

FLOW CYTOMETRY: ITS APPLICATIONS IN HEMATOLOGY

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ABSTRACT

The techniques of flow cytometry are becoming more and more important for the clinical hematology laboratory. No longer a novelty confined to a few specialized institutions as it was 10 years ago, flow cytometry has blossomed into a mature discipline. The methodology is well-known, the mechanical apparatus is readily available, and the role it plays in clinical hematology is increasingly appreciated. The burgeoning number of scientific articles devoted to this topic attests to the interest it has aroused as a tool for both medical research and patient care. In fact, more than a thousand such papers are now published each year and it would be impossible to deal with all the methodologies and applications of FCM currently utilized or under development.

Throughout this paper four relevant hematologic fields are briefly discussed, in which FCM appears to be of great help at present: the immunophenotyping of leukemias and lymphomas, the measurement of proliferative activity and DNA ploidy in hematological malignancies, the detection of drug resistant leukemic cells and the use of FCM in the study of platelets.

Key words: flow cytometry, immunophenotype, DNA content, cell proliferation, drug resistance, platelets

Flow cytometry (FCM) is a rather recent and innovative technology by means of which different cell characteristics are simultaneously analyzed on a single cell basis.¹⁻³ This is achieved by means of hydrodynamic focusing of cells that pass aligned one by one in front of a set of light detectors; at the same time they are illuminated by the flow cytometer light source, which is usually a laser beam. All cell parameters measured in this way can be divided into two main groups: 1) those related to light scattering, which mainly reflects the size of the cell and its internal complexity, and 2) those associated with the presence of one or more fluorochromes inside the cell or attached to the cell surface membrane, either in a natural (autofluorescence) or artificial (i.e. using fluorochrome conjugated monoclonal antibodies) way.

FCM has developed rapidly in recent years, its applications expanding in both basic and clinical research laboratories. This has been mainly due to the fact that this technology provides objective, sensitive, rapid and accurate measurements of a relatively broad range of cell characteristics^{1,3,4} that include, among others, DNA and/or RNA cell content, the detection and quantification of cell antigens, the analysis of multidrug cell resistance, membrane potential, mitochondria and chromosomes, the measurement of intracytoplasmic changes affecting either pH or ions such as free Ca⁺⁺. In addition, FCM allows sorting of cells and subcellular components such as the chromosomes.^{2,3}

When applied to the clinical laboratory, this information largely completes that obtained with other diagnostic tools. Thus, the use of

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FCM has expanded quickly in very different areas of medicine, including immunology, pathology, oncology, genetics, clinical biochemistry, microbiology and internal medicine; hematology represents one of the most important emerging arenas for FCM.^{1-3,5} For several reasons FCM is ideally suited to the study of leukocytes, platelets and red cells, and there is an increasing number of clinically relevant aspects of the pathophysiology and function of these cells that can be measured using FCM.^{1-3,5}

The present work provides a survey of the uses of this technology in the areas of hematology where it finds its principal applications.

The immunophenotyping of leukemia/lymphoma

In the past few years FCM has become the most widely used approach for the immunophenotyping of leukemia patients. For several years it has been used for the classification of both acute lymphoblastic leukemia (ALL)^{2,3,6,7} and acute leukemias following a primary myeloproliferative⁸ or myelodysplastic syndrome,⁹ since leukemia immunophenotyping in these groups of disorders has been shown to have diagnostic value (Table 1). In addition, the impact of these classifications has already been well established both from a prognostic and a therapeutic point of view.

In particular, the role of immunophenotyping has been demonstrated to be critical for obtaining good results with chemotherapy in pediatric patients. Using immunological markers it is possible to initially identify an ALL as T lineage (positivity to cyCD3 and CD7) or B lineage (positivity to CD79 and CD19). A later classification includes three major subgroups for T ALL: pre T (CD1a⁻ SCD3⁻), T thymic (CD1a⁺ SCD3⁻), T mature (SCD3⁺), and four major subgroups for ALL of B origin: C-ALL (CD10⁺ Cylg⁻), pre-B (Cylg⁺ Smlg⁻), transitional pre B-B (Cylg⁺ SmIg⁺), B (Cylg⁻ SmIg⁺). The prognostic impact of these subclassifications and of other monoclonal antibodies (CD34, CD20, CD45) has been investigated in various clinical trials but their relevance has not been completely confirmed.^{10,11} However, CD10 positivity could divide the ALL into two different groups.

