

World Journal of *Stem Cells*

World J Stem Cells 2024 May 26; 16(5): 462-614



EDITORIAL

- 462 Single-cell sequencing technology in diabetic wound healing: New insights into the progenitors-based repair strategies
Xiang Z, Cai RP, Xiao Y, Huang YC
- 467 Mesenchymal stem cells' "garbage bags" at work: Treating radial nerve injury with mesenchymal stem cell-derived exosomes
Mushtaq M, Zineldeen DH, Mateen MA, Haider KH
- 479 Deer antler stem cell niche: An interesting perspective
Cavallini C, Olivi E, Tassinari R, Zannini C, Ragazzini G, Marcuzzi M, Taglioli V, Ventura C

ORIGINAL ARTICLE**Basic Study**

- 486 Sinomenine increases osteogenesis in mice with ovariectomy-induced bone loss by modulating autophagy
Xiao HX, Yu L, Xia Y, Chen K, Li WM, Ge GR, Zhang W, Zhang Q, Zhang HT, Geng DC
- 499 Hydrogel loaded with bone marrow stromal cell-derived exosomes promotes bone regeneration by inhibiting inflammatory responses and angiogenesis
Zhang S, Lu C, Zheng S, Hong G
- 512 Patient-derived induced pluripotent stem cells with a *MERTK* mutation exhibit cell junction abnormalities and aberrant cellular differentiation potential
Zhang H, Wu LZ, Liu ZY, Jin ZB
- 525 Therapeutic potential of urine-derived stem cells in renal regeneration following acute kidney injury: A comparative analysis with mesenchymal stem cells
Li F, Zhao B, Zhang L, Chen GQ, Zhu L, Feng XL, Gong MJ, Hu CC, Zhang YY, Li M, Liu YQ
- 538 GATA binding protein 2 mediated ankyrin repeat domain containing 26 high expression in myeloid-derived cell lines
Jiang YZ, Hu LY, Chen MS, Wang XJ, Tan CN, Xue PP, Yu T, He XY, Xiang LX, Xiao YN, Li XL, Ran Q, Li ZJ, Chen L
- 551 Cardiac differentiation is modulated by anti-apoptotic signals in murine embryonic stem cells
Yehya A, Azar J, Al-Fares M, Boeuf H, Abou-Kheir W, Zeineddine D, Hadadeh O
- 560 Effects of interleukin-10 treated macrophages on bone marrow mesenchymal stem cells *via* signal transducer and activator of transcription 3 pathway
Lyu MH, Bian C, Dou YP, Gao K, Xu JJ, Ma P
- 575 Hepatocyte growth factor enhances the ability of dental pulp stem cells to ameliorate atherosclerosis in apolipoprotein E-knockout mice
Duan H, Tao N, Lv L, Yan KX, You YG, Mao Z, Wang CY, Li X, Jin JY, Wu CT, Wang H

- 591** Effect of ginsenoside Rg1 on hematopoietic stem cells in treating aplastic anemia in mice *via* MAPK pathway

Wang JB, Du MW, Zheng Y

SYSTEMATIC REVIEWS

- 604** Role of glioma stem cells in promoting tumor chemo- and radioresistance: A systematic review of potential targeted treatments

Agosti E, Zeppieri M, Ghidoni M, Ius T, Tel A, Fontanella MM, Panciani PP

ABOUT COVER

Editorial Board Member of *World Journal of Stem Cells*, Umberto Galderisi, PhD, Full Professor, Department of Experimental Medicine, Molecular Biology at the School of Medicine, University of Campania "Luigi Vanvitelli", Via Luigi De Crecchio 7, Naples I-80138, Italy. mberto.galderisi@unicampania.it

