Crimson Publishers
Wings to the Research

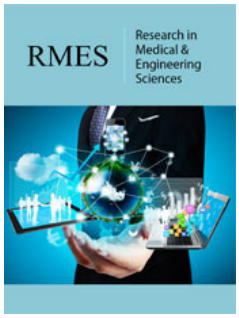
Mini Review

Single-cell RNA Sequence Applications in Abdominal Aortic Aneurysm: Mini review

Yousif A Algabri*

Department of Biomedical Engineering, School of Control Science and Engineering, Shandong University, Jinan, Shandong, 250061, China

ISSN: 2576-8816



***Corresponding author:** Yousif A Algabri, Department of Biomedical Engineering, School of Control Science and Engineering, Shandong University, Jinan, Shandong, 250061, China

Submission: December 12, 2022
Published: December 19, 2022

Volume 10 - Issue 1

How to cite this article: Yousif A Algabri*. Single-cell RNA Sequence Applications in Abdominal Aortic Aneurysm: Mini review. Res Med Eng Sci. 10(1). RMES.000729.2022. DOI: 10.31031/RMES.2022.10.000729

Abstract

Single-cell RNA sequencing (scRNA-seq) has revolutionized biomedical research by describing and analyzing single-cell transcriptomes. scRNA-seq has identified unique cell types, analyzed single-cell trajectory generation and stem or progenitor cell growth, and compared healthy and diseased tissues at single-cell resolution. These applications have enhanced cardiovascular research, particularly abdominal aortic aneurysm treatment. Mammalian heart and blood vessel cell atlases, cardiovascular development, and stem/progenitor cell differentiation pathways illustrate this. This review discusses scRNAseq applications in AAA research and how basic AAA research might be applied to clinical practice.

Keywords: Single-cell RNA sequencing; Cardiovascular disease; Abdominal aortic aneurysm; Biomedical research

Introduction

The biological processes through which the cells that make living beings function must be clarified to comprehend the phenomena of life. The biological functions of cells depend on RNA, and transcriptomes offer vital data directly related to cell phenotypes. A potent method for analyzing individual cells is single-cell RNA sequencing (scRNA-seq). While the traditional method of bulk RNA-seq examines the average gene expression across cells in a sample and identifies changes between sample conditions, scRNA-seq measures the gene expression of individual cells and can distinguish between cells in one or more samples. Although traditionally, cells are identified by their morphology or by molecules specific to each cell type, scRNA-seq enables automatic classification of cells through the clustering of transcriptomes and can identify heterogeneous cell types and molecular states even in a group that has been thought to consist of only one cell type [1,2].

Cardiovascular diseases (CVDs) are widespread throughout the world [3]. Congenital heart disease, for instance tetralogy of Fallot ventricular septal defect, affects one in every hundred children and is caused by an anomaly during the heart's formation process. One of these lethal CVDs is an aneurysm. Aneurysm patients have up to 90% less elastin than healthy artery patients, even though most arteries are fragmented [4]. Patients with aneurysms are more likely to have an underlying respiratory and cardiovascular illness. An Abdominal Aortic Aneurysm (AAA) is recognized as one of the most common cardiovascular disorders. Aortic aneurysms have grown during the last two decades, possibly due to improved diagnosis or increased aneurysm cases [4].

scRNAseq and AAA applications

Single-cell RNA expression profiling is fast becoming an indispensable approach for human, animal, and plant research, enabling more accurate, rapid identification of uncommon and unique tissue cells. Due to technical difficulties or a lack of cell type and developmental biology knowledge, scRNA-seq has been used in a few plants [5].

scRNA-seq can profile, identify, classify, and discover new or rare cell types and subtypes from different human organs and tissues, providing more insight into health and disease in development, immunology, diabetes, microbiology, Covid-19, cancer biology, vascular biology, neurobiology, clinical diagnosis, and many other fields [6]. Therefore, since AAA is recognized as a potentially fatal health condition worldwide [7], several research and applications of scRNAseq have been made in recent years [8-11].

Murine abdominal aortic aneurysm

Yang et al. [8] used scRNA-seq to map the murine AAA cell atlas and predicted the roles of cell types in macrophages, SMCs, and fibroblasts based on transcriptional patterns [8]. Their findings can be used to guide future research into the heterogeneity of vascular and immunological cells in AAA.

