Archives in Cancer Research©
3 (11) 2023 : 001-003 • MINI REVIEW

Cancer immunotherapy

Alaric Steve*

Molecular Development of the Immune System Section, USA

AUTHORS' CONTRIBUTION: (A) Study Design · **(B)** Data Collection . **(C)** Statistical Analysis · **(D)** Data Interpretation · **(E)** Manuscript Preparation · **(F)** Literature Search · **(G)** No Fund Collection

ABSTRACT

Immunotherapy is a cancer treatment. It boosts the immune system and helps the body detect and destroy cancer cells by using compounds created by the body or in a laboratory. Immunotherapy can be used to treat a wide range of cancers. It can be used alone or with chemotherapy and/or other cancer therapies.

Keywords: Cancer; Cancer treatment; Immunotherapy; Chemotherapy

Address for correspondence:

Alaric Steve,
Molecular Development of the Immune System Section, USA
E-mail: stevealaric@rediff.com

Word count: 1363 **Tables:** 00 **Figures:** 00 **References:** 10

Received: 02.05.2023, Manuscript No. ipacr-23-13684; **Editor assigned:** 04.05.2023, PreQC No. P-13684; **Reviewed:** 18.05.2023, QC No. Q-13684; **Revised:** 23.05.2023, Manuscript No. R-13684; **Published:** 30.05.2023

INTRODUCTION

Cancer immunotherapy is a strategy of tumour management and elimination that involves reactivating the body's cancer-immunity cycle and restoring its antitumor immune response. Increased data availability, along with advances in high-performance computers and novel artificial intelligence (AI) technologies, has resulted in an increase in the application of AI in cancer research. In immunotherapy research, cutting-edge AI models for functional categorization and prediction are increasingly being employed to supplement laboratory-based trials. This paper provides an overview of current AI applications in immunotherapy, such as neoantigen detection, antibody creation, and immunotherapy response prediction. Moving ahead in this manner will result in more powerful prediction models for identifying better targets, medicines, and therapies, and these developments will ultimately make their way into clinical settings, propelling AI forward in the field of precision oncology [1-5].

T cell antitumor immunity is critical to the effectiveness of cancer immunotherapy. Identifying the repertoire of T cell antigens expressed on the tumour cell surface is critical for many targeted immunotherapies designed to boost T cell-driven antitumor response. A scan of such antigens using mass spectrometry ("immunopeptidomics") in conjunction with other omics platforms and computational techniques has proved critical in discovering and quantifying tumor-derived T cell antigens. We examine the types of tumour antigens that have developed for targeted cancer immunotherapy, as well as the immunepeptidomics technologies that are critical in MHC peptide identification and quantification, in this review. We present an overview of the advantages and disadvantages of mass spectrometry-driven techniques, as well as how they have been used with other technologies to identify targetable T cell antigens for cancer immunotherapy. We discuss some of the new cancer immunotherapies that have effectively used immunopeptidomics, as well as their limitations and mass spectrometry-based tactics that can help them evolve.

Immunotherapy has long been used to treat cancer. Aside from standard chemotherapy, radiotherapy, and surgery, the ongoing development of biotechnology and the characterization of tumour molecular mechanisms have resulted in immunotherapy playing an increasingly important role in cancer treatment and becoming one of the leading cancer treatments. Immunotherapy, as opposed to standard cancer treatments, is a treatment technique that employs the body's own immune system to combat cancer by targeting various sites and dynamically modifying the immune system. Immune checkpoint

blockage (ICB) and adoptive cell therapy (ACT) are the two main cancer immunotherapies. ICB boosts the immune system's reaction to cancer cells, which has been repressed. Immune checkpoint inhibitors, such as antibodies neutralising programmed cell death protein 1 (PD-1) or cytotoxic T-lymphocyte-associated protein 4 (CTLA-4), are employed in the ICB method to reactivate tumor-specific T lymphocytes. By guiding or manipulating immune cells, therapeutic antibodies can aid to boost antitumor immunity. To guide immune responses, therapeutic antibodies (such as anti-CD20 rituximab) attach directly to tumor-associated antigens (TAs). The patient's own immune cells are taken and in vitro manipulated to improve their antitumor capabilities for the ACT method. CAR-T and TCR treatments, for example, entail the alteration of a patient's T cells to allow them to target known TAs. Both kinds of cancer immunotherapy rely on tumor-specific mutations in particular patients to trigger T-cell-mediated immune responses targeted to the malignancy. In this study, we will look at three key aspects in cancer immunotherapy: neoantigen detection, antibody design, and immunotherapy response prediction. Neoantigens are mutations that encode immunologically active proteins, causing the immune system to identify the afflicted cell as alien. Neoantigens are critical in the development of personalised cancer immunotherapies such personalised cancer vaccines, ICB, and ACT. Because only a small number of mutations are immunogenic, predicting neoantigens, also known as neoepitopes, is a major challenge for computational immunotherapy approaches and a requirement for narrowing down mutations for inclusion in vaccines or high-throughput methods assessing T-cell recognition in vitro. Many neoantigens predicted by next-generation sequencing (NGS) may be unable of being effectively translated into proteins or peptides, which might explain why NGS predictions of some tumours do not match actual therapy outcomes. The selection of safe target antigens is a major difficulty for immunotherapies that entail the transfer of TCRs into recipient patient T cells. The consequences of modified TCR-T cells cross-reacting with self-antigens in healthy tissue can be disastrous. Because not all tumours contain an adequate number of immunogenic mutations, identifying a broader range of shared TAs (gene fusions, alternative splicing, mutational frame shifts, and endogenous retroviruses) has the potential to broaden the scope and number of therapeutic cancer vaccines and immunotherapy efficacy assessments.