AIMS AND SCOPE

The primary aim of *World Journal of Stem Cells (WJSC, World J Stem Cells)* is to provide scholars and readers from various fields of stem cells with a platform to publish high-quality basic and clinical research articles and communicate their research findings online. *WJSC* publishes articles reporting research results obtained in the field of stem cell biology and regenerative medicine, related to the wide range of stem cells including embryonic stem cells, germline stem cells, tissue-specific stem cells, adult stem cells, mesenchymal stromal cells, induced pluripotent stem cells, embryonal carcinoma stem cells, hemangioblasts, lymphoid progenitor cells, *etc.*

INDEXING/ABSTRACTING

The *WJSC* is now abstracted and indexed in Science Citation Index Expanded (SCIE, also known as SciSearch®), Journal Citation Reports/Science Edition, PubMed, PubMed Central, Scopus, Biological Abstracts, BIOSIS Previews, Reference Citation Analysis, China Science and Technology Journal Database, and Superstar Journals Database. The 2023 Edition of Journal Citation Reports® cites the 2022 impact factor (IF) for *WJSC* as 4.1; IF without journal self cites: 3.9; 5-year IF: 4.5; Journal Citation Indicator: 0.53; Ranking: 15 among 29 journals in cell and tissue engineering; Quartile category: Q3; Ranking: 99 among 191 journals in cell biology; and Quartile category: Q3. The *WJSC*'s CiteScore for 2022 is 8.0 and Scopus CiteScore rank 2022: Histology is 9/57; Genetics is 68/325; Genetics (clinical) is 19/90; Molecular Biology is 119/380; Cell Biology is 95/274.

RESPONSIBLE EDITORS FOR THIS ISSUE

Production Editor: *Xiao-Mei Zheng*; Production Department Director: *Xu Guo*; Cover Editor: *Jia-Ru Fan*.

NAME OF JOURNAL

World Journal of Stem Cells

ISSN

ISSN 1948-0210 (online)

LAUNCH DATE

December 31, 2009

FREQUENCY

Monthly

EDITORS-IN-CHIEF

Shengwen Calvin Li, Carlo Ventura

EDITORIAL BOARD MEMBERS

<https://www.wjnet.com/1948-0210/editorialboard.htm>

PUBLICATION DATE

May 26, 2024

COPYRIGHT

© 2024 Baishideng Publishing Group Inc

INSTRUCTIONS TO AUTHORS

<https://www.wjnet.com/bpg/gerinfo/204>

GUIDELINES FOR ETHICS DOCUMENTS

<https://www.wjnet.com/bpg/GerInfo/287>

GUIDELINES FOR NON-NATIVE SPEAKERS OF ENGLISH

<https://www.wjnet.com/bpg/gerinfo/240>

PUBLICATION ETHICS

<https://www.wjnet.com/bpg/GerInfo/288>

PUBLICATION MISCONDUCT

<https://www.wjnet.com/bpg/gerinfo/208>

ARTICLE PROCESSING CHARGE

<https://www.wjnet.com/bpg/gerinfo/242>

STEPS FOR SUBMITTING MANUSCRIPTS

<https://www.wjnet.com/bpg/GerInfo/239>

ONLINE SUBMISSION

<https://www.f6publishing.com>

Single-cell sequencing technology in diabetic wound healing: New insights into the progenitors-based repair strategies

Zhen Xiang, Rui-Peng Cai, Yang Xiao, Yong-Can Huang

Specialty type: Cell and tissue engineering

Provenance and peer review: Invited article; Externally peer reviewed.

Peer-review model: Single blind

Peer-review report's scientific quality classification

Grade A (Excellent): 0
Grade B (Very good): 0
Grade C (Good): C
Grade D (Fair): 0
Grade E (Poor): 0

P-Reviewer: Jain R, India

Received: December 26, 2023

Peer-review started: December 26, 2023

First decision: February 24, 2024

Revised: March 8, 2024

Accepted: March 25, 2024

Article in press: March 25, 2024

Published online: May 26, 2024



Zhen Xiang, Rui-Peng Cai, Yong-Can Huang, Shenzhen Engineering Laboratory of Orthopaedic Regenerative Technologies, Department of Spine Surgery, Peking University Shenzhen Hospital, Shenzhen 518036, Guangdong Province, China

Yang Xiao, Department of Breast and Thyroid Surgery, Peking University Shenzhen Hospital, Shenzhen 518036, Guangdong Province, China

Co-first authors: Zhen Xiang and Rui-Peng Cai.

