Leveraging the power of high parameter cell sorting and single-cell multi-omics to profile intratumoral immune cells in a model of B cell lymphoma

Imaging

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The pathogenesis and progression of B-cell lymphomas is a dynamic process involving reciprocal interactions between malignant cells and surrounding components in the tumor microenvironment. Neoplastic B cells migrate to lymphoid sites and prompt the immune cell infiltration. The infiltrated cytotoxic lymphocytes potentially contribute to tumor cell killing and good prognosis. However, most immune cell types in the tumor niche often become unresponsive or end up promoting tumor growth. In this study we present a sorting strategy using the BD FACSymphony™ S6 Cell Sorter that enables concurrent isolation of six cell populations from a tumor niche in a murine B-cell lymphoma model. Single-cell sequencing was used downstream to unravel the respective roles of each cell subset for the tumor's progression and/or evasion. The six cell subsets were isolated from mice that had been inoculated with an OVA-expressing B-cell lymphoma cell line and subsequently with either wild-type or BTLA-deficient OVA-specific CD8+ T cells. The cell sorting aided more robust single-cell profiling of rare cell subsets within the sorted populations. In summary, we demonstrated a high-throughput approach that enabled a comprehensive characterization of critical cell populations in tumor responses. Since these cell populations constitute potential targets for the treatment of B-cell lymphomas, this platform, notably through the analysis of protein expression, offers an opportunity for identification of new therapeutic targets.

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