

BIOINFORMATIC PREDICTION AND COEXPRESSION NETWORK IDENTIFIES REPURPOSED NOVEL DRUGS FOR PAPILLARY THYROID CANCER

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Abstract

Thyroid cancer is a type of cancer that affects the endocrine system and has a high malignancy. Papillary thyroid cancer, the most common subtype of thyroid cancer, also has well-differentiated features. Early diagnosed and well-differentiated thyroid cancer is generally associated with a good prognosis and/or survival rate. Therefore, it is of great importance to determine the molecular signatures of the disease. In this study, five papillary thyroid cancer-related gene expression datasets were analyzed using linear models for microarray data (LIMMA) method. Differentially expressed genes (DEG) have been identified and gene set enrichment analysis was performed via ConsensusPathDB and the MetaScape tool. Coexpression network was constructed by using mutual DEG expression profiles and network modules were found a disease module with 21 nodes, 145 edges, 69% density, and significantly correlated genes in all datasets was obtained compared with normal thyroid tissues. Genes in the disease module were processed in L1000CDS², resulting in 42 drug lists and identified as drug repurposing candidates, and text mining analyzes was performed by using Python library urllib3. Doxorubicin hydrochloride, doxorubicin, and Dorsomorphin dihydrochloride drugs with the highest TF-IDF are already used in the treatment of thyroid cancer. FDA-approved AS605240, piperlongumine, and TWS119 drugs and/or small molecules that are not used in thyroid cancer have been identified as candidate drugs that can be used in the treatment of thyroid cancer. As a result of FDA-approved drugs piperlongumine, and TWS119 may be promising candidates for thyroid cancer. Preclinical testing, as well as additional drug validation, may ensure new cure preference for thyroid cancer.

Keywords : drug repurposing, papillary thyroid cancer, coexpression network, gene expression

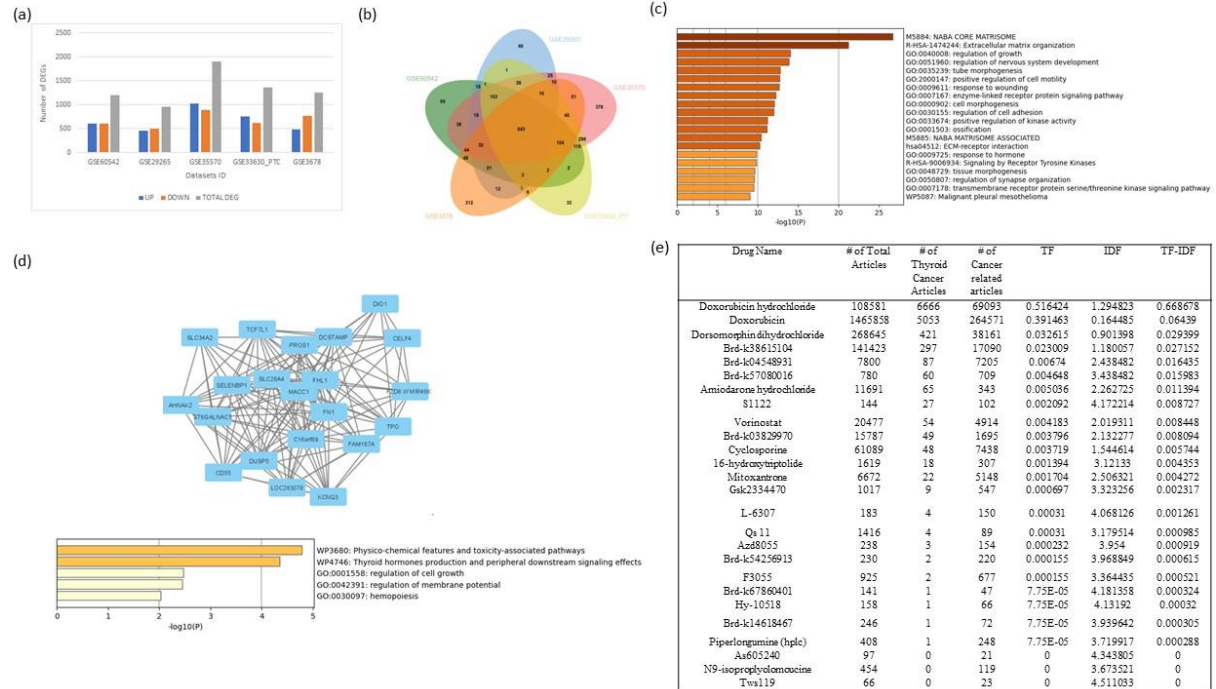


Figure 1 Identification of DEGs a) distribution of DEGs by datasets b) The overrepresentation pathway analysis of DEGs c) Venn diagram of common DEGs d) Potential gene set for papillary thyroid cancer: Coexpressed module genes and biological insights of the genes. e) Drug repurposing results