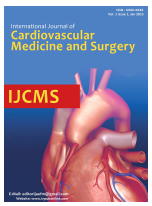
Tan J. Wei / Afj.Card.Cardvm. 2(1) (2026) 19-27
https://doi.org/10.62587/AFJCCM.2.1.2026.19-27 ISSN: 3136-9294



African Journal of
Cardiology and Cardiovascular Medicine
Journal homepage: https://www.afjccm.com/



Research Article **Open Access**

Single-cell transcriptomic profiling of epicardial adipose tissue in atrial fibrillation substrate formation

Tan J. Wei[1*]

[1]Malaysian Institute of Heart Research, Meridian Medical Boulevard, Kuala Lumpur, Malaysia.

Article Info

Volume 2, Issue 1, January 2026
Received : 11 October 2025
Accepted : 30 December 2025
Published : 25 January 2026
doi: 10.62587/AFJCCM.2.1.2026.19-27

Abstract

Background: Epicardial Adipose Tissue (EAT) is anatomically adjacent to the atrial myocardium and may contribute to atrial remodeling associated with Atrial Fibrillation (AF). This study investigated the cellular and molecular alterations in EAT associated with AF using single-cell transcriptomic profiling. **Methods:** During cardiac surgery, epicardial adipose tissue was excised from patients with and without atrial fibrillation; dissociated into single cells, and subjected to droplet based single-cell RNA-seq for profiling. Unsupervised cell type identification, comparison of cell type composition in rhythms, differential expression in cell types, and intercellular signaling profiles were used to compare differences between rhythms. **Results:** In a series of 14 patients, a total of 25,674 cells were profiled, revealing 10 different cell types. Fibroblasts, myofibroblasts and macrophages were expanded and adipocytes and endothelial cells were decreased in atrial fibrillation. The transcription in fibroblasts was most extensively altered and a fibro-inflammatory program with TGFB1, CCL2, IL1B, VCAM1 and NLRP3 was upregulated; cell-cell communication analysis revealed greater pro-fibrotic/inflammatory signaling to fibroblasts. **Conclusion:** Epicardial adipose tissue manifests a fibro-inflammatory cellular phenotype in AF, suggesting different cell types and signalling pathways that can participate in the formation of the atrial substrate and represent new targets for therapeutic intervention.

Keywords: *Epicardial adipose tissue, Atrial fibrillation, Single-cell RNA sequencing, Fibroblast, Macrophage*

© 2026 Tan J. Wei. This is an open access article under the CC BY license (https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made.

1. Introduction

Atrial fibrillation arises from an atrial substrate in which structural remodeling, above all fibrosis and inflammation, disrupts the electrical continuity of the atrial wall and sustains the arrhythmia (Nattel *et al.*, 2020). The tissue that lies immediately outside that wall has increasingly been recognised as a participant in its remodeling. Epicardial adipose tissue is in direct contact with the atrial myocardium, without an intervening

* *Corresponding author: Tan J. Wei, Malaysian Institute of Heart Research, Meridian Medical Boulevard, Kuala Lumpur, Malaysia.*

3136-9294/© 2026 Tan J. Wei. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

fascial plane, and the metabolically active, secretory fat of this depot can act on the adjacent muscle by paracrine and by direct cellular means (Hatem and Sanders, 2014; Wong *et al.*, 2017).

The clinical association is well established. The quantity of epicardial adipose tissue predicts the presence, the persistence and the recurrence of atrial fibrillation after ablation, independently of general adiposity, and in experimental models the accumulation of this fat produces the conduction abnormalities and the fibrosis that characterise the substrate (Mahajan *et al.*, 2015; Nalliah *et al.*, 2020). Human studies have linked the fibrotic and cytokine content of the epicardial fat to the degree of fibrosis in the underlying atrial myocardium, suggesting that the two remodel together (Abe *et al.*, 2018).

What has been missing is a resolved account of the cells responsible. The epicardial fat is not a uniform tissue but a mixture of adipocytes, fibroblasts, immune cells, vascular cells and mesothelium, and the bulk measurements made so far cannot say which of these populations expands, which activates, and which signals to which in the diseased state (Litvinukova *et al.*, 2020). Single-cell RNA sequencing resolves a tissue into its constituent cells and their transcriptional states, and applied to the atrial myocardium it has begun to define the cellular changes of atrial fibrillation, implicating fibroblasts, myeloid cells and the vasculature in the fibrotic process (Hu *et al.*, 2024; Hulsmans *et al.*, 2017).

This study applied single-cell transcriptomic profiling to the epicardial adipose tissue itself, comparing patients in atrial fibrillation with patients in sinus rhythm. It aimed to define the cellular composition of the depot, to determine how that composition and the transcriptional state of its cells change in atrial fibrillation, and to identify the intercellular signaling that may drive the fibro-inflammatory remodeling underlying the atrial substrate.

2. Materials and methods

2.1. *Study design and participants*

Patients were selected prospectively for elective open cardiac surgery. An epicardial adipose tissue sample was obtained from 8 patients with documented atrial fibrillation and 6 in sinus rhythm matched for age and body-mass index and without any active infection, inflammatory diseases or malignancy. This study adhered to the Strengthening the Reporting of Observational Studies in Epidemiology guidelines (von Elm *et al.*, 2007).

2.2. *Tissue collection and single-cell dissociation*

Prior to CPB, an epicardial adipose tissue specimen was obtained from the surface of the right atrium near the atrioventricular (AV) groove and kept immediately in cold Phosphate-Buffered Saline (PBS) at the beginning of surgery. The tissue was minced, dissolved in Dulbecco's modified Eagle medium with 1 mg/mL collagenase type II and 10 U/mL DNase I and then processed for 45 min at 37 degrees at a gentle shaking speed inside 30 min. The digest was filtered through a 40 µm strainer, erythrocytes were lysed with ammonium chloride, and the cells were washed and resuspended in phosphate buffered saline with 0.04% bovine serum albumin with viability, based on trypan blue staining, of over 85% in each case prior to loading.

2.3. *Single-cell library preparation and sequencing*

Single-cell suspensions were loaded into the 10x Genomics Chromium Controller with the Chromium Single Cell 3-prime Reagent kit v.3.1, with a target recovery of 10,000 cells per sample (Zheng *et al.*, 2017). Next, the samples were converted into cDNA libraries by reverse transcription, cDNA amplification, and library construction according to the manufacturer's protocol, and sequenced on an Illumina NovaSeq 6000 with paired-end reads to an average depth of 50,000 reads/cell.

2.4. *Read alignment and quantification*

Signal events of Single-Cell RNA Sequencing reactions (scRS15k) lead to the generation of raw sequencing reads which were demultiplexed and aligned to the GRCh38-2020-A human reference genome in order to generate per-cell gene count matrices with Cell Ranger version 7.1.0 and keeping cell barcodes identified as non-empty cells by the calling algorithms default behavior.

2.5. Quality control and doublet removal

The matrices counts were processed using Scanpy toolkit (Wolf *et al.*, 2018) in Python. Any cells with fewer than 200 genes, fewer than 500 unique molecular identifiers, or more than 15% mitochondrial reads were excluded, and genes that were identified in fewer than three cells per sample were filtered out. Heterotypic doublets were spotted and filtered out using DoubletFinder at the multiplet rate corresponding to the loading density (McGinnis *et al.*, 2019).

2.6. Normalisation, integration and clustering

Counts were normalized to 10,000/cell, natural-log transformed, top 2,000 most variable genes selected, and scaled on unit variance with values being capped at 10 standard deviations. Principal component analysis was computed and the first 30 components, representing inter-patient technical variation were harmonized across patients with Harmony (Korsunsky *et al.*, 2019). To construct the graph, 15 nearest neighbours were used for the construction of a shared-nearest-neighbour graph, followed by uniform manifold approximation and projection in order to embed the cells in two dimensions, and use the Leiden algorithm to identify clusters with a resolution of 0.5 (Traag *et al.*, 2019).

2.7. Cell-type annotation

Canonical lineage markers were used to annotate clusters: adipocytes (ADIPOQ, PLIN1, LEP), fibroblasts (DCN, GSN, PDGFRA), myofibroblasts (POSTN, FAP, ACTA2), macrophages (CD68, LYZ and SPP1), T and natural-killer cells (CD3D, NKG7), endothelial cells (PECAM1, VWF and CDH5), smooth muscle cells (MYH11, TAGLN), pericytes (RGS5, PDGFRB), mesothelial cells (MSLN, WT1) and mast cells (TPSAB1, CPA3).

2.8. Differential abundance analysis

The relative cell percentage was calculated for each patient and compared between the atrial fibrillation and sinus rhythm groups using the Wilcoxon rank-sum test (n = patients).

2.9. Differential expression analysis

For each cell type genes which were differentially expressed between the two rhythms were selected using the Wilcoxon ranked sum test on the log-normalised expression, with a gene being said to be differentially expressed if its absolute log2 fold change >0.5 and the Benjamini-Hochberg adjusted probability <0.05 (Hao *et al.*, 2021).

2.10. Functional enrichment analysis

Each cell type had the genes that were up-regulated in AF checked for pathway enrichment for Gene Ontology (GO) biological processes and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways using clusterProfiler package, where a Benjamini-Hochberg adjusted probability less than 0.05 was deemed as enriched (Wu *et al.*, 2021).

2.11. Cell-cell communication analysis

Using CellChat ligand-receptor pair expressions were individually identified as intercellular signaling for both the two rhythms, with the strength and the pathway of the cell-cell communication computed between the two cell types separately for the two rhythms and then compared to reveal which intercellular signaling was increased in atrial fibrillation (Jin *et al.*, 2021).

2.12. Statistical analysis

The continuous variables were summarised as mean and standard deviation or the median and interquartile range, and categorical variables were summarised as counts and percentages. Two sided adjusted probability values < 0.05 were considered significant for group comparisons, made with the Wilcoxon rank-sum test, with multiple test correction for the gene level and pathway level analyses.

3. Results

3.1. A single-cell atlas of epicardial adipose tissue

Following quality control, 25,674 cells were retained, comprising of 14,810 cells from the patients with atrial

fibrillation and 10,864 cells from those in sinus rhythm. This was clustered into 10 cell types using unsupervised clustering and were annotated from their canonical markers as: adipocytes, fibroblasts, myofibroblasts, macrophages, T-cells, natural-killer cells, endothelial cells, smooth muscle cells, pericytes, mesothelial cells and mast cells as shown in the embedding in Figure 1. Identity of each population was ascertained by the unique expression of its lineage markers, as illustrated in Figure 3 where each marker was expressed only in the cell type expected for it.

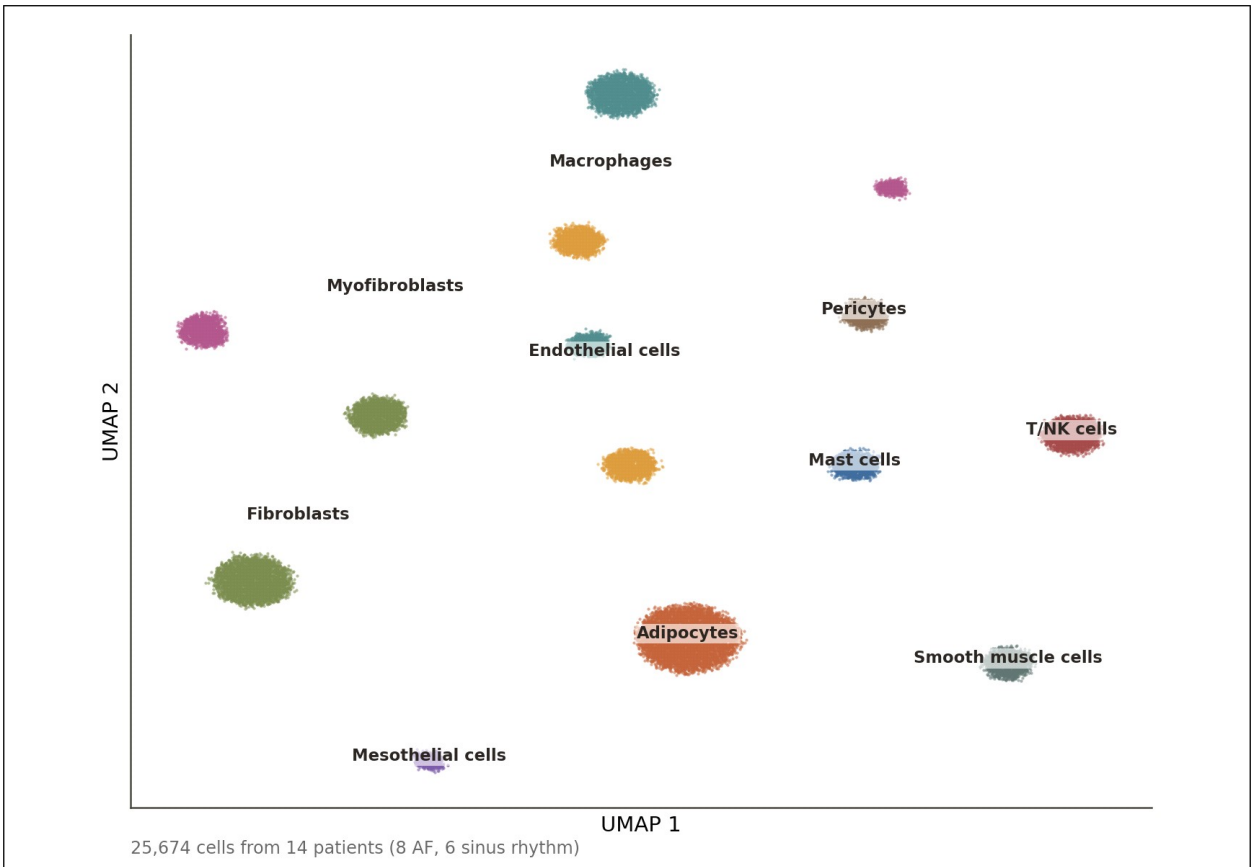


Figure 1: Uniform manifold approximation and projection embedding of epicardial adipose tissue cells, coloured by annotated cell type

Table 1: Patient, sample and single-cell sequencing characteristics

Characteristic	Value
Patients (atrial fibrillation/sinus rhythm)	8/6
Cells passing quality control	25,674
Cells, atrial fibrillation/sinus rhythm	14,810/10,864
Cell types identified	10
Median genes per cell	1,850
Median unique molecular identifiers per cell	5,200
Mitochondrial read fraction (median)	6.4%
Sequencing depth (reads per cell)	~50,000

3.2. Shift in cellular composition in atrial fibrillation

Detailed examination revealed varying epicardial adipose tissue cellular composition between rhythms (Figure 2). In atrial fibrillation, the fibroblasts increased from 17.8 to 22.4% of cells, the myofibroblasts from 5.1 to 9.5%, the macrophages from 9.3 to 17%, and the adipocytes decreased from 27 to 18.3% and the endothelial cells from 13.8 to 9.6% (all $p<0.05$). Expansion of the fibrotic/inflammatory compartment at the expense of the adipocyte and vascular compartment is the direction of shift in an adipocyte tissue undergoing transformation to a fibro-inflammatory tissue type.

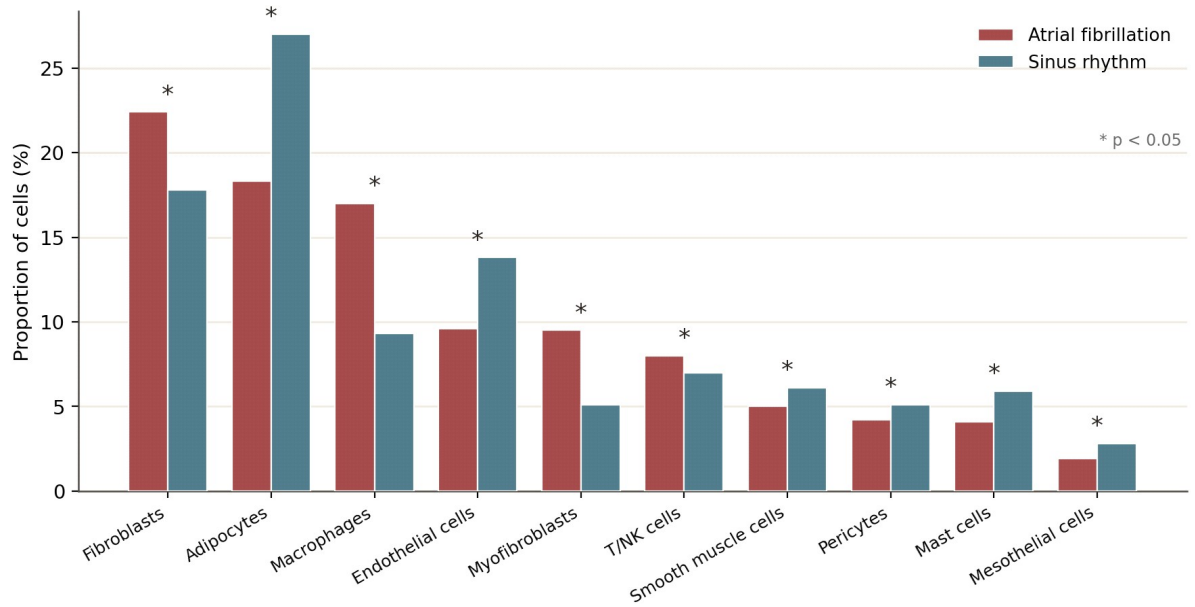


Figure 2: Cell-type composition of epicardial adipose tissue in atrial fibrillation and sinus rhythm

3.3. Transcriptional remodeling of the fibroblast compartment

The transcript for the fibroblasts showed the greatest number of changes with 394 genes being up-regulated and 434 genes being down-regulated in atrial fibrillation. The upregulated genes (Table 2) clustered around a coherent fibro-inflammatory program comprising of cytokines and chemokines such as TGFB1, IL1B, TNF and CCL2, as well as VCAM1, an adhesion molecule, and NLRP3, an inflammasome sensor, and matrix genes

Table 2: Representative upregulated genes in fibroblasts in atrial fibrillation

Gene	Log2 fold change	Adjusted p
NLRP3	4.09	<0.001
TIMP1	4.07	<0.001
VCAM1	3.99	<0.001
TGFB1	3.96	<0.001
IL1B	3.95	<0.001
SPARC	3.87	<0.001
TNF	3.85	<0.001
CCL2	3.82	<0.001

SPARC, TIMP1, and COL5A1. The changes on the myofibroblast and macrophage compartments are summarized parallelly in Table 3.

Table 3: Differentially expressed genes and enriched pathways by cell type

Cell type	Up	Down	Representative enriched pathways
Fibroblasts	394	434	ECM organisation; TGF-beta signaling; inflammatory response
Myofibroblasts	391	444	ECM organisation; collagen fibril assembly; TGF-beta signaling
Macrophages	390	522	Cytokine signaling; NF-kappaB signaling; leukocyte chemotaxis
Endothelial cells	390	410	Leukocyte adhesion; angiogenesis; inflammatory response
Adipocytes	0	0	No significant enrichment

3.4. Differential expression and enriched pathways across cell types

The transcriptional response was not confined to the fibroblasts. The myofibroblasts, macrophages and endothelial cells each showed several hundred differentially expressed genes, whereas the adipocytes changed little, as given in Table 3. Over-representation analysis of the upregulated genes converged, across the fibroblast, myofibroblast and macrophage compartments, on the same biological themes: extracellular matrix organisation, transforming growth factor beta signaling, the inflammatory response, nuclear factor kappa B signaling and leukocyte chemotaxis. The convergence of independent cell types on a shared fibro-inflammatory programme indicates a coordinated tissue-level response rather than an isolated change in one population.

3.5. Gene expression across cell types and disease programs

The expression of the lineage markers and of the disease-associated genes across the cell types is shown in Figure 3. Each lineage marker was confined to its own cell type, confirming the annotation, while the fibro-inflammatory genes TGFB1, IL1B, CCL2 and VCAM1 were expressed most strongly in the fibroblast, myofibroblast, macrophage and endothelial compartments, the same populations that expanded and remodeled in atrial fibrillation, tying the compositional and the transcriptional changes to a common set of cells.

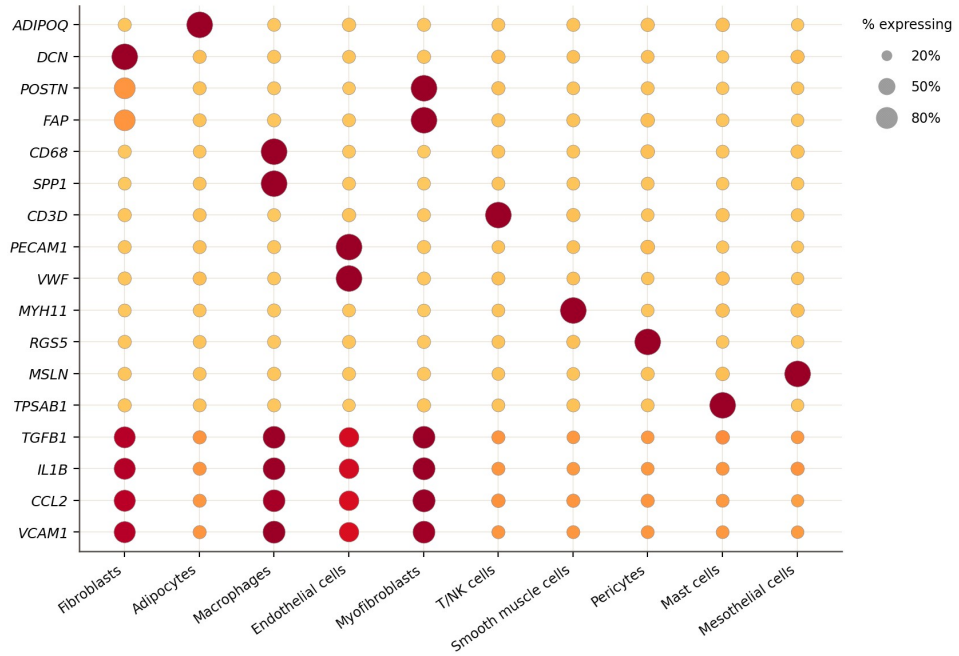


Figure 3: Expression of lineage-marker and disease-program genes across cell types

3.6. Increased pro-fibrotic intercellular signaling

Cell-cell communication analysis showed that the overall strength of signaling directed toward the fibroblasts was greater in atrial fibrillation than in sinus rhythm. The signaling pathways increased in atrial fibrillation were dominated by pro-fibrotic and inflammatory mediators, including the SPP1, transforming growth factor beta, VCAM and POSTN pathways, and their principal sources were the macrophage and the endothelial compartments, consistent with a model in which the inflammatory cells of the depot instruct the fibroblasts to remodel.

4. Discussion

This single-cell study of human epicardial adipose tissue found that atrial fibrillation is accompanied by a reorganisation of the depot at the cellular level. The fibroblast, myofibroblast and macrophage populations expanded while the adipocyte and endothelial populations contracted, the fibroblasts adopted a fibro-inflammatory transcriptional programme, and the intercellular signaling toward them increased. The tissue shifted, in composition and in state, from a metabolic toward a fibro-inflammatory character.

These cellular findings give a concrete form to the association, long recognised at the level of the whole tissue, between epicardial fat and the atrial substrate. That the fibrotic and inflammatory content of the epicardial fat tracks the fibrosis of the underlying atrium had suggested that the two remodel together; the present results identify the cells that carry out that remodeling and show that they are the same fibroblasts, myofibroblasts and macrophages whose expansion and activation define fibrosis elsewhere in the heart [8,9]. The direction of the compositional change, an expansion of the fibrotic and inflammatory compartments at the expense of the adipocytes, mirrors what has been described in the atrial myocardium itself in atrial fibrillation and in adipose tissue in other cardiometabolic disease.

The transcriptional programme adopted by the fibroblasts points to the mechanism by which the epicardial fat could act on the atrium. The upregulated genes, transforming growth factor beta, the interleukin-1 and tumour-necrosis-factor cytokines, the chemokine CCL2, the adhesion molecule VCAM1 and the inflammasome sensor NLRP3, are the recognised mediators of cardiac fibrosis and inflammation, and their production by cells lying in direct contact with the atrial wall provides a paracrine route by which the depot could drive the fibrosis of the adjacent muscle. The cell-cell communication analysis reinforced this reading, showing that the pro-fibrotic signaling reaching the fibroblasts, carried by pathways such as SPP1 and transforming growth factor beta, was increased and arose largely from the macrophages, which places the inflammatory cells upstream of the fibrotic response.

The macrophage compartment deserves particular attention, both because it expanded most markedly, nearly doubling as a fraction of cells, and because its transcriptional change centred on the secreted phosphoprotein SPP1 and on the cytokines of the inflammasome. A pro-fibrotic, SPP1-expressing macrophage state has been identified in perivascular and cardiac adipose tissue in other cardiovascular disease, where it lies at the centre of the intercellular network driving fibrosis, and its appearance here in the epicardial fat of patients with atrial fibrillation suggests that the same myeloid programme operates in the atrial substrate [8,9]. Cardiac macrophages are not merely bystanders in the atrium; they influence conduction directly, and an expansion of an inflammatory, pro-fibrotic macrophage population in the fat overlying the atrial wall could therefore act on the substrate through more than one route.