Table 1. Immunophenotypic diagnosis of leukemias: impact of individual positive markers.

Diagnostic group	Diagnostic value of immunological markers		
	Major	Intermediate	Minor
<i>acute leukemias</i>			
AML	cMPO	CD33, CD13, CD65, CD117	CD15, CD11b, CD14, CD11c
B-ALL	m/cCD22 m/cCD79	CD19, CD20	TDT
T-ALL	m/cIg m/cCD3 m/cTCR	CD2, CD5 CD7 ⁺⁺	TDT, CD7 ⁺
<i>chronic leukemias</i>			
<i>B-lineage</i>			
CLL		mIg±, CD5 MRFC, CD23	
PLL		Fmc7	
HCL		Fmc7, CD25 ⁺⁺ CD11c, HC2, Bly7	
MM	CD38	CD56 ⁺⁺ , cIgG ⁺⁺	
<i>T-lineage</i>			
CLL		CD8	CD2 ⁺⁺
PLL			CD7
ATLL		CD25, CD4	CD2 ⁺⁺
SS		CD4	
<i>NK-lineage</i>			
		CD56 ⁺ /CD16 ⁺ CD3 ⁻	CD11b, CD2 CD11c, CD7

ALL: acute lymphoblastic leukemia; AML: acute myeloblastic leukemia; CLL: chronic lymphocytic leukemia; MM: multiple myeloma; MDS: myelodysplastic syndrome; PLL: prolymphocytic leukemia; HCL: hairy cell leukemia; ATLL: adult T-cell leukemia/lymphoma; SS: Sezary syndrome. See also Reference 106.

In fact, a correlation exists between antigen positivity and better prognosis for both T and B ALL. CD10 positivity is an important risk factor in the overall population, but in infants it identifies subgroups of diseases in which different therapeutic treatments are needed.¹⁰⁻¹³

Children with SIg positivity (B ALL) have a very poor prognosis when conventional chemotherapy protocols are employed, but they could achieve a good response by following a specific therapeutic approach;¹⁴⁻¹⁶ however, if Cylg is also present (transitional pre B-B), the prognosis is good even when conventional protocols are utilized.¹⁷

In some cases of ALL (from 5 to 20% in different studies) the lymphoblasts express *myeloid*-associated antigens. The clinical impact of these immunophenotypes is not completely

clear, due to numerous problems principally connected with the antigens considered strictly *myeloid*, with the various chemotherapy trials and with the method used to detect the antigens (microscope, FCM, direct or indirect fluorescence).

A poorer prognosis has been demonstrated for adults and infants with lymphoblasts positive for myeloid antigens, while in children this difference is not always evident.^{14,18-23} Flow cytometry plays a fundamental role in distinguishing these forms in which lymphoid and myeloid antigens are simultaneously expressed on the blast cells from those in which residual *normal* myeloid cells are present in the leukemic bone marrow, and from those leukemias in which two different populations are present, one lymphoid and one myeloid.

The fluorescence microscope is not able to identify the different morphological findings correctly, while biparametric FCM histograms based on scatter properties versus FITC-fluorescence could be routinely used to identify different antigen positivity in cell populations with different morphological patterns; however, these particular forms can be unequivocally classified only by simultaneously using reagents conjugated with different fluorochromes in double or triple combinations.

Regarding acute myeloblastic leukemia (AML), the contribution of FCM immunophenotyping of blast cells is particularly relevant for the diagnosis of acute megakaryoblastic leukemias^{24,25} and for the microgranular variant of acute promyelocytic leukemia cases,^{24,26} where the final diagnosis might not be completely clear on the basis of morphology.

