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New discovery of genetic mutations in lung cancer and how it can be used in drug development

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According to GLOBOCAN 85% of the lung cancer cases include NSCLC. Despite having a variety of treatment options, NSCLC has a poor survival rate and poor prognosis. The major obstacle to the effectiveness of these treatments is the acquisition of drug resistance. Intrinsic resistance occurs due to the failure of malignant cancerous cells to the treatment because of genetic polymorphisms.

It has been found that genetic variants in the 3'-UTR regions destroy or create the miRNA binding sites and result in the deregulation of gene expression. As a result, miRNAs play an important role in tumorigenesis and tumour development by regulating the protooncogene and tumour suppressor expressions. It has been found that genetic variants in the 3'-UTR regions destroy or create the miRNA binding sites and result in the deregulation of gene expression. These polymorphisms might be implicated in the chemotherapy response, cancer prognosis and susceptibility and might be associated with the clinical outcome of NSCLC patients. In this research, we used publicly available bioinformatics databases to identify the driver genes which are dysregulated in non-small cell lung cancer (NSCLC). Also, we identified the mutations in the form of single nucleotide polymorphisms (SNPs) in the 3'-Untranslated regions (3'-UTR) of those genes. Furthermore, overall gene expression analysis of significant SNPs was conducted.

Biography

Kashmira Vishal Lele is postgraduated from Coventry University. She completed her masters in MSc. Pharmacology and Drug Discovery.

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