

# UNDERSTANDING OF PROTEIN INTERACTION NETWORKS BETWEEN NORMAL AND CANCER CONDITIONS USING SELECTED ATTRIBUTES

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## ABSTRACT

*Finding of expression and networks between cancer causing proteins are the principle and basic level of understanding in control of cancer. The present network analysis was provided an understanding of protein networks for selected proteins/genes AKT1, ALK, BRAF, EGFR, HER2, KRAS, MEK1, MET, NRAS, PIK3CA, RET, ROS1 AR, ER, FGFR1, FGFR2, PIK3CA, PR and PTEN oncogenes. The study showed that two genes, AKT1 and PIK3CA are largely associated with both lung and breast cancers.*

**Keywords:** Lung Cancer, Breast Cancer, Oncogenes, Interaction Networks.

## I. INTRODUCTION

The increasing amount of data generated and stored in molecular genetics laboratories is often difficult to build a sense of results due to vast number of different outcomes occurring during studies. The expression levels for genes in biological databases make intelligence findings and furnish a significant result for computing its associated (experiment-wise) statistical significance (Mark et al., 2003). Protein interaction network methods have become increasingly important and form integral part of research in the health sciences. The clustering and association techniques are used to assembly the transactional data based on literature (Auget et al., 2007).

Lung cancer is comprised of two main histologic subtypes: small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC). Over the past few decades it has become understandable that subsets of NSCLC can be further distinct at the molecular level by repeated 'driver' mutations occurring in multiple oncogenes, including AKT1, MET, ALK, BRAF, RET, HER2, KRAS, EGFR, NRAS, MEK1, PIK3CA, and ROS1 (<http://www.mycancergenome.org/content/disease/lung-cancer>).

Breast cancer is the most frequently diagnosed cancer leading cause of cancer death in female's worldwide, accounting for 23% (1.38 million) of the total new cancer cases and 14% (458,400) of the total cancer deaths in 2008. The gene involved in breast cancer includes AKT1, AR, HER2, PIK3CA, ER, FGFR1, FGFR2, PR and PTEN (<http://www.mycancergenome.org/content/disease/breast-cancer>).

## II. METHODOLOGY

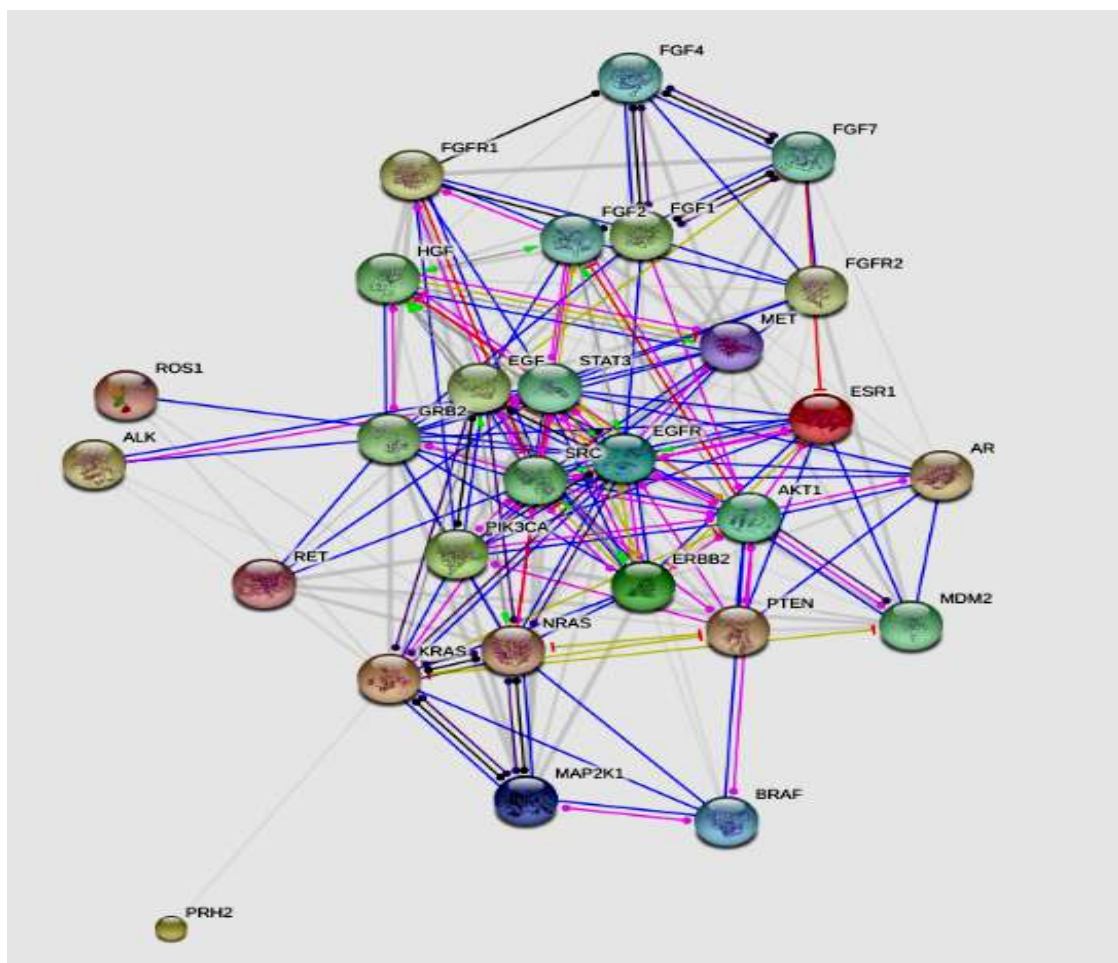
As there are more number of breast and lung cancers that are predicted in the available data from different sources, the genes that are shown above are tested for network analysis using string database. The query multiple proteins AKT1, ALK, BRAF, EGFR, HER2, KRAS, MEK1, MET, NRAS, PIK3CA, RET, ROS1 AR, ER, FGFR1, FGFR2, PIK3CA, PR and PTEN were submitted to string server for understanding protein interaction networks.

