of cancer molecular mechanisms. We know that cancer biomarkers hold the key to effectively manage health care indeed they are the gate keepers of personalized medicine [4].

Proteomics is a method for early detection of cancer and also important for lung cancer screening. Especially, protein microarrays and two-dimensional gel electrophoresis could play an important role in the early detection of neoplasia [5]. The detection of protein patterns could be a method for interpreting signalling pathways and other cellular processes that contribute to cancer development and metastasis [6]. Proteomics has a method of detecting markers of neoplasia with a particular emphasis on lung cancer and potential to sample the lung by Exhaled Breath Condensate (EBC). Proteomic techniques such as EBC are commonly used in the research laboratories as a potential screening tool for the early detection of lung carcinomas but these techniques have not become common place in the clinical laboratories [5].

Omic technologies are analytical methods to quantify gene expression (transcriptomics), proteins (proteomics), lipids (lipidomics) and metabolites (metabolomics) in the lungs or body liquids that define disease abnormalities. In addition they offer the promise of a comprehensive understanding of cancer [7,8].

Recent studies indicate that microarray based genomic and mass spectrometry based proteomic technologies are powerful tools for classification of tumour sub types. In addition, these techniques can be used for the identification of genes or proteins that may serve as diagnostic, predictive, or prognostic markers. Omic technologies' use for cancer staging and personalization of therapy at the time of diagnosis could improve patient care. Generated profiles of gene and protein expression in lung cancer specimens, relevant model systems make recommendations to facilitate the clinical application of omic technologies.

More research is needed before omic technologies can be applied in the clinical setting for the early detection of lung carcinomas.

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