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617.ACUTE MYELOID LEUKEMIAS: BIOMARKERS, MOLECULAR MARKERS AND MINIMAL RESIDUAL DISEASE IN DIAGNOSIS AND PROGNOSIS

Deep Immunophenotyping Using High Complexity Flow Cytometry in Acute Myeloid Leukemia

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Acute Myeloid Leukemia (AML) is a highly heterogenous disease with a diverse range of abnormal myeloid subpopulations resulting in challenges in clinical diagnosis and treatment of disease. While sequencing may provide precise information about mutations, the turnaround times make it impractical for routine tracking of disease progression. In contrast, flow cytometry utilizes the expression patterns of cellular markers to determine AML subpopulations with high accuracy. This, coupled with the limited turnaround time, makes flow cytometry an excellent tool for the identification and tracking of disease progression. AML lineage characterization and disease progression are found to be a predictor of both residual disease and the likelihood of relapse further emphasizing the need for effective and accurate characterization of AML populations.

Champions Oncology has developed a high-complexity 18-color flow cytometry panel to identify AML subpopulations at high resolution, named PhenoSeek AML ®. Clinical samples may be shipped to a central location for processing which requires sample populations to be retained during transit. Utilizing Champions' bank of primary AML samples, we have evaluated the stability of key AML subpopulations and found stability to be retained for up to 72 hours after collection. In addition to sample stability, assessing the lower limit of detection is critical for minimum residual disease and relapse screening. Flow cytometry provides an excellent tool for these tests due to its single cell nature, which allows for the interrogation of individual populations with as little as hundreds of cells. Indeed, the dilution of primary AML subpopulations was detected with as little as 10^{3}-10^{4} cells.

Finally, utilizing Champions' cryopreserved never-passaged AML models characterized by both flow cytometry and sequencing, we investigated how the cryopreservation processes impacted the expression of markers associated with specific AML subpopulations. We observed similar expression and detection of AML populations following cryopreservation indicating that these models can be utilized as an excellent tool for further studies.

Collectively, our data indicates that the panel developed at Champions Oncology provides robust detection and deconvolution of AML subpopulations and can be an excellent tool for the tracking of AML disease progression.

Disclosures No relevant conflicts of interest to declare.

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