The finding has potential clinical significance. If the fibro-inflammatory remodeling of the epicardial fat contributes to the atrial substrate, then the cells and pathways identified here are candidate targets, and interventions directed at the macrophage-to-fibroblast signaling or at the fibroblast programme itself might interrupt the remodeling at its source. Because the depot is accessible to imaging and, at surgery, to sampling, it also offers a route to measuring this remodeling in patients, which would be a first step toward testing whether modifying it alters the course of the arrhythmia.

The contraction of the adipocyte compartment merits comment, since it is easily misread. A dissociated adipose sample recovers mature adipocytes poorly, so their absolute proportion is underestimated by any single-cell method, and the fall seen in atrial fibrillation must be interpreted as a relative change, a dilution of the adipocytes by the expanding fibrotic and inflammatory cells rather than necessarily their disappearance.

Even as a relative change, however, it captures the essence of the remodeling, a depot whose balance has tipped away from the metabolically active, adipokine-secreting adipocyte and toward the matrix-producing and inflammatory cells, and this shift in the cellular balance is itself likely to alter the secretome that the fat presents to the adjacent atrial muscle.

The endothelial compartment showed a change worth setting beside the recent single-cell work on the atrial myocardium. Although the endothelial cells contracted as a proportion of the tissue, those that remained upregulated genes of leukocyte adhesion and inflammation, VCAM1 among them, a state that both recruits the inflammatory cells and, in the atrial wall itself, has been shown to feed the fibrotic process through endothelial-to-mesenchymal signaling. That the endothelium of the epicardial fat adopts an activated, adhesive phenotype in atrial fibrillation places the vasculature of the depot within the same fibro-inflammatory network as its fibroblasts and macrophages, and suggests that the recruitment of circulating cells into the fat, across an activated endothelium, is one of the steps by which the remodeling is amplified and sustained.

Placed within the wider picture of epicardial fat and atrial fibrillation, these cellular findings supply a missing link. The epidemiology has established that the volume and the activity of the epicardial fat predict the arrhythmia, and the physiology has shown that the fat can slow and disorganise atrial conduction, but the step between an enlarged, active depot and a remodeled atrium has remained a matter of inference. By resolving the depot into cells and showing that atrial fibrillation is accompanied by the expansion and activation of precisely the fibrotic and inflammatory populations that would be expected to act on the atrium, the present work makes that step explicit and identifies the cellular machinery through which the clinical and the physiological observations may be connected. The natural next step is to test, in larger and longitudinal cohorts and with functional models, whether this machinery is a cause of the substrate and whether interrupting it can prevent it.

6. Conclusion

Single-cell transcriptomic profiling showed that atrial fibrillation is associated with a shift of the epicardial adipose tissue toward a fibro-inflammatory cellular phenotype, in which fibroblasts, myofibroblasts and macrophages expand, the fibroblasts adopt a pro-fibrotic and inflammatory transcriptional programme, and the intercellular signaling that drives them is increased. These findings resolve, at the level of the individual cell, the remodeling of the epicardial fat that accompanies atrial fibrillation, and they identify the cell populations and signaling pathways that may form the atrial substrate and that merit study as targets for its prevention.

Ethical approval

The study was approved by the Institutional Ethics Committee and was conducted in accordance with the Declaration of Helsinki. Written informed consent was obtained from every participant.

Conflict of interest

The authors declare that no conflict of interest exists in relation to this work.

Funding

This work received no specific grant from any funding agency in the public, commercial, or not-for-profit sectors.

Data availability

The data supporting the findings of this study are available from the corresponding author on reasonable request.

References

Abe, I., Teshima, Y., Kondo, H., Kaku, H., Kira, S., Ikebe, Y. *et al.* (2018). Association of fibrotic remodeling and cytokines/chemokines content in epicardial adipose tissue with atrial myocardial fibrosis in patients with atrial fibrillation. *Heart Rhythm*, 15(11): 1717-27.

