Standardized multi-parameter flow cytometry panels for clinical trial immunomonitoring

P. Barennes, H.P. Pham, M. Touati, V. Quiniou

Parean BIOTECHNOLOGIES
Deep Immune Phenotyping

Introduction

The immune system plays a pivotal role in determining disease outcomes, especially in oncology where tumor-infiltrating lymphocytes (TILs) can be either anti-tumorigenic or pro-tumorigenic, significantly influencing patient prognosis. Standardized multi-parameter flow cytometry panels are essential for monitoring and analyzing these interactions. Our standardized multi-parameter flow cytometry panels enable precise identification and characterisation of various immune cell subsets, to identify the phenotypic and chemokine profiles of these cell populations, facilitating a deeper understanding of their roles. Using our platform, researchers gain critical insights into the immune landscape, enhancing immunomonitoring and therapeutic interventions.

Methods

Our platform addresses these challenges head-on by offering a standardized and optimized flow cytometry analysis pipeline. We have meticulously designed and validated protocols that ensure reproducibility and consistency across experiments. Our advanced analytical tools and optimized gating strategies enable researchers to obtain high-dimensional data, allowing for a more profound exploration of immune cell phenotypes.

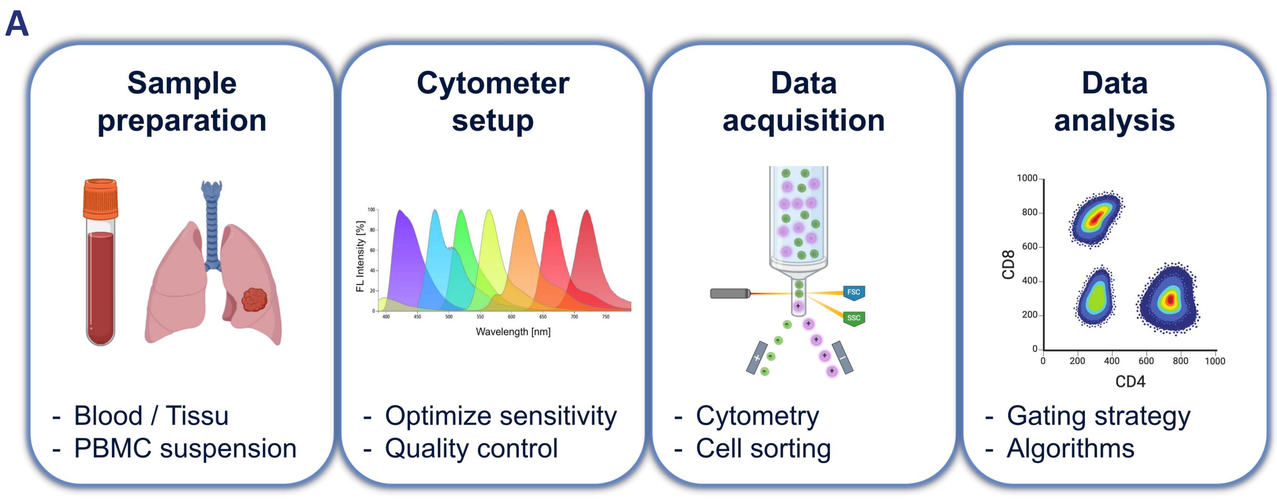

Figure 1. A. Parean standardised and integrated workflow for immunomonitoring, from biological samples to advanced data science. B. Gating strategy allowing the detection of 42 phenotypes from one single blood sample.

Results

For the deep immunophenotyping of clinical trial, we developed reproducible pipeline to investigate several immune phenotype during the treatment course. Five multi-parameter panels (T cell, B cell, Innate Cell, T Helper, Treg) were designed for reproducible immuno-monitoring. These panels allowed to identify more than 40 distinct phenotypes within a single blood sample.

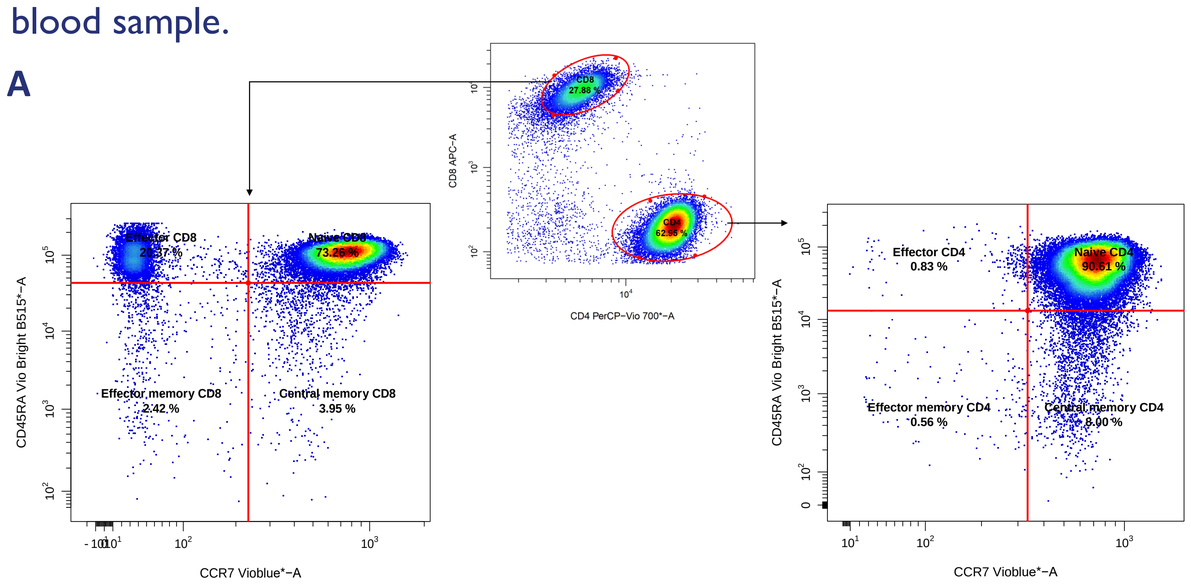

Figure 2. Example of T cell panel acquisition and quantification on PBMCs.

