

ABSTRACT

Angiogenesis – the formation of new blood vessels from pre-existing ones – requires interaction between several cell types and involves signaling molecules, secreted as well as membrane-tethered and their cognate receptors, of many different types. My laboratory focuses on mechanisms of angiogenic sprouting, and the involvement of distinct endothelial phenotypes (tip cells and stalk cells) in this process. We are also investigating the mechanisms leading to the recruitment of vascular mural cells (pericytes and vascular smooth muscle cells) to blood vessels and the role of these cells, in particular the pericytes, in vascular development and function. However, pericyte identification remains challenging due to a paucity of defining markers, and there are not yet any good tools available for their specific genetic manipulation. As a consequence, there is not an accepted consensus about how pericytes should be defined, where they reside, how heterogeneous they are, and what they do. To resolve this problem, we use single cell RNA sequencing to define pericytes and other vascular and vessel-associated cell types of the brain, as well as in other organs. In addition to providing cell type and subtype definitions based on genome-wide quantitative transcriptional information, our data also reveal new insights in the arterio-venous zonation and organotypicity of vascular cell, as well as the identification and definition of hitherto unrecognized vascular cell types.