Hao, Y., Hao, S., Andersen-Nissen, E., Mauck, W.M., Zheng, S., Butler, A. *et al.* (2021). Integrated analysis of multimodal single-cell data. *Cell*, 184(13): 3573-87.

Hatem, S.N. and Sanders, P. (2014). Epicardial adipose tissue and atrial fibrillation. *Cardiovasc Res*, 102(2): 205-13.

Hu, Z., Wang, J., Yan, Y., Zhang, Y., Wang, H., Chen, J. *et al.* (2024). Single-cell RNA sequencing reveals the contribution of smooth muscle cells and endothelial cells to fibrosis in human atrial tissue with atrial fibrillation. *Mol Med*, 30(1): 247.

Hulsmans, M., Clauss, S., Xiao, L., Aguirre, A.D., King, K.R., Hanley, A. *et al.* (2017). Macrophages facilitate electrical conduction in the heart. *Cell*, 169(3): 510-22.

Jin, S., Guerrero-Juarez, C.F., Zhang, L., Chang, I., Ramos, R., Kuan, C.H. *et al.* (2021). Inference and analysis of cell-cell communication using CellChat. *Nat Commun*, 12(1): 1088.

Korsunsky, I., Millard, N., Fan, J., Slowikowski, K., Zhang, F., Wei, K. *et al.* (2019). Fast, sensitive and accurate integration of single-cell data with Harmony. *Nat Methods*, 16(12): 1289-96.

Litvinukova, M., Talavera-Lopez, C., Maatz, H., Reichart, D., Worth, C.L., Lindberg, E.L. *et al.* (2020). Cells of the adult human heart. *Nature*, 588(7838): 466-72.

Mahajan, R., Lau, D.H., Brooks, A.G., Shipp, N.J., Manavis, J., Wood, J.P. *et al.* (2015). Electrophysiological, electroanatomical, and structural remodeling of the atria as a consequence of sustained obesity. *J Am Coll Cardiol*, 66(1): 1-11.

McGinnis, C.S., Murrow, L.M. and Gartner, Z.J. (2019). DoubletFinder: Doublet detection in single-cell RNA sequencing data using artificial nearest neighbors. *Cell Syst*, 8(4): 329-37.

Nalliah, C.J., Bell, J.R., Raaijmakers, A.J.A., Waddell, H.M., Wells, S.P., Bernasochi, G.B. *et al.* (2020). Epicardial adipose tissue accumulation confers atrial conduction abnormality. *J Am Coll Cardiol*, 76(10): 1197-211.

Nattel, S., Heijman, J., Zhou, L. and Dobrev, D. (2020). Molecular basis of atrial fibrillation pathophysiology and therapy: A translational perspective. *Circ Res*, 127(1): 51-72.

Traag, V.A., Waltman, L. and van Eck, N.J. (2019). From Louvain to Leiden: Guaranteeing well-connected communities. *Sci Rep*, 9(1): 5233.

von Elm, E., Altman, D.G., Egger, M., Pocock, S.J., Gotzsche, P.C. and Vandenbroucke, J.P. (2007). The Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) statement: Guidelines for reporting observational studies. *Lancet*, 370(9596): 1453-7.

Wolf, F.A., Angerer, P. and Theis, F.J. (2018). SCANPY: Large-scale single-cell gene expression data analysis. *Genome Biol*, 19(1): 15.

Wong, C.X., Ganesan, A.N. and Selvanayagam, J.B. (2017). Epicardial fat and atrial fibrillation: Current evidence, potential mechanisms, clinical implications, and future directions. *Eur Heart J*, 38(17): 1294-302.

Wu, T., Hu, E., Xu, S., Chen, M., Guo, P., Dai, Z. *et al.* (2021). ClusterProfiler 4.0: A universal enrichment tool for interpreting omics data. *Innovation (Camb)*, 2(3): 100141.

Zheng, G.X., Terry, J.M., Belgrader, P., Ryvkin, P., Bent, Z.W., Wilson, R. *et al.* (2017). Massively parallel digital transcriptional profiling of single cells. *Nat Commun*, 8: 14049.

Cite this article as: Tan J. Wei (2026). Single-cell transcriptomic profiling of epicardial adipose tissue in atrial fibrillation substrate formation. *African Journal of Cardiology and Cardiovascular Medicine*. 2(1), 19-27. doi: 10.62587/AFJCCM.2.1.2026.19-27.