Corresponding author: Yong-Can Huang, PhD, Associate Professor, Shenzhen Engineering Laboratory of Orthopaedic Regenerative Technologies, Department of Spine Surgery, Peking University Shenzhen Hospital, Lianhua Road, Shenzhen 518036, Guangdong Province, China. y.c.huang@connect.hku.hk

Abstract

Diabetes mellitus (DM), an increasingly prevalent chronic metabolic disease, is characterised by prolonged hyperglycaemia, which leads to long-term health consequences. Although much effort has been put into understanding the pathogenesis of diabetic wounds, the underlying mechanisms remain unclear. The advent of single-cell RNA sequencing (scRNAseq) has revolutionised biological research by enabling the identification of novel cell types, the discovery of cellular markers, the analysis of gene expression patterns and the prediction of developmental trajectories. This powerful tool allows for an in-depth exploration of pathogenesis at the cellular and molecular levels. In this editorial, we focus on progenitor-based repair strategies for diabetic wound healing as revealed by scRNAseq and highlight the biological behaviour of various healing-related cells and the alteration of signalling pathways in the process of diabetic wound healing. ScRNAseq could not only deepen our understanding of the complex biology of diabetic wounds but also identify and validate new targets for intervention, offering hope for improved patient outcomes in the management of this challenging complication of DM.

Key Words: Single-cell sequencing; Diabetic wound healing; Cell subpopulations; Heterogeneity; Pathogenesis; Progenitor cells

©The Author(s) 2024. Published by Baishideng Publishing Group Inc. All rights reserved.

Core Tip: Understanding the mechanism of diabetic wound healing is crucial for the development of novel therapeutic strategies. In this editorial, we focus on advances in the biological behaviour of various healing-related cells and the alteration of signalling pathways in the process of diabetic wound healing. Single-cell RNA sequencing (scRNAseq) has emerged as a powerful tool to explore cellular heterogeneity, reveal new cell subpopulations and predict developmental trajectories. Summarising the current results of scRNAseq in diabetic wounds has provided new insights into progenitor-based repair strategies and possible therapeutic targets.

Citation: Xiang Z, Cai RP, Xiao Y, Huang YC. Single-cell sequencing technology in diabetic wound healing: New insights into the progenitors-based repair strategies. *World J Stem Cells* 2024; 16(5): 462-466

URL: <https://www.wjgnet.com/1948-0210/full/v16/i5/462.htm>

DOI: <https://dx.doi.org/10.4252/wjsc.v16.i5.462>

INTRODUCTION

The prevalence of diabetes mellitus (DM), currently affecting an estimated 550 million individuals, continues to escalate [1]. Diabetic foot ulcer (DFU) is a common and severe complication in patients with diabetes, characterised by its stubbornness, difficulty in treating, and high recurrence rate. It mainly manifests as peripheral neuropathy, lower limb arterial sclerosis and local infection, which profoundly impact the patient's quality of life and disease prognosis. Without proper treatment or inadequate management, it can easily lead to lower limb paralysis, disability and even amputation. Approximately 19% to 34% of diabetes patients worldwide will develop DFU, and about 20% of DFU cases will require lower limb amputation[2]. Current treatment approaches for DFU predominantly encompass wound debridement, offloading strategies, glycemic control, and the management of infections[3]. Recently, several innovative therapeutic modalities have surfaced, including hyperbaric oxygen therapy, application of dressings, negative pressure wound therapy, growth factor therapy, stem cell-based therapy and application of tissue-engineered skin[4]. Despite the development of various innovative technologies and drugs to treat DFU, their therapeutic effects remain unsatisfactory. Progenitor- and stem cell-based therapies, including embryonic stem cells, adult stem cells and mesenchymal stem cells, have been introduced in clinical settings to enhance diabetic wound healing, but the intricacies of stem cell application and tissue interactions are not fully comprehended. The advent of single-cell RNA sequencing (scRNAseq) technology offers a promising avenue for elucidating these complex biological processes, thereby potentially unlocking novel therapeutic targets for DFU.

SINGLE-CELL SEQUENCING TECHNOLOGY

ScRNAseq represents a technique for amplifying the entire transcriptome at the individual cell level. This process involves the reverse transcription of mRNA into cDNA, subsequent amplification of the cDNA, and high-throughput sequencing[5]. As a quintessential instrument for single-cell analysis (Figure 1), scRNAseq facilitates unbiased, high-throughput investigations requiring minimal initial sample volumes. It allows for the detection of cell-specific attributes and intercellular variances through cell mapping, delves into the cooperative functions of cells, and examines the heterogeneity within tissues[6]. Thus, using scRNAseq to investigate progenitor-based repair strategies may yield novel insights into the mechanisms of diabetic wound healing.

SINGLE-CELL SEQUENCING IN DIABETIC WOUND HEALING

Traditionally, it is believed that endothelial cells, epithelial cells, fibroblasts, keratinocytes, macrophages, inflammatory cells and tissue stem cells are the main contributors to wound healing. ScRNAseq has shown that endothelial cells, fibroblasts, epithelial cells, keratinocytes, monocytes, macrophages, B cells, T cells and tissue stem cells are significantly present in both non-healing and healing DFU wounds. By applying scRNAseq, we can gain a clearer understanding of the biological behaviour of various cell types during diabetic wound healing. The following content presents five applications of scRNAseq in studying diabetic wounds and unveiling cellular behaviour and molecular changes during the healing process (Table 1). The samples, primarily from DFUs, non-DFUs and healthy subjects, exhibited cell quantities ranging from 21819 to 174962, facilitating the identification of cell populations, such as fibroblasts, keratinocytes, macrophages, vascular endothelial cells and the discovery of associated signal pathways.

Through a cluster analysis of the data from the GEO database, Li *et al*[7] and Wang *et al*[8] found that the proportions of macrophages, leukocytes and monocytes were higher in patients with DFUs, which indicated a higher level of inflammation; also, the elevated proportions of pluripotent stem cells and stromal cells were observed in patients with DM, which indicated a higher level of dryness. These findings were in line with research by Theocharidis *et al*[9], who noted that DFU healers had a higher presence of naive and early differentiated progenitor T-lymphocytes, while non-healers had more cytotoxic natural killer T cells at the systemic level. Additionally, the proportion of M1 macrophages (classically

Table 1 The results of single-cell sequencing in diabetic wound healing

Objective	Major findings	Cell quantity	Changes at molecular level	Changes at cellular level	Signaling pathway changes	Ref.
Of 11 healthy subjects, 9 DFU healings, and 5 DFU non-healings	Some targeting genes, such as ANPEP, BID, CYBA, CYBB, FCER1G, ITGA1, and PLAUR were found in DFUs	94325	ANPEP, BID, CYBA, CYBB, FCER1G, ITGA1, PLAUR, CD19, ITGAM, and HLA-DR up-regulated in patients with DFUs	Macrophages, white blood cells, and monocytes increased in DFUs; pluripotent stem cells and stromal cells increased in DMs	-	[7]
Of 10 non-DMs and 17 DMs (11 DFUs and 6 non-DFUs)	The CCL2-ACKR1 signal pathway may be closely associated with DFU wound healing	-	CXCL11, MMP1, HS3ST2, CALML, LCK, LDLRAD2, S100A1, and MAMDC2 up-regulated	Tissue stem cells and endothelial cells increased in DFUs	CCL, PROS, EDN, PERIOSTIN, and PARs activated in healing DFU tissues; FGF, SEMA3, MK, PIN, and TGF activated in DFUs	[8]
Of 10 non-DMs, 6 DMs, and 11 DFUs (7 healers; 4 Non-healers)	A new type of fibroblast named HE-Fibro was found in the DFUs	174962	IL7R, TCF7, CCR7, IL1B, S100A, HIF1A, TNF, STAT5a/b, TLR7, TLR9, IL17R/C, IL6, PLA2G2A, FOS, TNFAIP6, MMP1, and CHI3L1 up-regulated, while CD44, TGFβ1, CCL5, NFKBIA, SOX4, TGFβ1, and NANOG down-regulated in DFU-healers; NKG7, GNLY, CCL5, KLRD1, DAB2, CD163, TYMP, and ANXA1 up-regulated in DFU-non-healers	CCR7+, LEF1+ naive T cells, M1 macrophage, IL17+ cells, and HE-fibroblasts increased in DFU-healers; M2 macrophage increased in DFU-non-healers	IL-6, IL-8, CD28 signaling pathways, iCOS-iCOSL pathways inhibited in DFU-healers; RhoGDI, EIF2 signaling pathways; IL6, HIF1A, ILK signaling pathways activated in DFU-healers	[9]
Of 1 non-DM, 2 T2DMs	Some differentially expressed genes were found as keratinocyte-related gene, such as LUCAT1, MAL2 and MXD1	21819	ARG1, PHYH, PKLR, PHKG1, ADH4, AQP9, HADH, PC, and ARG2 up-regulated in T2DM patients	-	Oxidative phosphorylation pathway, antigen processing and presentation pathway, tight junction pathway, amyotrophic lateral sclerosis pathway, vasopressin-regulated water reabsorption pathway activated in T2DM patients	[10]
DMs, non-DMs, STZ-induced diabetic mice	RAB17 in DFU-HDMECs may be the key factor of angiogenic capacity in DFUs	-	RAB17, CD200, HIF-1α and VEGF-A down-regulated in DFU patients	-	Hallmark-KRAS-signaling-on activated in DFU HDMECs; hallmark-angiogenesis, hallmark-epithelial-mesenchymal-transition, hallmark-inflammatory-responses, and hallmark-TNFα-signaling-via-NFκB inhibited in DFU HDMECs	[11]

DM: Diabetes mellitus; T2DM: Type 2 diabetes mellitus; DFU: Diabetic foot ulcer; MMP: Matrix metalloproteinase; CXCL11: CXC chemokine ligand 11; TNFAIP6: Tumor necrosis factor-alpha-stimulated gene-6; IL: Interleukin; TGF: Transforming growth factor; HIF: Hypoxia inducible factor; TNF: Tumor necrosis factor; NFκB: Nuclear factor-kappaB.

activated macrophages that promote inflammation) was higher in DFU-healer than in DFU-non-healers, compared to that of M2 macrophages (alternatively activated macrophages with anti-inflammatory properties)[9]. These results implied that suppressing systemic immuno-inflammatory responses while activating local responses in the wound environment could facilitate diabetic wound healing. Liao *et al*[10] found highly expressed keratinocyte genes in the diabetic wound, including SFN, LYPD3, S100A8, KRT1, KRT10, KRT6A, KRT5, and KRT16, underscoring the crucial role of keratinocytes in diabetic wound healing. By analysing the skin specimens of DFU patients and healthy controls using scRNAseq, Du *et al*[11] found that human dermal microvascular endothelial cells (HDMECs) isolated from DFU patients showed considerably impaired tube formation compared to those from healthy controls; they also found that the significantly under-expressed RAB17 in DFU-HDMECs may be the key factor leading to the impaired angiogenic capacity in DFUs. Moreover, it was proven in the diabetic mouse wound-healing model that the STZ-induced diabetic mice injected with an RAB17-overexpressing rAAV vector had a higher wound perfusion and a significant acceleration of wound closure[11]. Theocharidis *et al*[9] profiled 174962 single cells from the foot, forearm and peripheral blood mononuclear cells using

