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Immunogenetics: Open Access

Short Communication

Predictive Cancer Medicine with High-Throughput Immunogenetics

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ABSTRACT

The biochemical backdrop of cancer is exceedingly complex, making individualized therapeutic interventions difficult. Predictive medicine promises to remove this barrier by combining data from various 'subsystems,' including as the host, the external environment, the tumours, and the tumours micro-environment. Immunogenetics is a crucial technique for understanding lymphoid cancer ontogeny at both a cell-intrinsic and cell-extrinsic level, *i.e.* by analyzing micro-environmental interactions, with the goal of developing predictive treatment. Next Generation Sequencing (NGS), which allows for a detailed analysis of immunological receptors. Indeed, NGS immunogenic analysis (immune-seq) has emerged as a critical tool for understanding cancer pathophysiology and increasing clinical decision-making accuracy in oncology. Immune-seq has uses in lymphoid malignancies, such as helping in diagnosis by distinguishing between reactive and non-reactive diseases as well as disease monitoring through reliable minimal residual disease diagnosis.

Keywords: Next Generation Sequencing (NGS); Immunological receptors; Immunogenetics

INTRODUCTION

Immunogenetics is the study of how genetics, the immune system, hereditary immune response regulation, disease vulnerability, immune system bioinformatics, immunologically relevant molecular arrangement, reproductive biology immune genetics, tissue separation, and development interact. Sequences, nucleotides, genes, proteins, immune globins, and antibodies such as T-cell receptor, Major Histocompatibility Complex (MHC), and human leukocyte antigen are all part of immune genetics (HLA). Immune genetics can be used to diagnose, treat, and engineer autoimmune disorders, as well as acquired immunodeficiency diseases (such as cancer, AIDS, and other infectious diseases) [1]. Rapid advancements in cancer immunology should lead to a better knowledge of the molecular mechanisms underpinning cancer formation, progression, and therapy response. As evidenced by the recent breakthrough in cancer immunotherapies, adaptive immune responses inside the tumours microenvironment appear to be key drivers of the clinical course in each cancer patient. Immunotherapeutic treatments include immune checkpoint inhibitors, adoptive cell therapies, and therapeutic cancer vaccines, all of which attempt to improve anti-tumor responses in solid tumours and hematological malignancies [2].

DESCRIPTION

Antigen recognition in adaptive immune cells is based on a remarkably diverse repertoire that is consolidated by the coordinated action of primarily two mechanisms during differentiation: (i) DNA recombination of the IG/TR Variable (V), Diversity (D), and Joining (J) genes; and (ii) antigen-dependent maturation, which is critically dependent on selection processes. Immune-seq strives to capture the characteristics of both pathways in molecular detail, which obviously raises various problems. Immune-seq analysis has been used to investigate B and T cells, namely the B cell Receptor Immunoglobulin (BcR IG) and the T cell Receptor (TR). The introduction of NGS based techniques has given clonally evaluation a whole new meaning. Unlike prior methods like Genes can analysis/spectra typing, NGS based locality evaluation uses BcR IG/TR collotype computation, which takes into consideration the makeup of each unique sequence. In both health and disease, locality assessment using NGS based IG/TR gene rearrangement sequences could be widely used for in-depth

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qualitative and quantitative characterization of B and T cell populations. This method may also be useful for determining the clonal association of BcR IG/TR gene rearrangements from different anatomical regions or throughout time, as well as assessing intraclonal diversity in mature B cell malignancies due to ongoing somatic hyper mutation. Immune-seq is also effective for determining locality in materials with poor DNA quality, such as formalin tissue samples, paraffin-embedded tissues [3-5].

Immune-seq has a lot of promise for overcoming this constraint because it allows for systematic, longitudinal, and thorough clone characterization and tracking even at extremely low frequencies, allowing for rapid clinical treatments. This is especially important given that early repertoire diversity recovery has been identified as a marker for reduced risk of graft-versus-host illness and relapse. Furthermore, detailed characterization of the TR repertoire in patients undergoing allogeneic hematopoietic stem cell transplantation for hematological malignancies could be used to monitor graft clones with potential anti-leukemia effects as well as cytotoxic clones that eventually cause graft-versus-host disease. Because of the large number of available TR specificities, T cells are intrinsically capable of attacking and eliminating cancer cells *via* neo-antigen identification.

Immune-seq allows researchers to analyse the repertoire of T cells across a variety of tumours types in detail, providing information into both antigen selection mechanisms and the sorts of antigens implicated (albeit only indirectly). Due to the various micro environmental impacts, the TR repertoire may differ dramatically between different anatomical sites; as a result, when comparing Tumours Infiltrating Lymphocytes (TILs) to peripheral blood T cells in the same patient, distinct TR profiles have been documented. Although specialized anti-tumor T cells have been found in cancer patients' tumours and peripheral blood, and TIL density has been linked to a positive prognosis in many cancer types, total tumours elimination is impossible [6-8]. Adoptive Cell Transfer (ACT) is a cancer treatment that involves the highly tailored growth and injection of immune cells with anti-tumor characteristics. Melanoma patients were the first to receive this treatment, and it was a huge success. Immune-seq data was utilized to discover the TR beta chain motifs responsible for the recognition of Melan-A, the most often recognized antigen by peripheral T cells and TILs in HLA-$A2^+$ melanoma patients, with apparent therapeutic implications [9].

CONCLUSION

Immune-seq has already proven to be extremely useful in the research of cancer, in line with precision medicine approaches. Immune-seminal seq's contribution to lymphoid malignancies diagnosis and monitoring, as well as the study of both hematological and solid cancers, through the identification and characterization of lymphoid clones with putative anti-tumor capacity in the context of immunotherapy, exemplifies this notion.

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