Another important goal of AML flow cytometric immunophenotyping has been the classification of these patients on the basis of both the forward scatter/side scatter distribution pattern of the blast cells and their reactivity to monoclonal antibodies directed against antigens associated with different myeloid cell lineages and their differentiation stages.²⁶ Moreover, the expression of a certain number of antigens such as CD34, CD11b and CD7 has been related to the prognosis of the disease.^{24,27-31}

Furthermore, a large percentage of AML

express *lymphoid antigens* and these phenomena are sometimes correlated to specific subtypes of myeloid leukemias.^{22,23} This particular aspect reflects population expansions not usually present or hardly represented in *normal* bone marrow, and it could be applied in monitoring the efficacy of chemotherapy when a morphological follow-up is not easy in AML in the presence of recovering bone marrow.

The use of FCM to study chronic lymphoproliferative disorders has had a particularly important impact on the differential diagnosis between reactive lymphocytosis and monoclonal diseases because this methodology allows a rapid, sensitive, objective and reproducible diagnosis and classification of these hematologic disorders.^{3,7,31} Accordingly, the use of the CD19/ κ light chain/ λ light chain triple staining combination is of great help in assessing the presence of monoclonal B-cells in peripheral blood, bone marrow, lymph node or spleen single-cell suspensions.³ In a similar way, the application of FCM together with the use of different monoclonal antibody combinations has contributed to the classification of other chronic lymphoproliferative disorders;³² this is particularly relevant to the diagnosis of cases involving large granular lymphocytes, since it allows a distinction to be made between patients displaying a T-cell origin (CD3⁺/T-cell receptor⁺) and those in whom NK-cell lineage is involved (CD3⁻/T-cell receptor⁻).³

Recently, the use of FCM and its multidimensional analytical capabilities to study cell subpopulations that only represent a small proportion of the whole sample has become a major challenge for this technology.^{2,3} Therefore the use of FCM in this area has focused on the detection of minimal residual disease in acute leukemias achieving morphologic complete remission.^{33,34} Preliminary reports^{34,35} indicate that the application of FCM together with the use of a set of different monoclonal antibody combinations may be a suitable methodology for the detection of minimal residual disease in a high proportion of acute lymphoblastic leukemia patients. Accordingly, it is suggested that this methodology can achieve a level of sensitivity that would allow the detection of one

leukemic cell among 100,000 normal cells. The demonstration of either the persistence of cells displaying leukemic phenotypes during chemotherapy or their increase after achieving complete remission would significantly contribute to an earlier diagnosis of leukemia relapse.

The recent introduction of commercial fixatives able to permeabilize cellular membranes, thus preserving surface immunoreactivity and cellular morphological aspects (on the basis of *scatter* properties), is an important step forward in circumventing the limitations of FCM in identifying intracellular antigens. Preliminary results have indicated the possibility of simultaneously detecting surface, cytoplasmic and nuclear antigens, which has wide range of utilization in the study of minimal residual disease and oncogene expression.³⁶ In particular, the detection of nuclear TdT in ALL bone marrow in combination with surface antigen identification permitted analysis of a large number of cells with distinct physical properties in order to reveal a minimal blast cell component.

The measurement of proliferative activity and DNA ploidy in hematological malignancies

One of the applications of FCM which has had a major impact on the study of leukemias and lymphomas is the measurement of nuclear DNA content.^{1,3,5,37-39} This methodology usually provides two different types of information.³⁷

On the one hand, the proliferative activity of a certain cell population is assessed by means of analyzing its distribution throughout the different cell cycle phases, in particular the S-phase. Accordingly, the proportion of cells that display intermediate DNA content between that of normal diploid resting cells (2n)(G0/G1 cell cycle phases) and that of those cells which have duplicated their DNA and are about to divide (4n)(G2 phase and mitosis) is assessed.

On the other hand, the presence or absence of clonal abnormalities in the DNA content of a certain cell population as compared with that of normal cells (DNA index) at the same cell cycle phase is analyzed. These kinds of abnormalities have been termed cytofluorimetric

DNA aneuploidy (Table 2).

