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

REFERENCES:

- [1] Xu X, Ramanujam M, Visvanathan S, et al. Transcriptional insights into pathogenesis of cutaneous systemic sclerosis using pathway driven meta-analysis assisted by machine learning methods. *PLoS One* 2020;15(11):e0242863. doi: 10.1371/journal.pone.0242863 [published Online First: 2020/12/01].
- [2] Xu C, Meng LB, Duan YC, et al. Screening and identification of biomarkers for systemic sclerosis via microarray technology. *Int J Mol Med* 2019;44(5):1753-70. doi: 10.3892/ijmm.2019.4332 [published Online First: 2019/09/24].
- [3] Zhou Y, Zhou B, Pache L, et al. Metascape provides a biologist-oriented resource for the analysis of systems-level datasets. *Nat Commun* 2019;10(1):1523. doi: 10.1038/s41467-019-09234-6 [published Online First: 2019/04/05].

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POS0848

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-PAH. At present, there are not many sensitive markers for the diagnosis of SSc-PAH. Therefore, it is necessary to mine more sensitive markers as more accurate 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 v.s 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 ($|\log_2\text{FC}| > 1$; $P < 0.05$). 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 derived, 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 provided new molecular markers for its diagnosis and treatment, but also provided new ideas for its related biological research.

REFERENCES:

- [1] Zheng JN, Li Y, Yan YM, et al. Identification and Validation of Key Genes Associated With Systemic Sclerosis-Related Pulmonary Hypertension. *Front Genet* 2020;11:816. doi: 10.3389/fgene.2020.00816 [published Online First: 2020/08/15].
- [2] Zhou Y, Zhou B, Pache L, et al. Metascape provides a biologist-oriented resource for the analysis of systems-level datasets. *Nat Commun*

2019;10(1):1523. doi: 10.1038/s41467-019-09234-6 [published Online First: 2019/04/05].

- [3] Szklarczyk D, Gable AL, Lyon D, et al. STRING v11: protein-protein association networks with increased coverage, supporting functional discovery in genome-wide experimental datasets. *Nucleic Acids Res* 2019;47(D1):D607-D13. doi: 10.1093/nar/gky1131 [published Online First: 2018/11/27].

Figure 1: (A) Volcano map of gene expression: The horizontal axis is log₂ FC, the vertical axis is log₁₀ adj.P.Val. Each dot represents a gene, blue indicates low expression genes, red indicates high. (B) Heat map of the top 100 up-regulated differentially expressed genes: Each small square represents a gene; the color indicates the expression level of the gene. Each column indicates the expression level of the genes in a sample; each row indicates the expression level of a gene in different samples; the right side is the gene name. (C,D,E and F) Visualization GO enrichment analysis and KEGG pathway enrichment analysis. (G) Protein-protein interactions network.

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POS0849

SEXUAL FUNCTION IS IMPAIRED IN WOMEN WITH IDIOPATHIC INFLAMMATORY MYOPATHIES COMPARED TO HEALTHY CONTROLS

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