Overcoming immune evasion mechanisms in cancer therapy.

Stein Rivert*

Department of Oncology, University College London, United Kingdom

Introduction

The field of clinical cancer immunology has witnessed remarkable advancements with the introduction of immune checkpoint inhibitors targeting PD-1 and CTLA-4. However, the pursuit of more effective and comprehensive immunotherapies continues to drive research into alternative strategies to overcome immune evasion mechanisms employed by tumors [1].

Beyond PD-1 and CTLA-4, researchers are exploring other immune checkpoint pathways such as LAG-3 (lymphocyte-activation gene 3), TIM-3 (T-cell immunoglobulin and mucin-domain containing-3), and TIGIT (T-cell immunoreceptor with Ig and ITIM domains). These checkpoints play distinct roles in regulating T-cell function and are frequently upregulated in various cancers, contributing to immune evasion. Therapeutic agents targeting these pathways are currently under investigation in preclinical and clinical trials, showing potential to overcome resistance to PD-1/PD-L1 and CTLA-4 inhibitors [2].

For instance, combining ICIs with chemotherapy, radiotherapy, or targeted therapies can create a more favorable tumor microenvironment. Additionally, combinations involving multiple checkpoint inhibitors, such as PD-1 with LAG-3 or TIGIT, are being evaluated for their synergistic potential in boosting immune responses [3].

Approaches include targeting immunosuppressive cells such as regulatory T-cells (Tregs) and myeloid-derived suppressor cells (MDSCs), as well as enhancing the activity of tumor-infiltrating lymphocytes (TILs). Drugs that modulate cytokines, chemokines, and metabolic pathways within the TME are also under active development [4].

Advances in genomics and proteomics have paved the way for personalized cancer immunotherapy. Neoantigen-based vaccines, which target tumor-specific mutations, are being developed to elicit robust immune responses. Additionally, biomarker-driven approaches are helping identify patients most likely to benefit from specific therapies, optimizing treatment outcomes [5].

Cellular immunotherapies, such as chimeric antigen receptor (CAR) T-cell therapy, are expanding the horizons of cancer treatment. While initially successful in hematologic malignancies, efforts are underway to adapt CAR-T therapies for solid tumors by addressing challenges like the immunosuppressive TME and antigen heterogeneity. Other cell-based approaches, including tumor-infiltrating lymphocyte (TIL) therapy and natural killer (NK) cell therapy, are also showing promise in preclinical and clinical studies [6].

Oncolytic viruses are engineered to selectively infect and kill tumor cells while stimulating an anti-tumor immune response. These viruses can also be modified to deliver immunostimulatory molecules, further enhancing their therapeutic potential. When combined with ICIs, oncolytic viruses may provide a dual attack on cancer by directly lysing tumor cells and boosting systemic immunity [7].

The integration of cutting-edge technologies such as artificial intelligence (AI) and machine learning is expected to accelerate the discovery and optimization of novel immunotherapies. AI-driven analysis of large-scale genomic, transcriptomic, and proteomic data can identify new therapeutic targets and predict patient responses more accurately [8].

Furthermore, ongoing research aims to expand the applicability of immunotherapy to a broader range of cancers and earlier disease stages. Efforts are also focused on mitigating immune-related adverse events (irAEs) to improve the safety and tolerability of these treatments [9].

Combining immune checkpoint inhibitors with other modalities has emerged as a promising strategy to enhance anti-tumor efficacy. The tumor microenvironment (TME) plays a critical role in cancer progression and immune evasion. Emerging strategies aim to reprogram the TME to support immune activation [10].

Conclusion

Overcoming immune evasion mechanisms in cancer therapy remains a central challenge in achieving durable and effective treatments. By targeting additional immune checkpoints, reprogramming the TME, and leveraging personalized and cell-based therapies, the next generation of immunotherapies promises to bring us closer to achieving durable cancer control and improved patient survival.

References

1. Makarem N, Chandran U, Bandera EV, et al. Dietary fat in breast cancer survival.Annu Rev Nutr.2013;33:319–348.
2. Jung S, Wang M, Anderson K, et al. Alcohol consumption and breast cancer risk by estrogen receptor status: in a pooled analysis of 20 studies.In J Epidemiol.2016;45:916–928.

***Correspondence to:** Stein Rivert, Department of Oncology, King Abdullah Medical City, Saudi Arabia. E-mail: steinri@hotmail.com

***Received:** 02-Dec-2024, Manuscript No. AAJCIT-24-155304; **Editor assigned:** 03-Dec-2024, Pre QC No. AAJCIT-24-155304(PQ); **Reviewed:** 17-Dec-2024, QC No AAJCIT-24-155304; **Revised:** 23-Dec-2024, Manuscript No. AAJCIT-24-155304(R); **Published:** 30-Dec-2024, DOI:10.35841/aajcit-7.6.245*

***Citation:** Rivert S. Overcoming immune evasion mechanisms in cancer therapy. J Cancer Immunol Ther. 2024;7(6):245*

3. Ravdin PM, Cronin KA, Howlader N. et al. The decrease in breast-cancer incidence in 2003 in the United States.N Engl J Med.2007;356:1670–1674.

4. Catsburg C, Miller AB, Rohan TE. Active cigarette smoking and risk of breast cancer.Int J Cancer.2015;136:2204–2209.

5. Desmedt C, Zoppoli G, Gundem G, et al. Genomic Characterization of Primary Invasive Lobular Breast Cancer.J Clin Oncol.2016;34:1872-1881.

6. Su Y, Wang X, Li J, et al. The clinicopathological significance and drug target potential of FHIT in breast cancer, a meta-analysis and literature review.Drug Design Deve Therapy.2015;9:5439–5445.

7. Berardi R, Morgese F, Onofri A, et al. Role of maspin in cancer.Clin Transl Med.2013;2:8.

8. Dabiri S, Moeini Aghtaei M, Shahryari J, et al. Maspin Gene Expression in Invasive Ductal Carcinoma of Breast. Ira J Pathol.2016;11:104–111.

9. Navarro SL, Chang JL, Peterson S, et al. Modulation of human serum glutathione S-transferase A1/2 concentration by cruciferous vegetables in a controlled feeding study is influenced by GSTM1 and GSTT1 genotypes.*Cancer Epidemiol Biomarkers Prev.*2009;18:2974-8.

10. Inoue K, Fry EA. Aberrant expression of cyclin D1 in cancer.Signal Transduction Insights.2015;4:1–13.

Citation: *Rivert S. Overcoming immune evasion mechanisms in cancer therapy. J Cancer Immunol Ther. 2024;7(6):245*