Tumor-infiltrating myeloid cells are conserved between human and mouse lung cancers

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Tumor-infiltrating myeloid cells (TIM) have emerged as key cancer regulators and potential next-generation immunotherapy targets. TIMs include monocytes, macrophages, dendritic cells, and neutrophils. These cells develop into a range of diverse states, many of which can in turn affect tumor initiation, growth, and progression. TIM state heterogeneity, particularly in human cancers and as compared to lymphocytes, remain poorly understood. To address this knowledge gap, we used single-cell RNA sequencing to map TIMs in non-small cell lung cancer patients. We uncovered over twenty TIM states, most of which were reproducibly found across patients. To facilitate translational research of these populations, we also profiled TIMs in mice. In systematically comparing TIMs across species, we identified a near-complete congruence of population structures among dendritic cells and monocytes; conserved neutrophil subsets; and species differences among macrophages. By contrast, myeloid cell population structures in patients' blood showed limited overlap with those of TIMs. We further identified unique markers, which both defined TIM states and associated with clinical prognosis. This study comprehensively maps the lung TIM landscape and sets the stage for future investigations into the potential of TIMs as immunotherapy targets.

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