Using an exploratory data analysis approach, complemented by high-dimensional visualization workflows, we were able to effectively discriminate patient markers between responders and non-responders. This methodology proved valuable in correlating specific markers with treatment responses, providing critical insights for patient stratification and therapeutic efficacy.

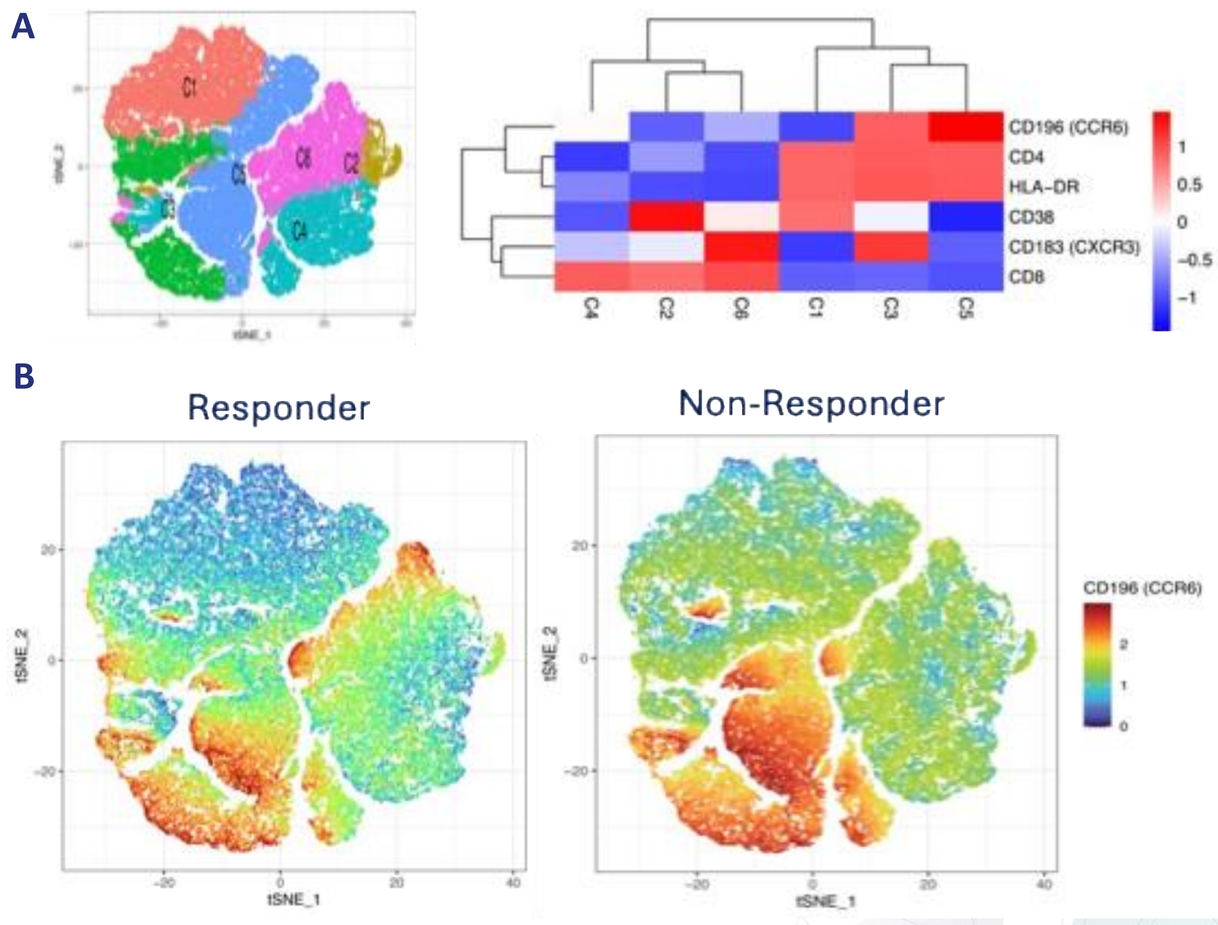

Figure 3. A. Cluster identification based on cells markers expression. The tSNE represent the different clusters. The heatmap highlight some of the markers significantly different between the clusters. B. Identification of CCR6 expression discriminated the responder and non-responder group.

Conclusion

Our standardized multi-parameter flow cytometry panels have demonstrated their utility in providing precise and reproducible immuno-monitoring. By identifying and characterising over 42 phenotypic profiles within a single blood sample, these panels enable a comprehensive understanding of the immune landscape. The integration of high-dimensional visualization workflows facilitates the discrimination of patient-specific markers, crucial for assessing treatment responses. This approach not only enhances our understanding of immune cell dynamics in oncology but also supports the development of more effective therapeutic interventions. Through our platform, researchers can achieve a deeper, more actionable insight into the complex interactions within the immune microenvironment.