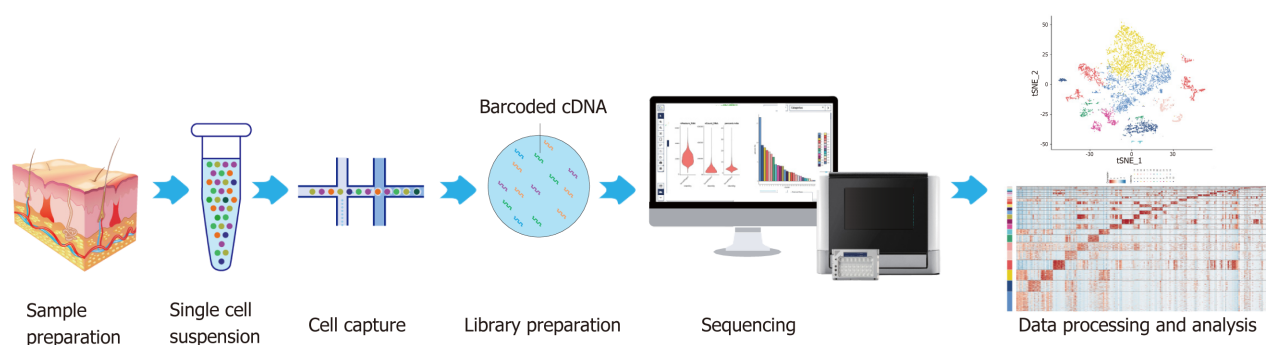


Figure 1 Brief procedures for single-cell sequencing. Single-cell sequencing involves isolating individual cells, capturing their genetic material and amplifying it to create a library for high-throughput sequencing. The generated data are then processed and analysed to uncover cellular diversity and understand the function of individual cells within a complex tissue. This technique allows for the exploration of cellular heterogeneity at an unprecedented resolution, providing insights into the molecular mechanisms that govern processes and diseases.

scRNAseq; based on the differential expression of genes, the fibroblast population was divided into 14 subclusters, in which an unique population of fibroblasts overexpressing matrix metalloproteinase 1 (MMP1), MMP3, MMP11, hypoxia inducible factor 1-alpha (HIF1A), chitinase 3-like protein 1 and tumor necrosis factor (TNF)-alpha-stimulated gene-6 was defined as a new type of fibroblast, namely HE-Fibro. HE-Fibro were found to preferentially locate at the wound bed compared to the wound edge or unwounded skin and increase M1 macrophage polarisation in the DFU patients with healing wounds, suggesting that particular subtypes of fibroblasts play pivotal roles in the healing process of DFUs and targeting these specific fibroblast subtypes may represent a viable therapeutic strategy[9]. The differential gene expression revealed by scRNAseq also suggested the activation or inhibition of the corresponding signalling pathway in the process of diabetic wound healing. The diabetic healing-related differentially expressed gene analysis and gene ontology functional enrichment analysis identified significant differential genes, including CD19, Integrin Subunit Alpha M, HLA-DR, CXC chemokine ligand 11, MMP1, heparan sulfate 3-O-sulfotransferase 2, CALML, interleukin (IL)7R, IL6, TCF7, CCR7, IL1B, S100A8, HIF1 α , TNF, CD44, transforming growth factor β 1, C-C chemokine ligand 5, SOX4, RAB17, CD200 and vascular endothelial growth factor A[7,10]. These genes were predominantly associated with the immune and inflammatory signalling pathways, oxidative phosphorylation and cytokine receptor interactions, suggesting that the immune and inflammatory environment is critical for diabetic wound healing. Alterations in the metabolic processes of cells within diabetic wounds have also been implied[7,10]. Additionally, genes such as ANPEP, BID, CYBA, CYBB, FCER1G, ITGA1 and PLAUR, which were overexpressed in the diabetic wound microenvironment, might serve as potential drug targets[7]. Currently, scRNAseq is extensively applied in the analysis of pathological tissues, the identification of cell populations and the discovery of novel cell subpopulations in diabetic wound healing. However, advanced applications, such as spatial transcription and research into cell development and differentiation, remain underexplored and represent promising frontiers for investigation.

