The comparison of gene expression and flow cytometry for immune profiling in Chronic Lymphocytic Leukemia

Background

Understanding how cancer and cancer therapies affect the immune system is integral to the rational application of immunotherapies. Flow cytometry is the gold standard method of peripheral blood immune cell profiling. However, the requirement for viable cells can limit its applicability, especially in studies of retrospective clinical cohorts.

Research Question

Can gene expression analyzed using the NanoString platform be used to quantify immune populations present in cryopreserved PBMCs from patients with Chronic Lymphocytic Leukemia (CLL)?

Cell Types Included in the nCounter Gene Expression Immune Cell Profiling

B Cells	Cytotoxic Cells
T Cells	Dendritic Cells
TH1	Macrophages
Regulatory T cells (Treg)	Mast Cells
CD45	Neutrophils
CD8+ T Cells	Natural Killer (NK) Cells
Exhausted CD8+ T Cells	NK CD56dim cells

Experimental Setup

Sample Type	Cryopreserved; Thawed Materials; PBMC
Tissue Type	Human
Assay	PanCancer Immune Profiling Panel
Analyte	RNA
Instrument	nCounter® Analysis System

"Cell abundance scores derived from gene expression analysis were significantly correlated with the population frequency quantified by flow cytometry for all subsets analyzed, including T cells, NK cells and Monocytes."

Sharpe et. al.

Results & Conclusions

- Relative abundance scores significantly correlated with the respective immune population frequency calculated by flow cytometry.
- Strongest correlation observes in the most abundant cell types (B cells and T cells.)
- Gene expression analysis and flow cytometry resulted in significantly correlated immune abundance measurements for all cell types assessed.
- Allows for snapshot of immune population abundance using less sample compared to flow cytometry.

Sharpe C., Davis, J., Mason, K. et al. Comparison of gene expression and flow cytometry for immune cell profiling in chronic lymphocytic leukemia. Journal of Immunological Methods 463, 97-104 (2018). https://doi.org/10.1016/j.jim.2018.09.013

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