Antibody design is critical for therapeutic antibodies or antibody-single bonddrug conjugates (ADCs) used in cancer therapy. There are eleven ADCs and two bispecific antibodies, blinatumomab and amivantamab, that are authorised anticancer antibodies in alternate forms. The efficacy of these antibodies in treating cancer, particularly haematological malignancies, has fueled increased attempts to generate next-generation anticancer antibodies with higher response rates or durations. The prediction of antibody structure has several implications in antibody engineering. The capacity to forecast 'developability' is another problem in computational antibody creation. An antibody's 'developability' already includes a number of desired drug-like features, including as its manufacturability, storage stability, simplicity of administration, and favourable pharmacological behaviour in patients. This method is comparable to the Lipinski rule of five, which has shown to be quite useful in the creation of small molecule drugs. It is believed that the antibody sequence space contains up to 1018 distinct molecules. Creating phage display libraries is a conventional method for discovering novel antibodies. These libraries provide users access to up to 1011 different molecules, which is only a small portion of the total available space. The task for antibody engineers is to devise a computational approach for exploring the antibody sequence space and discovering novel functional antibodies. Furthermore, all protein-based therapies, including monoclonal antibodies (mAbs), have the potential to be immunogenic and induce immunological responses in humans. The immunogenicity of monoclonal antibodies (mAbs) and anti-drug antibodies (ADAs) can produce adverse responses is also a serious issue [6-10]. AI technology comprises a variety of technologies that all share the objective of computationally mimicking human intellect. Over the last decade, deep learning (DL) algorithms such as deep neural networks (DNNs) have gained extraordinary success in processing natural data types such as photos, text, and audio. Cancer diagnosis, molecular characterisation, tumour microenvironment characterization, pharmacogenomics discovery, and clinical outcome prediction are just a few of the uses of AI in cancer research and precision medicine. AI is great for complicated pattern identification in vast amounts of data and can deliver quantitative judgements automatically. By amassing medical data, such as omic, radiography, pathology, and clinical data, and related outcomes, AI techniques enable computers to get better at performing certain jobs and developing decision support systems.

CONCLUSION

Cancer immunotherapy based on T cells has emerged as a potent weapon in the fight against cancer. Nonetheless, it required many years of fundamental science discoveries and subsequent clinical translation to conclusively establish the potential of immune system modulation in cancer treatment. Further study into the control of T cells and other immune cells, such as APCs and natural killer cells, may help us to improve the efficacy of this technique. The impact sizes found in clinical studies of checkpoint blockade medicines, ATC transfer treatments, and cancer vaccines in 'difficult to treat' cancers were significantly greater than the most successful chemotherapeutic agents. Despite the fact that immune-related side effects are widespread; these novel immune-targeting medicines are better tolerated than standard chemotherapeutic drugs. Cancer immunotherapy is a developing discipline that is expanding as indications for presently authorised medicines increase and the quest for novel druggable targets continues. The cancer immunotherapy success stories we've shared demonstrate the inextricable link between fundamental scientific research and clinical practise. They also show how

a bench-to-bedside approach based on sound basic research may be successful in combating one of humanity's most feared illnesses.

REFERENCES

1. **Gao B**. Cytokines, STATs, and liver disease. *Cell Mol Immunol*. 2005; 2(6):92–100.
2. **Huang D, Chen X, Zeng X, et al**. Targeting the regulator of G protein signaling 1 in tumor-specific T cells enhances their trafficking to breast cancer. *Nat Immunol*. 2021; 22:865–879.
3. **Lu T, Bankhead A, Neamati N, et al**. Multi-omics profiling reveals key signaling pathways in ovarian cancer controlled by STAT3. *Theranostics*. 2019; 9(1):5478–5496.
4. **Calò V, Migliavacca M, Bazan V, et al**. STAT proteins: from normal control of cellular events to tumorigenesis. *J Cell Physiol*. 2003; 197 (6):157–68.
5. **Machida K, Tsukamoto H, Liu JC, et al**. C-jun mediates hepatitis c virus hepatocarcinogenesis through signal transducer and activator of transcription 3 and nitric oxide-dependent impairment of oxidative DNA repair. *Hepatology*. 2010; 52 (8):480–492.
6. **Darnell JE Jr., Kerr IM, Stark GR**. Jak-STAT pathways and transcriptional activation in response to IFNs and other extracellular signaling proteins. *Sci.* 1994; 264(4):1415–1421.
7. **Siegel RL, Miller KD, Fuchs HE, et al**. Cancer statistics, 2022. *CA Cancer J Clin.* 2022; 72(4):7-33.
8. **Groen RS, Gershenson DM, Fader AN**. Updates and emerging therapies for rare epithelial ovarian cancers: one size no longer fits all. *Gynecol Oncol*. 2015; 136 (6):373–383.
9. **Robson M, Im SA, Senkus E, et al**. Olaparib for metastatic breast cancer in patients with a germline BRCA mutation. *N Engl J Med*. 2017; 377 (7):523–533.
10. **Chang SJ, Hodeib M, Chang J, et al**. Survival impact of complete cytoreduction to no gross residual disease for advanced-stage ovarian cancer: a meta-analysis. *Gynecol Oncol*. 2013; 130(7):493–498.