clinical disease activities. This result could serve as a template for future studies to design stratified approaches for SSC patients.

REFERENCES:

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POSO849 IDENTIFICATION OF POTENTIAL CRUCIAL GENES AND KEY PATHWAYS IN PULMONARY ARTERIAL HYPERTENSION WITH SYSTEMIC SCLEROSIS BY BIOINFORMATIC ANALYSIS

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Background: Pulmonary arterial hypertension with systemic sclerosis (SSc-PAH) is the main cause of death in patients with SSc. Early diagnosis and timely treatment are very important to reduce the mortality of patients with SSc-PAH1. At present, there are not many sensitive markers for the diagnosis of SSc-PAH. Therefore, it is necessary to mine more sensitive markers and practical predictors, which is of great significance for the diagnosis and treatment of SSc-PAH.

Objectives: To discover the differentially expressed genes (DEGs) and activated signaling pathways in SSc-PAH.

Methods: Fifty-five samples (27 SSc-PAH vs 28 normal controls) in GSE33463 chip data obtained from Gene Expression Omnibus (GEO) were included in this study. DEGs in SSc-PAH patients were screened by R, key pathways and hub genes were discovered by Metascape2, STRING3 and Cytoscape. 

Results: Total 431 genes with large differences were identified, including 238 up-regulated genes and 193 down-regulated genes, after standardizing the data (log2FC > 1; P < 0.05). GO analysis showed that the upregulated genes were mainly involved in defense response to virus, hemoglobin complex, platelet alpha granule membrane and cytokine binding. The downregulated genes were mainly characterized by positive regulation of cell death, regulation of MAPK cascade, regulation of DNA-binding transcription factor activity and transcription factor AP-1 complex. Several significant enriched pathways obtained in the KEGG pathway analysis were Influenza A, Hepatitis C, IL-17 signaling pathway, MAPK signaling pathway, Toll-like receptor signaling pathway. Finally, after the selected differential genes were introduced into STRING online software, the data information of protein interaction network was obtained, and 12 core genes in the network were identified, they were CXCL8, PPBP, LPAR1, FPR2, GNG11, CXCL10, LPAR5, JUN, C3AR1, CCR2, CCR3, IRF2.

Conclusion: The genes and signal pathways related to SSc-PAH discovered by bioinformatics methods could not only provide new molecular markers for its diagnosis and treatment, but also provided new ideas for its related biological research.

REFERENCES: