



Identification of Hub Genes and Pathways in Acute Respiratory Distress Syndrome Based on Differential Expression Network

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ABSTRACT This study aimed to investigate significant genes and pathways in acute respiratory distress syndrome (ARDS) based on differential expression network (DEN). Firstly, differentially expressed genes (DEGs) between ARDS samples and normal controls were identified using linear models for microarray data (Limma) package. Secondly, differential interactions and non-differential interactions were selected to construct a DEN. Thirdly, topological centrality analysis (degree) was performed for exploring hub genes. Finally, to investigate functional biological processes related to hub genes, pathway enrichment analysis was conducted. A total of 229 DEGs were detected for ARDS. There were 759 nodes and 576 edges which included 550 differential edges and 26 non-differential interactions. By accessing topological centrality analysis, the researchers obtained 6 hub genes, *UBC*, *CSNK2A2*, *CUL5*, *SOX2*, *PARK2* and *CHAF1A*. The most significant pathway enriched by hub genes was T cell receptor signaling pathway. The hub genes and pathways would be potential biomarkers for ARDS diagnosis and treatment.