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Comparison of the transcriptome of human mesenchymal cells isolated from right ventricle and epicardial fat

Authors:
J Stepniewski¹, U Florczyk¹, K Bukowska-Strakova¹, K Szade¹, T Cichon², M Mikula³, M Zembala⁴, M Zembala⁴, A Jozkowicz¹, J Dulak¹, ¹Jagiellonian University, Department of Medical Biotechnology - Krakow - Poland, ²Maria Sklodowska-Curie Memorial Cancer Center and Institute of Oncology, Center for Translational Research and Molecular Biology of Cancer - Gliwice - Poland, ³Maria Sklodowska-Curie Memorial Cancer Center and Institute of Oncology, Department of Genetics - Warsaw - Poland, ⁴Silesian Center for Heart Diseases (SCHD) - Zabrze - Poland,

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Background: Mesenchymal stem/stromal cells isolated from different tissues are claimed to demonstrate similar therapeutic potential. However, thorough comparison of such cells are lacking.

Purpose: The aim of this study was to compare transcriptome of mesenchymal cells with the same phenotype isolated from two different tissues, before and after culture.

Methods: Cells were isolated from biopsies of right ventricle and epicardial fat collected from patients who underwent heart transplantation. Immunophenotyping revealed three distinct populations in both tissues: i) CD31-CD45-CD90+CD34+CD146-, ii) CD31-CD45-CD90+CD34-CD146+ and iii) CD31-CD45-CD90-CD34-CD146+, from which only the first could be grown after sorting. Thus, material for RNA-seq was collected from these cells before culture (250 cells) and on the passage 6 (5000 cells).

Results: Transcriptomic analysis revealed that cells of the same phenotype upon isolation preferentially clustered according to the tissue of origin, not the patient they were isolated from. Additionally, cells from epicardial fat demonstrated higher heterogeneity. After 6 passages, heart- and fat-derived cells did not acquire similar transcriptome. Cell culture itself, however, significantly changed gene expression within both tissues.

Conclusion: This is an important indication that mesenchymal cells isolated from different tissues do not demonstrate similar properties. Accordingly, ease of isolation cannot be considered as a criterion in any therapeutic utilization of such cells.