LETTER TO THE EDITOR

An omics-based tumor microenvironment approach and its prospects

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ABSTRACT

Multi-omics approaches are revolutionizing cancer research and treatment by integrating single-modality omics methods, such as the transcriptome, genome, epigenome, epi-transcriptome, proteome, metabolome, and developing omics (single-cell omics). These technologies enable a deeper understanding of cancer and provide personalized treatment strategies. However, challenges such as standardization and appropriate methods for funneling complex information into clinical consequences remain. The tumor microenvironment (TME) is a complex system containing cancer cells, immune cells, stromal cells, and secreted molecules. To overcome these challenges, researchers can establish standardized protocols for data collection, analysis, and interpretation. Collaborations and data sharing among research groups and institutions can create a comprehensive and standardized multi-omics database, facilitating cross-validation and comparison of results. Multi-omics profiling enables in-depth characterization of diversified tumor types and better reveal their function in cancer immune escape. Datasets play a fundamental role in multi-omics approaches, with artificial intelligence and machine learning (AI) rapidly advancing in multi-omics for cancer.

Key words: multi-omics; TME; cancer

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Multi-omics approaches are revolutionizing cancer research and treatment by integrating multiple single-modality omics methods, such as the transcriptome, genome, epigenome, epi-transcriptome, proteome, metabolome, and developing omics (single-cell omics) [1]. These technologies have proven to be the most effective tools for dissecting the core mechanisms of cancer, with the Cancer Genome Atlas (TCGA) serving as an example. Researchers can uncover intricate molecular interactions and identify novel biomarkers and therapeutic targets by integrating various omics data, which single-modal approaches alone would have missed. This enables a deeper understanding of cancer and paves the way for more personalized and effective treatment strategies. However, multi-omics approaches also present challenges, such as standardization and appropriate methods for funneling complex information into clinical consequences. The tumor microenvironment (TME) is a complex system that contains cancer cells, tumor-infiltrating immune cells, stromal cells, the extracellular matrix (ECM), and other secreted molecules [2]. To overcome these challenges, researchers can establish standardized protocols and guidelines for data collection, analysis, and interpretation. Collaborations and data sharing among different research groups and institutions can help create a comprehensive and standardized multi-omics database, which can facilitate cross-validation

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and comparison of results. Based on their features, we can classify tumors as cold or hot, with hot tumors characterized by T cell infiltration and immune activation, presenting efficient responses to immunotherapy, and cold tumors characterized in the opposite way. Developing multi-omics profiling will enable in-depth characterization of diversified tumor types and better reveal their function in cancer immune escape. Multi-omics analysis of the TME is an important research direction in precision medicine, as it can reveal the heterogeneous composition of tumor and immune cells, evaluate disease progression, and guide therapeutic regimens for each patient.

Datasets play a fundamental role in multi-omics approaches in cancer research, providing the raw material for comprehensive analyses that integrate various molecular layers. They serve as centralized platforms for integrating diverse omics data, providing structured storage systems, and enhancing data accessibility for researchers to collaborate and validate findings. Artificial intelligence and machine learning (AI) are rapidly advancing in multi-omics for cancer, offering sophisticated analytical approaches with predictive capacities. While multi-omics approaches offer unprecedented insights into cancer biology and personalized medicine, addressing technical, computational, and ethical challenges is essential to harnessing their potential. Since the late 1990s, medical diagnostics have used AI and ML approaches for imaging, immunotherapy, diagnosis, and prognosis of cancer [3]. In the upcoming years, AI and ML-based methods will become increasingly important in digital healthcare for both diagnosis and therapy. In conclusion, multi-omics approaches are revolutionizing cancer study and treatment by enabling in-depth characterization of diversified tumor types and better understanding of their function in cancer immune escape. Still, problems like standardization, finding the right ways to turn complicated data into useful clinical information, and the possibility of using multi-omics approaches to find cancer earlier are still there.

Conflict of interest
Author declare no conflict of interests.

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