CONCLUSION

The advent and integration of scRNAseq into the study of diabetic wound healing have afforded unprecedented insights into cellular functions, pathophysiological processes and the intricate microenvironment of wounds. This technology enables the precise delineation of cellular subpopulations, the elucidation of pivotal molecular mechanisms and the identification of novel therapeutic targets. Future longitudinal studies that build a map of the diabetic wound healing timeline, and combine scRNAseq and spatial transcription may provide a better way to explore tissue regeneration and repair mechanisms. Collectively, the application of scRNAseq in diabetic wounds has provided new insights into the mechanism of diabetic wound healing and possible directions for further treatment.

FOOTNOTES

Author contributions: Xiang Z and Cai RP contributed equally to this editorial, they drafted and revised the manuscript; Xiao Y read and revised the manuscript; Huang YC conceived the study and approved the final manuscript; and all authors approved the final version of the paper.

Supported by Shenzhen Science and Technology Program, No. GJHZ20210705142543019; and Guangdong Basic and Applied Basic Research Foundation, No. 2023A1515220074.

Conflict-of-interest statement: All the authors report no relevant conflicts of interest for this article.

Open-Access: This article is an open-access article that was selected by an in-house editor and fully peer-reviewed by external reviewers. It is distributed in accordance with the Creative Commons Attribution NonCommercial (CC BY-NC 4.0) license, which permits others to

distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: <https://creativecommons.org/licenses/by-nc/4.0/>

Country/Territory of origin: China

ORCID number: Zhen Xiang [0009-0007-9156-4467](https://orcid.org/0009-0007-9156-4467); Rui-Peng Cai [0009-0003-7000-3151](https://orcid.org/0009-0003-7000-3151); Yang Xiao [0009-0008-0012-7067](https://orcid.org/0009-0008-0012-7067); Yong-Can Huang [0000-0001-8548-8233](https://orcid.org/0000-0001-8548-8233).