Cellular heterogeneity

The heterogeneity and relative contributions of various vascular cells in healthy and aneurysmal aortas are poorly understood, despite the fact that the primary aortic cell types throughout the whole aorta are well characterized [12,13]. scRNA-seq, which was developed recently, offers the chance to completely and objectively characterize the molecular profile and heterogeneity of numerous individual cells in healthy or affected aortas [12]. Recent research has employed scRNA-seq to show the locations of immune cells, macrophages, perivascular adipose tissue stem cells, adventitial cells, and endothelial cells (ECs) inside the aorta [12].

Future Directions

scRNA-seq has given new insights into healthy and diseased cardiology. scRNA-seq revealed several critical cardiac development and pathophysiology molecular pathways. Human pathogenesis has been studied using this innovative method. scRNA-seq analysis now uses molecular information across cells and organs with remarkable spatial and temporal accuracy. Like in these other organs, integrating scRNA-seq and clinical data of cardiovascular disorders such as AAA may reveal new insights and treatments. This involves translating basic research into clinical medicine.

References

1. Lafzi A, Moutinho C, Picelli S, Heyn H (2018) Tutorial: guidelines for the experimental design of single-cell RNA sequencing studies. Nat Protoc 13(12): 2742-2757.
2. Yamada S, Nomura S (2020) Review of single-cell RNA sequencing in the heart. Int J Mol Sci 21(21): 8345.
3. Algabri YA, Rookkapan S, Gramigna V, Espino DM, Chatpun S (2019) Computational study on hemodynamic changes in patient-specific proximal neck angulation of abdominal aortic aneurysm with time-varying velocity. Australas Phys Eng Sci Med 42(1): 181-190.
4. Kaewchoothong N, Algabri YA, Assawalertsakul T, Nuntadusit C, Chatpun S (2022) Computational study of abdominal aortic aneurysms with severely angulated neck based on transient hemodynamics using an idealized model. Applied Sciences 12(4): 2113.
5. Shaw R, Tian X, Xu J (2021) Single-cell transcriptome analysis in plants: Advances and challenges. Molecular Plant 14(1): 115-126.
6. Jovic D, Liang X, Zeng H, Lin L, Xu F, et al. (2022) Single-cell RNA sequencing technologies and applications: A brief overview. Clinical and Translational Medicine 12(3): e694.
7. Algabri YA, Altwijri O, Chatpun S (2019) Visualization of blood flow in AAA patient-specific geometry: 3-D reconstruction and simulation procedures. BioNanoSci 9(4): 966-976.
8. Yang H, Zhou T, Stranz A, DeRoo E, Liu B (2021) Single-cell RNA sequencing reveals heterogeneity of vascular cells in early stage murine abdominal aortic aneurysm. Arterioscler Thromb Vasc Biol 41(3): 1158-1166.
9. Davis FM, Tsoi LC, Ma F, Wasikowski R, Moore BB, et al. (2022) Single-cell transcriptomics reveals dynamic role of smooth muscle cells and enrichment of immune cell subsets in human abdominal aortic aneurysms. Ann Surg 276(3): 511-521.
10. Yu L, Zhang J, Gao A, Zhang M, Wang Z, et al. (2022) An intersegmental single-cell profile reveals aortic heterogeneity and identifies a novel Malat1+ vascular smooth muscle subtype involved in abdominal aortic aneurysm formation. Sig Transduct Target Ther 7(1): 125.
11. Zhao G, Lu H, Chang Z, Zhao Y, Zhu T, et al. (2021) Single-cell RNA sequencing reveals the cellular heterogeneity of aneurysmal infrarenal abdominal aorta. Cardiovasc Res 117(5): 1402-1416.
12. Dobnikar L, Taylor AL, Chappell J, Oldach P, Harman JL, et al. (2018) Disease-relevant transcriptional signatures identified in individual smooth muscle cells from healthy mouse vessels. Nat Commun 9(1): 4567.
13. Kalluri AS, Vellarikkal SK, Edelman ER, Nguyen L, Subramanian A, et al. (2019) Single-cell analysis of the normal mouse aorta reveals functionally distinct endothelial cell populations. Circulation 140(2): 147-163.