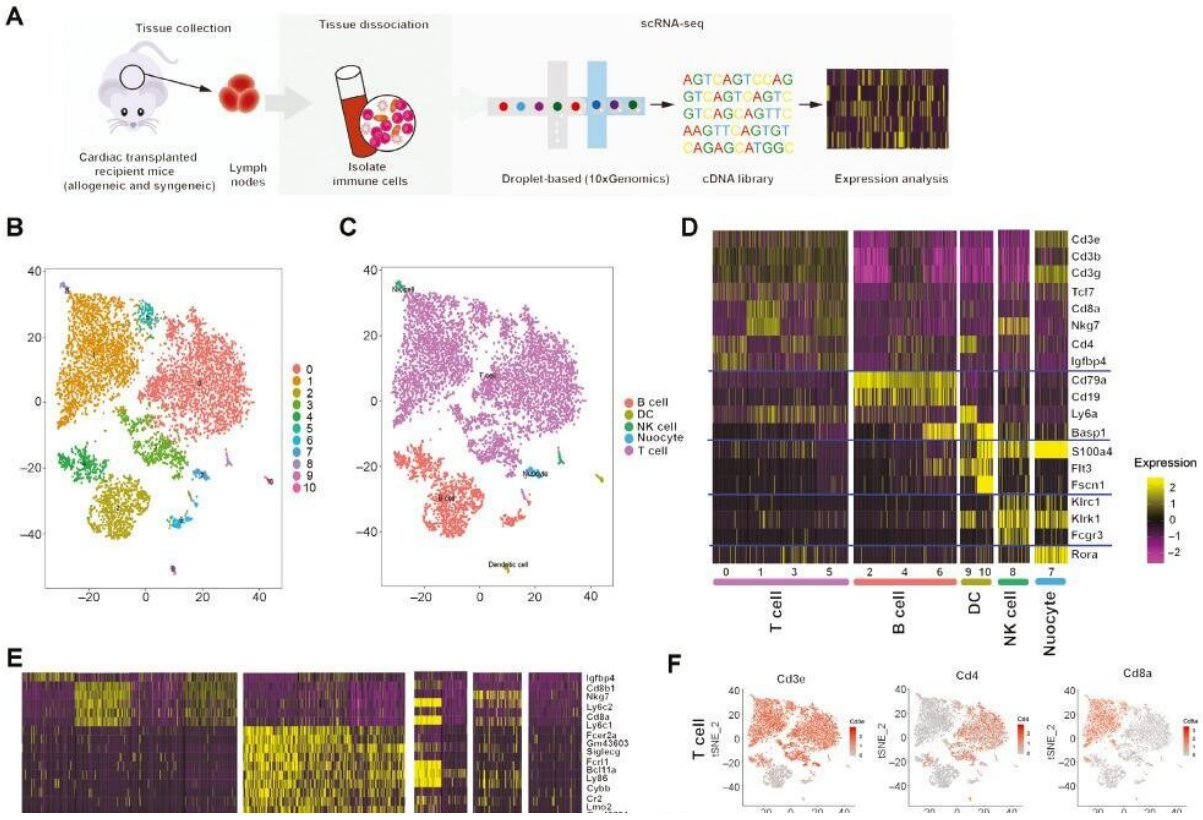
Single-cell RNA sequencing maps immune cell heterogeneity in mice with allogeneic cardiac transplantation

May 25 2023



Single-Cell RNA Sequencing of Immune Cells in Lymph Nodes Reveals the Presence of 11 Cell Clusters. A. Scheme of the overall study design. Single-cell RNA sequencing was applied to immune cells of lymph nodes derived from cardiac transplanted mice, and the output data were used for expression analyses. B. t-SNE projection of 7967 single immune cells (each point represents a single cell) in lymph nodes from syngeneic cardiac transplanted mice sharing similar

transcriptome profiles, grouped by color according to unsupervised clustering results. C. Cluster map showing the assigned identity for each cluster defined in (B). D. Heatmap analysis with known gene expression profiles of T cells, B cells, DC cells, NK cells, and nuocytes. E. Top ten upregulated DEGs (ranked by log fold change) of each cluster in immune cells, plotted in a heatmap. F-I. t-SNE maps indicating the expression of selected well-established cellular markers in cell populations identified as (F), T cells, (G), B cells, (H), DC cells, and (I), NK cells. Credit: *Cardiovascular Innovations and Applications* (2023). DOI: 10.15212/CVIA.2023.0023

Immune cells play important roles in mediating allograft rejection and tolerance after cardiac transplantation. However, immune cell heterogeneity at the single-cell level, and how immune cell states shape transplantation immunity, remain incompletely characterized.

The authors of a new study, published in *Cardiovascular Innovations and Applications*, performed single-cell RNA sequencing (scRNA-seq) on immune cells in LNs from a mouse syngeneic and allogeneic cardiac transplantation model. Nine T cell clusters were identified through unsupervised analysis. Pathway enrichment analysis was used to explore the functional differences among cell subpopulations and to characterize the metabolic heterogeneity of T cells.

The transcriptional landscape of immune cells was determined, particularly T cells, and their metabolic transcriptomes in LNs during mouse cardiac transplantation. On the basis of molecular and functional properties, we also identified T cell types associated with transplantation-associated immune processes, including cytotoxic $CD8^+$ T cells, activated conventional $CD4^+$ T cells, and dysfunctional Tregs. The contribution of JunB to the induction of Th17 cell differentiation and restriction of Treg development was further elucidated, and the authors identified that HIF-1a participates in T cell metabolism and function.

The first systematic single-cell analysis of transcriptional variation within the T cell population is presented in this article, providing new insights for the development of novel therapeutic targets for allograft rejection.

More information: Zhonghua Tong et al, Single-Cell RNA Sequencing Maps Immune Cell Heterogeneity in Mice with Allogeneic Cardiac Transplantation, *Cardiovascular Innovations and Applications* (2023). DOI: 10.15212/CVIA.2023.0023