S-Editor: Wang JJ

L-Editor: A

P-Editor: Zhang YL

REFERENCES

- 1 **Armstrong DG**, Tan TW, Boulton AJM, Bus SA. Diabetic Foot Ulcers: A Review. *JAMA* 2023; **330**: 62-75 [PMID: [37395769](https://pubmed.ncbi.nlm.nih.gov/37395769/) DOI: [10.1001/jama.2023.10578](https://doi.org/10.1001/jama.2023.10578)]
- 2 **McDermott K**, Fang M, Boulton AJM, Selvin E, Hicks CW. Etiology, Epidemiology, and Disparities in the Burden of Diabetic Foot Ulcers. *Diabetes Care* 2023; **46**: 209-221 [PMID: [36548709](https://pubmed.ncbi.nlm.nih.gov/36548709/) DOI: [10.2337/dci22-0043](https://doi.org/10.2337/dci22-0043)]
- 3 **Bardill JR**, Laughter MR, Stager M, Liechty KW, Krebs MD, Zgheib C. Topical gel-based biomaterials for the treatment of diabetic foot ulcers. *Acta Biomater* 2022; **138**: 73-91 [PMID: [34728428](https://pubmed.ncbi.nlm.nih.gov/34728428/) DOI: [10.1016/j.actbio.2021.10.045](https://doi.org/10.1016/j.actbio.2021.10.045)]
- 4 **Huang F**, Lu X, Yang Y, Li Y, Kuai L, Li B, Dong H, Shi J. Microenvironment-Based Diabetic Foot Ulcer Nanomedicine. *Adv Sci (Weinh)* 2023; **10**: e2203308 [PMID: [36424137](https://pubmed.ncbi.nlm.nih.gov/36424137/) DOI: [10.1002/advs.202203308](https://doi.org/10.1002/advs.202203308)]
- 5 **Zhang X**, Liu L. Applications of single cell RNA sequencing to research of stem cells. *World J Stem Cells* 2019; **11**: 722-728 [PMID: [31692946](https://pubmed.ncbi.nlm.nih.gov/31692946/) DOI: [10.4252/wjsc.v11.i10.722](https://doi.org/10.4252/wjsc.v11.i10.722)]
- 6 **Armand EJ**, Li J, Xie F, Luo C, Mukamel EA. Single-Cell Sequencing of Brain Cell Transcriptomes and Epigenomes. *Neuron* 2021; **109**: 11-26 [PMID: [33412093](https://pubmed.ncbi.nlm.nih.gov/33412093/) DOI: [10.1016/j.neuron.2020.12.010](https://doi.org/10.1016/j.neuron.2020.12.010)]
- 7 **Li Y**, Ju S, Li X, Li W, Zhou S, Wang G, Cai Y, Dong Z. Characterization of the microenvironment of diabetic foot ulcers and potential drug identification based on scRNA-seq. *Front Endocrinol (Lausanne)* 2022; **13**: 997880 [PMID: [36686438](https://pubmed.ncbi.nlm.nih.gov/36686438/) DOI: [10.3389/fendo.2022.997880](https://doi.org/10.3389/fendo.2022.997880)]
- 8 **Wang Z**, Wei D, Li S, Tang Q, Lu G, Gu S, Lu L, Liang F, Teng J, Lin J, Yu Y, Fang D, Huang Z. Healing mechanism of diabetic foot ulcers using single-cell RNA-sequencing. *Ann Transl Med* 2023; **11**: 210 [PMID: [37007553](https://pubmed.ncbi.nlm.nih.gov/37007553/) DOI: [10.21037/atm-23-240](https://doi.org/10.21037/atm-23-240)]
- 9 **Theocharidis G**, Thomas BE, Sarkar D, Mumme HL, Pilcher WJR, Dwivedi B, Sandoval-Schaefer T, Sirbulescu RF, Kafanas A, Mezghani I, Wang P, Lobao A, Vlachos IS, Dash B, Hsia HC, Horsley V, Bhasin SS, Veves A, Bhasin M. Single cell transcriptomic landscape of diabetic foot ulcers. *Nat Commun* 2022; **13**: 181 [PMID: [35013299](https://pubmed.ncbi.nlm.nih.gov/35013299/) DOI: [10.1038/s41467-021-27801-8](https://doi.org/10.1038/s41467-021-27801-8)]
- 10 **Liao B**, Ouyang Q, Song H, Wang Z, Ou J, Huang J, Liu L. Characteristic analysis of skin keratinocytes in patients with type 2 diabetes based on the single-cell levels. *Chin Med J (Engl)* 2022; **135**: 2461-2466 [PMID: [36583863](https://pubmed.ncbi.nlm.nih.gov/36583863/) DOI: [10.1097/CM9.0000000000002323](https://doi.org/10.1097/CM9.0000000000002323)]
- 11 **Du H**, Li S, Lu J, Tang L, Jiang X, He X, Liang J, Liao X, Cui T, Huang Y, Liu H. Single-cell RNA-seq and bulk-seq identify RAB17 as a potential regulator of angiogenesis by human dermal microvascular endothelial cells in diabetic foot ulcers. *Burns Trauma* 2023; **11**: tkad020 [PMID: [37605780](https://pubmed.ncbi.nlm.nih.gov/37605780/) DOI: [10.1093/burnst/tkad020](https://doi.org/10.1093/burnst/tkad020)]



Published by **Baishideng Publishing Group Inc**
7041 Koll Center Parkway, Suite 160, Pleasanton, CA 94566, USA
Telephone: +1-925-3991568
E-mail: office@baishideng.com
Help Desk: <https://www.f6publishing.com/helpdesk>
<https://www.wjgnet.com>

