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Opinion Article

The Incredible Impact of Cytarabine and Anthracycl on Acute Myeloid Leukemia

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DESCRIPTION

After decades of cytarabine plus anthracycline therapy for acute myeloblastic leukaemia, tailored medicines have since been developed, initially based on monoclonal antibodies (anti-CD52, anti-CD123), and more recently, on particular inhibitors of molecular alterations (anti-IDH, IDH2, or FLT3). What role should these therapeutic alternatives play in cure of the tumors heterogeneity that leukemia diagnoses entail as well as the tumors type's propensity for clonal drift? For targeted medications, it would be necessary to examine the numerous therapeutic targets not at the population level but rather at the cellular level. In fact, whether a given molecular target is a cell in terminal differentiation with low proliferative capacity or, on the other hand, a stem cell with great proliferative and self-renewal capacities, their prognostic value and therapeutic interest are unquestionably not the same. The drawbacks to this cell-by-cell study are numerous.

The first one is scientific because, despite using several approaches aimed at standardizing the data, comparing two independent single cell analysis experiments is delicate. The second trap is a practical one because it takes a lot of time and money to do a single cell experiment. The ability to handle several samples at once, which is the uniqueness of the cell hashing technique, is the answer. This study shows that acute myeloid leukemia cells may be analyzed using the cell hashing technique. In the comparison of the cell hashing method with the traditional single cell analysis, good agreement across a number of metrics, including quality control, gene expression correlation, and expression analysis of leukemia blast markers in both cases has been demonstrated. Thus, the method may be used to evaluate the biology of acute myeloid leukemia and help to individualize and improve the treatment of the condition, particularly when using targeted medicines. Acute Myeloid Leukemia (AML) is a genetically, epigenetically, and clinically heterogeneous disease that is characterized by proliferative, clonal, abnormally differentiated, and occasionally poorly differentiated hematopoietic system cells infiltrating the bone marrow, blood, and other tissues, ultimately impairing normal hematopoiesis. AML is more common in older persons, is associated with major complications and high mortality, and accounts for a disproportionately high proportion of malignancy-related fatalities.

Recent advancements in illness treatment have increased the cure rate for patients under 60% to about 40% and for those over 60% to 15%. Treatment for hematological malignancies and acute leukemia's in particular, has advanced significantly thanks to molecular analysis techniques. For a variety of causes, tumors might develop resistance to chemotherapy and immunotherapy. The identification of metabolic pathways of escape and the total population expression of resistance markers (such as *P-gp MRP, GST, Bcl-2, TGFb, Gal-9, CLIP*) are of interest. The data provided by this whole population analysis is insufficient, nevertheless, as it does not allow for the identification of the cell populations affected by these expressions. Even if it has not been demonstrated, it is conceivable that the expression of a certain resistance component has a varied prognostic value depending on whether it affects a terminally differentiated cell with a low capacity for proliferation or a leukemic stem cell with a high capability for mitogenesis. Flow cytometry techniques have made it possible to analyze many markers on the same cell in order to get over this limitation, although not more than 50 markers and typically less than 20 on the cytometrics used in routine tests. Less than 100 parameters can be analyzed using mass spectrometry. Even while there are currently a lot of markers, they are absolutely excessive compared to the 20,000 or so genes that a cell may express. This approach is supported by current single cell RNA analysis tools. Single-cell RNA sequencing, or scRNA-seq, is an effective technique for studying the complex cellular transcriptome at single-cell resolution in biological systems with cellular heterogeneity.

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