The tool we propose could be a valid support in accurately assessing the joint and indirectly skin involvement of sclerodactyly in this type of patient, especially in the context of a clinical trial to evaluate the efficacy of a treatment.

Further studies are needed to compare with other methods to assess hand disability in SSc such as the use of HAMIS (Hand Mobility in Scleroderma) test.

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POS0846

SEXUAL FUNCTION IS IMPAIRED IN WOMEN WITH SYSTEMIC SCLEROSIS COMPARED TO HEALTHY CONTROLS

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Background: Systemic sclerosis (SSc) is a multisystem, connective tissue disorder characterized by fibrosis of the skin and internal organ involvement, which can influence all aspects of life, including sexual life.

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

Methods: In total, 90 women with SSc (mean age: 49.1, disease duration: 6.1 years, lcSSc/dcSSc: 62/28, mRSS: 9.3, ESSG activity index: 2.1), who fulfilled the ACR/EULAR 2013 criteria, and 90 healthy controls (mean age: 49.1) without rheumatic diseases filled in 12 well-established and validated questionnaires assessing sexual function (FSFI, BISF-W, SFQ-28, SQoL-F), pelvic floor function (PISQ-12, PFIQ-7), 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 SSc reported significantly greater prevalence and severity of sexual dysfunction (FSFI, BISF-W, SFQ28 – in all subscales as well as total scores), worse sexual quality of life (SQoL-F) and pelvic floor dysfunction (PISQ-12, PFIQ-7) compared to HC (table 1). The prevalence of sexual dysfunction in patients with SSc according to the FSFI cut-off score was 77%. Worse scores in SSc patients were associated with longer disease duration [BISF-W-total ($r=-0.243, p=0.026$), FSFI-lubrication ($r=-0.229, p=0.035$)], higher disease activity [ESSG activity index: BISF-W-total ($r=-0.291, p=0.010$), FSFI-arousal ($r=-0.299, p=0.007$)], increased inflammation [CRP: BISF-W-receptivity/initiation ($r=-0.301, p=0.007$)], more pronounced fatigue [FIS-total: BISF-W-total ($r=-0.412, p<0.0001$)], more severe depression [BDI-II: FSFI-total ($r=-0.506, p<0.0001$), SQoL-F ($r=-0.369, p<0.0001$)], worse functional disability [HAQ: FSFI-total ($r=-0.394, p<0.0001$)], reduced physical activity [HAP: FSFI-total ($r=0.535, p<0.0001$)], and decreased overall quality of life [SF-36 PCS: FSFI-total ($r=0.428, p<0.0001$), SF-36 MCS: SQoL-F ($r=0.472, p<0.0001$)].

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

Questionnaire: score range (meaning)	SSc (n=90)	HC (n=90)	p-value
FSFI: Female sexual function index: 2 (worst) - 36 (best)	19.4 (3.9-26.8)	30.1 (23.1-32.9)	p<0.0001
BISF-W: Brief Index of Sexual Function for Women: -16 (worst) - 75 (best)	14.3 (2.1-35.1)	38.2 (19.3-46.2)	p<0.0001
SQoL-F: Sexual Quality of Life Questionnaire-61.1 (34.4-81.1)	61.1 (34.4-81.1)	91.1 (70.0-96.7)	p<0.0001
PISQ-12: Pelvic Organ Prolapse/Urinary Incontinence Sexual Questionnaire short form: 0 (best) - 48 (worst)	13.0 (9.0-17.0)	7.0 (5.0-12.0)	p<0.0001
PFIQ-7: Pelvic Floor Distress Inventory Questionnaire: 0 (best) - 300 (worst)	9.5 (0.0-48.8)	0.0 (0.0-8.3)	p<0.0001
SFQ-28: Sexual Functioning Questionnaire-28 desire: 5 (worst) - 31 (best)	17.0 (12.0-20.0)	21.0 (17.0-23.0)	p<0.0001
SFQ-28 arousal sensation: 4 (worst) - 20 (best)	10.0 (8.0-13.0)	12.0 (9.0-15.0)	p=0.0031
SFQ-28 arousal lubrication: 2 (worst) - 10 (best)	5.0 (4.0-7.0)	8.0 (5.2-9.0)	p<0.0001
SFQ-28 arousal cognitive: 2 (worst) - 10 (best)	5.0 (4.0-6.0)	7.0 (5.0-8.0)	p<0.0001
SFQ-28 orgasm: 1 (worst) - 15 (best)	10.0 (6.5-12.0)	12.0 (10.0-13.0)	p<0.0001
SFQ-28 pain: 2 (worst) - 15 (best)	12.0 (9.5-15.0)	15.0 (13.0-15.0)	p<0.0001
SFQ-28 enjoyment: 6 (worst) - 30 (best)	19.0 (12.5-24.0)	24.0 (20.0-25.8)	p<0.0001
SFQ-28 partner: 2 (worst) - 10 (best)	9.0 (8.0-10.0)	10.0 (9.0-10.0)	p=0.0182

