Network-based Identification of Key Proteins and Repositioning of Drugs for Non-Small Cell Lung Cancer

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Abstract

NSCLC is a highly prevalent cancer and accounts for 85% of cases of lung cancer. Conventional cancer treatments, such as chemotherapy and radiation, frequently exhibit limited efficacy and notable adverse reactions. Therefore, a drug repurposing method is proposed for effective NSCLC treatment. This study aims to evaluate candidate drugs that are effective for NSCLC at the clinical level using systems biology and network analysis approach. Differentially expressed genes of transcriptomics data were identified using the systems biology and network analysis approach. A network of gene co-expression was developed with the aim of detecting two modules of gene co-expression. Subsequently, the Drug-Gene interaction database was employed to pinpoint potential pharmaceutical agents that target crucial genes within two gene co-expression modules associated with non-small cell lung cancer (NSCLC). The construction of a drug-gene interaction network was facilitated with the utilisation of Cytoscape. Finally, the gene set enrichment analysis was done to validate candidate drugs. Unlike previous research on repositioning drugs for NSCLC, which uses a gene co-expression network, this project is the first to research both gene co-expression and co-occurrence networks. And the co-occurrence network also accounts for differentially expressed genes in cancer cells and their adjacent normal cells. Drugs exhibiting elevated gene regulation and gene affinity within the drug-gene interaction network are deemed noteworthy for the efficacious management of non-small cell lung cancer (NSCLC). According to this discourse, NSCLC genes exert a high degree of regulation over medications such as vincristine, fluorouracil, methotrexate, clotrimazole, etoposide, tamoxifen, sorafenib, doxorubicin, and pazopanib. Hence, there is a possibility of repurposing these drugs for the treatment of non-small cell lung cancer. Key words: Non-small cell lung cancer (NSCLC), drug repurposing, network analysis, drug-gene interaction, therapeutics

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