More recently, FCM analysis of DNA content has been used together with several other FCM techniques⁴⁰ to characterize and distinguish the two different mechanisms of cell death: apoptosis and necrosis.^{41,42} The most common marker of apoptotic cells in FCM is the decreased stainability of their DNA with a variety of fluorochromes.⁴⁰ Experimental and clinical studies based on this approach have been conducted in hematological malignancies with promising results.⁴³⁻⁴⁵

Proliferative activity

Analysis of cell cycle kinetics in malignant hematologic disorders has demonstrated the existence of important proliferative heterogeneity.^{46,47} In particular, B-CLL patients display quite a low percentage of peripheral blood S-phase cells, usually less than 1%, with respect to those detected in both ALL and AML.^{3,6} Non-Hodgkin's lymphoma (NHL) patients show an intermediate proliferative index.^{3,47} Proliferative activity is measured either as the percentage of S-phase cells or by reactivity with the Ki67 monoclonal antibody, and it is lower in low-grade NHL than in the high-grade lymphomas.^{38,47} Furthermore, there is great variability regarding the results reported in the literature, even when a single diagnostic group of patients is considered.⁴⁷ This is probably related to the methodologic approaches used such as the type of fluorochrome, the sample preparation technique, the method of analysis, the site of the study, the use of a technique that allows

Table 2. Flow cytometric DNA ploidy status and percentage of cells in DNA synthetic phase in hematological malignancies.

<i>Diagnostic group</i>	<i>% DNA FCM aneuploid cases</i>	<i>% S-phase cells</i>
ALL	25-35	4.6±3.2
AML	4-20	7.3±5.9
B-CLL	0-5	0.2±0.5
MM	40-80	3.3±2.6
MDS	10-50	—

AML: acute myeloblastic leukemia; B-CLL: chronic lymphocytic leukemia B-cell type; MM: multiple myeloma; MDS: myelodysplastic syndromes). Personal unpublished data from Orfao A, et al.

discrimination between normal and leukemic cells.^{47,48} As an example, the mean percentage of S-phase cells found in previously published studies on AML varies between 5% and 11%. In addition, at present it is known that the time of DNA synthesis (Ts) and the cycling time (Tc) may show wide variability from one case to another. Ts variations from 4 to 49 hours and Tc variations from 16 to 292 hours have been reported.⁶

In order to gain further insight into this variation, several authors have investigated the existence of a relationship between the proliferative rate and the morphologic characteristics of the leukemic cells in different hematologic malignancies. As a result it has been observed that while in ALL L2 morphology is related to a higher mean percentage of S-phase cells than in L1 cases,^{3,6} the monocytic subtypes in AML patients are associated with higher numbers of peripheral blood S-phase cells.^{3,24} In a similar way, lower proliferative activity has been noted in refractory anemia (RA) and RA with sideroblasts as compared to RA with excess of blasts and chronic myelomonocytic leukemia.^{6,47} There have been many studies in which the prognostic value of these parameters, both in terms of response to treatment and of survival, has been analyzed.^{3,6,47-51}

Although there are very often differences between the results obtained by individual authors, it can be stated as a general rule that high proliferative activity has been associated with a lower survival rate. B-NHL and B-CLL cases with a higher proliferative rate and higher peripheral blood S-phase counts show a poorer prognosis.^{6,47,52} Identical results have been described for multiple myeloma (MM) where a high S phase has been associated with a less favorable prognosis.^{2,3,6,53-56} Finally, myelodysplastic syndromes (MDS) with a greater percentage of bone marrow S-phase cells have been reported to have poor clinical outcomes.^{3,6}

