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

S. Feng¹, S. X. Zhang^{2,3,4}, R. Zhao^{2,3,4}, C. Zheng⁵, L. Cheng⁵, T. Kong⁵, X. Sun⁵, Q. Wang⁶, X. Li^{2,3,4}, Q. Yu^{5,7}, P. F. He⁷. ¹Shanxi Medical University, School of Humanities and Social Sciences, Taiyuan, China; ²The Second Hospital of Shanxi Medical University, Department of Rheumatology, Taiyuan, China; ³Shanxi Li Xiaofeng Medical Groups, Department of Rheumatology, Taiyuan, China; ⁴Ministry of Education, Key laboratory of Cellular Physiology at Shanxi Medical University, Taiyuan, China; ⁵Shanxi Medical University, School of Management, Taiyuan, China; ⁶Shanxi Medical University, Basic Medical College, Taiyuan, China; ⁷Shanxi Medical University, Medical Data Sciences, Taiyuan, China

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 ($|\log_2FC| > 1$; $P < 0.05$). 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 $\log_2 FC$, the vertical axis is $\log_{10} \text{adj.P.Val.}$. 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

B. Heřmáňková^{1,2}, M. Špiritović^{1,2}, S. Oreska^{2,3}, H. Štorkánová^{2,3}, H. Smucrova², M. Komarc⁴, M. Klein^{2,3}, K. Pavelka^{2,3}, L. Šenolt^{2,3}, H. Mann^{2,3}, J. Vencovsky^{2,3}, M. Tomčík^{2,3}. ¹Faculty of Physical Education and Sport, Charles University, Department of Physiotherapy, Prague, Czech Republic;

²Institute of Rheumatology, Department of Rheumatology, Prague, Czech Republic; ³First Faculty of Medicine, Charles University, Department of Rheumatology, Prague, Czech Republic; ⁴Faculty of Physical Education and Sport, Charles University, Department of Methodology, Prague, Czech Republic

Background: Idiopathic inflammatory myopathies (IIM) are rare diseases characterized by chronic muscle inflammation and multiple organ involvement. These serious clinical manifestations can be associated with significant impairment of quality of life, including sexual life.

Objectives: This study aimed to compare sexual function in patients with IIM to age-/sex-matched healthy controls (HC) and determine the potential impact of clinical features on sexual function.

Methods: In total, 62 women with IIM [mean age: 53.1, disease duration: 5.2 years, dermatomyositis (DM, 29)/ polymyositis (PM, 27)/ necrotizing myopathy (IMNM, 5)/ inclusion body myositis (IBM, 1)], who fulfilled the Bohan/Peter 1975 criteria for DM/PM, or ENMC criteria for IMNM or IBM, and 62 healthy controls (HC) (mean age: 53.1) without rheumatic diseases filled in 11 well-established and validated questionnaires assessing sexual function (FSFI, SFQ28, BISF-W, SQoL-F), pelvic floor function (PFIQ-7, PISQ-12), fatigue (FIS, Fatigue Impact Scale), physical activity (HAP, Human Activity Profile), disability (HAQ, Health Assessment Questionnaire), depression (BDI-II, Beck's Depression Inventory-II), and quality of life (SF-36, Medical Outcomes Study Short Form 36 – PCS, Physical Component Summary; MCS, Mental Component Summary). A routine laboratory testing was performed. Data are presented as median (IQR).

Results: Patients with IIM reported significantly greater prevalence and severity of sexual dysfunction (FSFI, BISF-W, SFQ28, SQoL-F) and pelvic floor dysfunction (PISQ-12, PFIQ-7) compared to HC (Table 1). The prevalence of sexual dysfunction in patients with IIM according to the FSFI cut-off score was 59%. Worse scores in IIM patients were associated with greater muscle weakness of m. gluteus maximus [MMT: FSFI ($r=0.289$, $p=0.035$), PFIQ-7 ($r=-0.407$, $p=0.003$)], m. gluteus medius [MMT: PFIQ-7 ($r=-0.381$, $p=0.005$)], more pronounced fatigue [FIS: SQoL-F ($r=-0.412$, $p=0.003$)], severer depression [BDI-II: SQoL-F ($r=-0.459$, $p=0.0007$)], worse functional disability [HAQ: FSFI ($r=-0.436$, $p=0.005$)], reduced physical activity [HAP: FSFI ($r=0.403$, $p=0.001$), SQoL-F ($r=0.368$, $p=0.007$)], and decreased quality of life [SF-36 PCS: FSFI-total ($r=0.381$, $p=0.002$), SF-36 MCS: SQoL-F ($r=0.407$, $p=0.002$)]. We did not observe any associations with disease duration, the current prednisone dose, or serum levels of muscle enzymes.

Conclusion: Women with IIM reported significantly impaired sexual function and pelvic floor function compared to age-/sex-matched healthy controls. Worse scores in IIM were associated with disease-related features.