## III. RESULTS AND DISCUSSIONS

Proteins are key biological molecules that performs network of associations that pass from health to disease conditions and vice-versa (Nageswara et al., 2010). A research field available in clinical and biochemical approaches help in understanding of function of enzymes and proteins in various living systems such as microbes, plants and animals (Kaladhar et al., 2012).

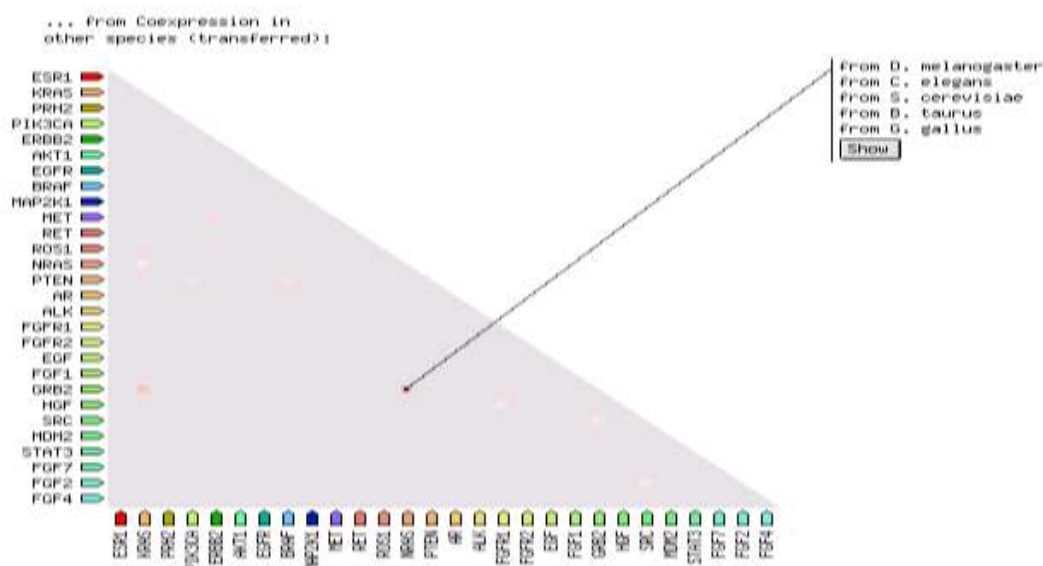
The data collected are shown good interactive profile and network for cancer genes. Two genes AKT1 and PIK3CA are largely associated with both lung and breast cancers.

Figure no. 1 was provided the cancer gene association network using database.



**Fig. 1: Breast and Lung Cancer Gene Network**

Figure no. 2 was shown the gene association with other species like *D.melanogaster*, *C. elegans*, *S.cerevisiae*, *B.Taurus* and *G.gallus*.



**Fig. 2: Species-Network Association for Cancer Genes**

Germline mutations in PTEN on 10q23 were found to cause 85% of Cowden syndrome with high risks of breast, thyroid, and other cancers (Orloff et al., 2013). PIK3CA and AKT pathway networks are common in cancers (Stemke-Hale et al., 2008). The genomic and proteomic studies can provide better understanding in cause of occurrences in various types of cancers. PIK3CA oncogene mutations direct PI3K-dependent tumorigenesis through activation of the AKT/PKB kinase (Vasudevan et al., 2009; Janku et al., 2011).

#### IV. CONCLUSION

The genes AKT1 and PIK3CA are associated with both the breast and lung cancers. The ligand protein interaction profile provides better understanding on available drugs used by patients in further studies.

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## BIOGRAPHICAL NOTES

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