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

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POS0847

IDENTIFICATION OF MOLECULAR PHENOTYPES IN SYSTEMIC SCLEROSIS BY INTEGRATIVE SYSTEMS ANALYSIS

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Background: Systemic sclerosis (scleroderma, SSc) is a systemic autoimmune disease characterized by inflammation, fibrosis and vasculopathy and associated with high mortality and high morbidity¹. Stratification based on whole-genome gene expression data could provide a new basis for clinical diagnosis from a micro perspective².

Objectives: The objective of this study is to stratify patients with SSc, combine with clinical skin scores and clinical features, and provide a preliminary assessment and novel insights for assessing disease severity, and treatment design.

Methods: The original data mRNA expression profiles of GSE95065 (including 18 SSc patients and 4 healthy controls) and GSE130955 (including 58 SSc patients and 33 healthy controls) were downloaded from the public Gene Expression Omnibus (GEO) database. After batch correction, background adjustment, and other pre-processing, a large gene matrix was obtained to identify the differentially expressed genes (DEGs) of SSc compared with healthy controls. Then the gene expression matrix decomposition was used to identify SSc subtypes by NMF algorithm. The cluster-based signature genes were applied to pathway enrichment analysis by Metascape³. Immune infiltrating cells and clinical skin scores were evaluated in all SSc subtypes.

Results: Total 325 DEGs were imputed to NMF unsupervised machine learning algorithm. Patients were divided into 2 subtypes (Figure 1A), one of which (sub1) was mostly enriched in the defense response to bacterium and cellular response to lipopolysaccharide pathway and another subtype (sub2) was enriched in the PPAR signaling and alcohol metabolic process pathway (Figure 1B-C). According to immune infiltration, sub1 had higher level of immune cells such as B cells, CD4+T cells, DC cells, Th2 cells and Tregs compared with sub2 ($P < 0.01$). Sub2 had more skin-related cells, including Epithelial cells, Fibroblasts and Sebocytes ($P < 0.05$). Interestingly, combined with clinical information, sub1 showed a severe clinical skin score over those of Sub2 patients ($P < 0.05$) (Figure 1D-E).

Conclusion: Our findings indicated that SSc patients could be stratified into 2 subtypes which had different molecular profiles of disease progression and

Figure 1 NMF clustering function enrichment, immune cells infiltration and clinical skin scores in SSc patients. (A) The relationship between cophenetic with respect to number of clusters. (B-C) Genetic functional enrichment for sub1 and sub2. (D) The box plot shows the difference in the clinical skin scores between the two subtypes. (E) Violin plot visualizing the differently infiltrated immune cells and skin cells (red represents sub1 and blue represents sub2). (ns, no significant; * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).

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

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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 ($|\log_2FC| > 1$; $P < 0.05$). 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.

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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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