## Identification of the Red Pulp Macrophage Niche in the Mouse Spleen

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The spleen filters the blood, removes circulating microorganisms, aging cells and cellular debris. It is composed of lymphoid islands collectively known as the white pulp surrounded by the red pulp. The red pulp is populated by a dense community of red pulp macrophages (RPM) endowed with important biological functions, including the phagocytosis of senescent red blood cells and the recycling of iron.
The development and homeostasis of macrophages are controlled by the availability and proper positioning of soluble and surface bound survival factors such as Fractalkine (CX3CL1), Interleukine-34 (IL34) and colony stimulating factor (CSF) 1 and 2. Indeed, mice deficient for these molecules display various alterations of their mononuclear phagocyte system. These dependencies suggest that macrophages are located in and depend on “niches” that are thought to provide an anchoring scaffold, appropriate nurturing as well as microenvironmental cues responsible for the pronounced tissue-specificity of distinct macrophage populations. The cellular identity of such niches, however, remains elusive and is currently the subject of intense research efforts.
While the biological functions of RPM have been extensively studied, the identification of their cellular niche remains to be determined. Using advanced imaging techniques and genetic tools, we showed that RPM reside among a network of fibroblastic stromal cells located in the splenic red pulp. We then characterized these stromal cells by flow cytometry, confocal imaging and transcriptomics. Finally, in vivo deletion of RPF and conditionally ablation of Csf1 in these cells drastically reduced the population of RPM.
Altogether, our results unraveled a novel type of splenic fibroblasts that acts as an essential component of the RPM niche in the mouse.

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