Background: High-throughput bulk immune repertoire sequencing technologies have emerged as powerful tools with diverse applications in immunotherapy and immunology research. These technologies enable scientists to unravel the complexities of immune responses, facilitating the identification of biomarkers and informing therapeutic interventions. Traditional high-throughput sequencing techniques for immune repertoire (IR) profiling often focus on a single immune cell type, limiting our understanding of complex B-cell/T-cell interactions.

Methods: To address this limitation, we have developed immunoPETE, a gDNA-based immune repertoire sequencing technology capable of capturing multiple adaptive immune cell types in a single reaction. By incorporating unique molecular identifiers (UMIs), immunoPETE accurately captures and reports heavy chains of T and B cells receptors. immunoPETE enables precise characterization of immune repertoires at the cell and clone levels, reporting crucial information such as CDR3 sequences, VDJ profile, diversity metrics, and extensive quality control measures.

In this study, we highlight the successful application of immunoPETE in immune repertoire profiling and adverse event analysis of patients diagnosed with infectious and autoimmune diseases such as COVID-19 and multiple sclerosis (MS). Our findings emphasize the importance of analyzing multiple lymphocyte cell types concurrently, enabling a comprehensive understanding of the behavior and dynamics of the adaptive immune system during disease progression and treatment.

Conclusions: Understanding the dynamics of disease and treatment response requires a thorough analysis of the adaptive immune response. Through immunoPETE, we gain insights into the intricate interplay between B-cells and T-cells, shedding light on the complex immune response mechanisms involved. This approach provides a more comprehensive understanding of disease dynamics and facilitates the development of targeted therapies and personalized treatment strategies.

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