Title:
ScRNAseq based analysis of the stromal immune cell composition in murine pre-weaning and adult white adipose tissues

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Abstract

Early postnatal adipose growth is essential to establish a functional metabolism. Conversely, proportional adipose expansion in adults results in insulin resistance. Despite adipocytes, immune cells play a pivotal role in orchestrating adipose tissue function and expansion. To this end, we performed an in-depth analysis of scRNAseq data of immune cell populations of 2 weeks (pre-weaning) and 8 weeks old (adult) murine subcutaneous and perigonadal adipose depots. Our analysis revealed 15 distinct immune cell clusters. Most immune cell types were found in all depots and ages. Among the detected T-cell populations, we only observed differences in the abundance of naïve T cells, which were predominantly found in in subcutaneous white adipose tissue, irrespective of age. Similar to human, we could define several murine macrophage subtypes. Among them, perivascular macrophages (PVM) were predominantly found in subcutaneous white adipose tissue of 2 weeks old mice. RNA-velocity analysis and pseudotime trajectory construction suggested a developmental trajectory from lipid-associated macrophages (LAM) to PVM, which was further corroborated by analysis of gene expression dynamics resolved along latent time of white adipose tissue macrophages from 2 weeks old mice. Further analysis revealed that the top-ranked 100 genes of LAM were associated with the regulation of endothelial cell migration and proliferation (Nrp1, Grn, Glul, Sash1, Ccl24), blood vessel morphogenesis (Nrp1, Tgfbr2) and the regulation of epithelial cell proliferation. In summary, we provide a comprehensive overview of the immune cell composition of pre-weaning and adults murine adipose tissues. Moreover, we provide in-depth analysis of T-cell and macrophage populations and their relationship and dependency based on mRNA expression analysis.