Monocyte heterogeneity and monocyte subsets specific to kawasaki disease revealed by single-cell RNA-seq

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Abstract

Kawasaki disease (KD) is characterized by a disorder of immune response, but its etiology remains unknown. Monocyte is an important member of body's innate immune system, however its role in KD is still elusive due to its ambiguities heterogeneity and complex functions. Here, single-cell RNA-seq was performed to map monocyte subsets and identify the KD specific monocyte subsets. Single-cell RNA-seq was used to transcriptionally profile the circulating monocytes that were separated from peripheral blood mononuclear cells and Seurat R package was used to identify the monocyte subsets. Four monocyte subsets were identified in healthy children, in which three clusters were mainly CD14+CD16- monocytes and one cluster was mainly CD14-CD16+ monocytes. Transcriptional markers of each subset were identified and the four monocyte subsets represent a linear differentiation. Two monocyte subsets specific to KD were identified, including one subset expressing FOLR3, S100A12 and IL1R2 and the other expressing MT-TN specifically. Moreover, KD specific monocyte subsets were mainly classical monocytes that poorly differentiated, and their function mainly involved in neutrophil activation. In conclusions, a relatively comprehensive map of circulating monocyte subsets was plotted for the first time in healthy children. KD specific monocyte subsets and their transcriptional markers were revealed respectively, which will contribute to the confirmation of diagnostic markers and development of a novel therapeutic strategy.

Biography:

Zhimin Geng is a medical doctor reading in Zhejiang University School of Medicine and her research expertise is Kawasaki disease. Her tutors is Prof. Fangqi Gong, who has published more than 20 papers in reputed journals and has been serving as a leader of Chinese medical association.

Speaker Publications:

1. "Microarray Analysis of Differential Gene Expression Profile Between Human Fetal and Adult Heart"; Pediatric Cardiology. / 2017 / 38(4) /pp 700-706

2. "Microarray analysis reveals a potential role of LncRNAs expression in cardiac cell proliferation"; BMC Developmental Biology / 2016 / Vol 16 (1)

17th International Conference on Pediatrics and Pediatric Cardiology; Webinar; June 18-19, 2020.

Abstract Citation:

Zhimin Geng, Monocyte heterogeneity and monocyte subsets specific to kawasaki disease revealed by single-cell RNA-seq, Pediatric Cardiology 2020, 17th International Conference on Pediatrics and Pediatric Cardiology; Webinar; June 18-19, 2020
(https://pediatriccardiology.conferenceseries.com/europe/abstract/2020/monocyte-heterogeneity-and-monocyte-subsets-specific-to-kawasaki-disease-revealed-by-single-cell-rna-seq)