



Analysis of protein-protein interaction network in chronic obstructive pulmonary disease

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ABSTRACT. Chronic obstructive pulmonary disease (COPD) is a growing cause of morbidity and mortality throughout the world. The purpose of our study was to uncover biomarkers and explore its pathogenic mechanisms at the molecular level. The gene expression profiles of COPD samples and normal controls were downloaded from Gene Expression Omnibus. Matlab was used for data preprocessing and SAM4.0 was applied to determine the differentially expressed genes (DEGs). Furthermore, a protein-protein interaction (PPI) network was constructed by mapping the DEGs into PPI data, and functional analysis of the network was conducted with BiNGO. A total of 348 DEGs and 765 interactive genes were identified. The hub genes were mainly involved in metabolic processes and ribosome biogenesis. Several genes related to COPD in the PPI network were found, including CAMK1D, ALB, KIT, and DDX3Y. In conclusion, CAMK1D, ALB, KIT, and DDX3Y were chosen as candidate genes, which have the potential

to be biomarkers or candidate target molecules to apply in clinical diagnosis and treatment of COPD.

Key words: Chronic obstructive pulmonary disease; Biomarker; Protein-protein interaction network