Abstract

Biomedical area of research is grown dynamical for identification of various diseases and prediction of disease, among the most cancer is vital and critical disease caused from various sources of gene mutation. Now a day’s Lung cancer has been malignancy and primary related cause of cancer deaths mostly worldwide. Our work is based on the observation of Inimitable mutations frequency patterns of cancer are found in lung subtypes, or in tumor, target drug that cause genetic mutations, characteristic cancer and transduction signal pathway is beneficial to the patients. Our work is based on Ampliseq Ion Torrent cancer sequence of 800 loci of 50 cancer Oncogenes and genes for identification of mutation related to genetic for 48 fixed-formalin taken from samples of Indian patients on human lung cancer disease. Genetic gene mutation of lung cancer is identified by using interaction network method.

Mutations occur frequent in PIK3CA, KRAS, TP53 AND EGFR genes, according to our observation from samples gained from lung cancer, one or more mutations occur in the gene is the basic key for finding the cancer disease. Our study narrates or gives flexibility in identifying
genetic mutation for lung cancer individually through tumors.

References

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**Index Terms**

| Computer Science | Biomedical |

**Keywords**

lungs cancer, genetic mutations, targeted sequencing, targeted therapy, algorithms, pathways, statistical significance, cancer genomes, SPI Network-Shortest Path Interactive Network.