Table 1. Sexual function and pelvic floor function in women with IIM and healthy controls

Questionnaire: score range (meaning)	IIM (n=62)	HC (n=62)	p-value
FSFI: Female Sexual Function Index: 2 (worst) - 36 (best)	18.2 (3.2-28.5)	28.4 (14.4-32.1)	p=0.006
BISF-W: Brief Index of Sexual Function for Women: -16 (worst) - 75 (best)	18.6 (2.7-32.3)	34.0 (8.0-44.7)	p=0.004
SQoL-F: Sexual Quality of Life Questionnaire – Female: 0 (worst) - 100 (best)	60.0 (41.4-83.6)	86.7 (70.8-95.6)	p<0.0001
PISQ-12: Pelvic Organ Prolapse/Urinary Incontinence Sexual Questionnaire short form: 0 (best) - 48 (worst)	14.5 (9.0-18.0)	8.0 (5.0-12.0)	p<0.0001
PFIQ7: Pelvic Floor Impact Questionnaire – short form 7: 0 (best) - 300 (worst)	4.8 (0.0-23.8)	0.0 (0.0-4.8)	p=0.052
SFQ-28: Sexual Functioning Questionnaire-28 desire: 5 (worst) - 31 (best)	18.0 (13.3-20.0)	19.0 (17.0-22.0)	p=0.042
SFQ-28 arousal sensation: 4 (worst) - 20 (best)	9.5 (7.0-11.0)	12.0 (9.0-14.3)	p=0.082
SFQ-28 arousal lubrication: 2 (worst) - 10 (best)	6.0 (4.0-8.0)	7.0 (5.0-9.0)	p=0.112
SFQ-28 arousal cognitive: 2 (worst) - 10 (best)	6.0 (4.3-7.0)	6.0 (5.0-7.3)	p=0.235
SFQ-28 orgasm: 1 (worst) - 15 (best)	11.0 (8.0-13.0)	12.0 (9.8-13.0)	p=0.279
SFQ-28 pain: 2 (worst) - 15 (best)	12.0 (10.0-15.0)	15.0 (13.0-15.0)	p=0.004
SFQ-28 enjoyment: 6 (worst) - 30 (best)	19.0 (14.3-24.3)	23.0 (19.0-25.0)	p=0.027
SFQ-28 partner: 2 (worst) - 10 (best)	9.0 (8.0-10.0)	10.0 (9.0-10.0)	p=0.012

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POS0850

NAILFOLD CAPILLARY DILATIONS IN RAYNAUD'S PHENOMENON: QUANTIFYING A PREDICTIVE THRESHOLD FOR THE 'SCLERODERMA PATTERN'

G. Pacini¹, M. Pendolino¹, C. Pizzorni¹, E. Gotelli¹, A. Sulli¹, L. Carmisciano², S. Paolino¹, V. Smith^{3,4}, M. Cutolo¹. ¹IRCCS Policlinic San Martino, University of Genova, Laboratory of Experimental Rheumatology and Academic Division of Rheumatology, Postgraduate School of Rheumatology, Department of Internal Medicine and Specialties, Genova, Italy; ²University of Genova, Biostatistics Unit, Department of Health Sciences, Genova, Italy; ³Ghent University Hospital, Department of Internal Medicine, Department of Rheumatology, Gent, Belgium; ⁴VIB-UGent Center for Inflammation Research, Unit for Molecular Immunology and Inflammation, Gent, Belgium

Background: Non-specific abnormalities could be detected by nailfold videocapillaroscopy (NVC) in subject with primary Raynaud's Phenomenon (RP) several years before the clinical onset of connective tissue diseases (CTD)s [1]. Previous findings from our group proved that ≤ 30 μ m capillary dilations in RP patients have a negative predictive value for developing the 'scleroderma pattern' during follow-up [2].

Objectives: To investigate the role of NVC >30 μ m capillary dilations as positive predictive factors of the 'scleroderma pattern' in RP patients later developing systemic sclerosis (SSc)-related RP.

Methods: A 10-year retrospective NVC-based investigation evaluated the dataset of sequential NVCs of 18 RP patients later developing SSc (cases) and 19 sex- and age-matched RP patients later developing other CTDs (controls). Both cases and controls had ≥ 1 NVC performed before the 'scleroderma pattern'/CTD diagnosis (basal NVC) showing >30 μ m dilated capillaries. Each NVC was qualitatively and semi-quantitatively assessed, recording number of total capillaries, number and average/site-specific diameters (arterial, apical, venous) of >30 μ m dilated capillaries [3]. Statistical analysis was performed to stratify the risk of developing the 'scleroderma pattern'.

Results: Significant differences of capillary diameters were observed between cases and controls both at basal NVC and during follow-up ($p<0.001$). The proportion of >30 μ m dilated capillaries in basal NVC was the strongest predictor of 'scleroderma pattern' in a median 3-year time, with a 27% cut-off (PPV 0.79, 95%CI 0.54,0.94; $p<0.001$). Additional "Higher risk" NVC hallmarks for 'scleroderma pattern' development were apical diameter >40 μ m ($p<0.001$), venous diameter >25 μ m ($p<0.05$) and average diameter ≥ 35 μ m ($p<0.005$). Conversely, CTDs patients showed a stable NVC 'non-scleroderma pattern' over a median 10-year time.

Conclusion: This is the first study to show that NVC-detected homogeneous and progressive capillary loop dilations in RP patients significantly contribute to predict the 'scleroderma pattern' evolution within a median 3-year time, possibly providing a "very early" window of opportunity in SSc pre-clinical stages.

REFERENCES:

- [1] Cutolo M et al. Expert Rev Clin Immunol. 2019;15(7):753–64. [2] Trombetta AC et al. J Rheumatol 2016;43:599–606. [3] Smith et al. Autoimmun Rev 2020; 19(3):102458.

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