Deciphering the Links between Microbiome and Immune Profiles by Single-Cell Multi-Omics Analysis.

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Precision medicine, also known as "personalized medicine," embodies a pioneering approach for disease treatment and prevention, considering unique variations in genes, environment, and lifestyles. This method necessitates comprehensive high-throughput and dimensional analysis to garner multi-omics data, offering insights into individual disease variances. We have been developing the novel platforms for single-cell technologies that enabled detailed cellular profiling, establishing cell atlases across various tissues and disease stages, enhancing our understanding of potential drivers in complex biological processes.

We focused on the development of innovative platforms for immune profiling and microbiome profiling utilizing CITE-seq, split-pool scRNA-seq, Drop-seq, 16S rRNA-seq, and advanced FACS analysis, striving to unveil pivotal drivers impacting disease progression. Our findings highlight new immune cell clusters and delineate immune cell dynamics during murine atherosclerosis progression and helminth-induced aortic plaque regression. Distinct myeloid and T cell populations were identified in inflamed tissues, a finding further corroborated by additional scRNA-seq datasets from inflammatory bowel disease (IBD) patients.

Furthermore, leveraging the CITE-seq technique, we proficiently profiled peritoneal fluid cells using a tailored oligonucleotide-label antibody panel, isolating 14 unique markers expressed solely on tissue-resident macrophages at the proteomic level. A specialized CITE-seq panel, reacting with 154 unique human cell surface antigens, has been crafted, enabling simultaneous acquisition of transcriptomic and proteomics data at the single-cell tier. Our ongoing efforts include the high-parameter FACS analysis to profile diverse surface markers on murine and human immune cells, aiming to uncover vital immune cell clusters that signify disease progression.

In conclusion, employing machine learning models enhances our capacity to pinpoint crucial microbiota closely linked with distinct immune profile variations on multi-omics data. This integrative approach of single-cell multi-omics analysis and machine learning models stands to significantly contribute to the identification of future therapeutic avenues by unraveling the intricate associations between microbiota and immune profiles.