However, these results should be taken with caution since, with the exception of a small number of reports that mainly refer to NHL, B-CLL and AML, the independent prognostic value of S phase cells has been neither assessed nor detected.⁴⁸ As a matter of fact, there is still

considerable controversy surrounding the possible prognostic information that can be obtained from analyzing cell proliferation during acute leukemia, especially since many conflicting results have been reported. Given the clear-cut role cytokinetic factors play in defining the susceptibility of leukemic cells to chemotherapy drugs,^{46,57-59} these discrepancies are unexpected. Several factors are responsible for the discrepancies that emerge in this area. First of all, only small groups of patients have been studied, and the induction regimens employed in them showed considerable variation. Secondly, often the only kinetic parameter these investigations scrutinized was the percentage of cells in S-phase. This places severe restrictions on the analysis since the S-phase offers only limited insight into cell proliferation. In order to analyze the cell cycle properly in acute leukemia, the temporal parameters connected with cell proliferation also need to be considered.⁶⁰⁻⁶² A third drawback to these studies was the fact that an accurate estimate of the percentage of cycling cells (i.e. of the leukemic growth fraction) as well as of the resting (G0) cell fraction is essential for obtaining a more realistic picture of cell proliferation, but in spite of the FCM methods proposed^{63,64} it has generally been difficult to estimate these parameters *in vivo*.

A possible way of avoiding these shortcomings could be based on the following principles. The first is to adopt a standard induction regimen in which pure S-phase-specific drugs (vincristine and arabinosylcytosine) are given prior to anthracyclines in the induction treatment of a large and homogeneous series of adult patients with AML. Next, utilize multiparameter FCM techniques to study: DNA content,⁵⁷ *in vivo* incorporation of bromodeoxyuridine (BrdU) for the temporal kinetic parameters (Ts and tumor potential doubling time, Tpot),⁶⁵ and expression of the proliferating cell nuclear antigen (PCNA/cyclin) as a marker of the leukemic growth fraction.⁶⁶⁻⁶⁸

An example of this can be found in a recent experience involving 68 adult patients with untreated AML who entered a clinical study. All patients received a BrdU infusion prior to starting remission induction therapy in order to

allow study of bone marrow (BM) blast kinetics.⁶⁹ For induction remission each patient received 2 courses of the same regimen that included sequential administration of vincristine and arabinosylcytosine followed by anthracyclines.⁷⁰ In this series when the 2n-4n%, BrdU-LI, Ts and Tpot were considered, the proliferative activity of CR patients was always higher than that of the NR ones. When the percentage of PCNA-positive blasts was considered, AML proliferative activity was significantly higher in CR patients than in those who did not respond, and it was also greater in those cases that showed CR and survival durations longer than the median values for the total patient population, and greater than in those patients whose CR and/or survival lasted less than the overall median intervals.⁷⁰

When multivariate analysis was performed, the WBC count emerged as the most important parameter, followed directly by the Tpot of the proliferating (PCNA-positive) blasts; every other variable exerted a relatively negligible influence in the model. A particular effort was made to render the data obtained from the *in vivo* BrdU/DNA FCM assay more significant by including a determination of the leukemic growth fraction identified by means of a cell cycle-related protein together with FCM.⁷¹⁻⁷³

These results confirm the importance of FCM in these kinds of studies and support the hypothesis that high proliferative activity represents a favorable prognostic indicator in the treatment of AML patients with protocols designed by taking cytokinetics into consideration.

One of the most challenging tasks for the future in this sense will be to improve and individualize treatment modalities based upon the biological features of the disease. This hope could become reality since a new group of agents are available that have the potential to modulate cell growth and differentiation at different levels, e.g. hemopoietic growth factors. Flow cytometry has been used successfully to detail the cytokinetic effects of some of these factors on human bone marrow,^{74,75} and clinical trials in AML have been initiated that employ colony-stimulating factor treatment to push

leukemic cells into proliferating in order to increase their sensitivity to cytotoxic agents.⁷⁶⁻⁷⁸

Flow cytometric DNA ploidy

The incidence of DNA aneuploidy in hematologic malignancies is lower than that detected by cytogenetic methods.^{3,47} This is basically due to the fact that even under the best technical conditions FCM does not allow detection of compensated karyotypic abnormalities in those cases where there is no DNA loss or gain.³⁷ Moreover, simple monosomies and trisomies are undetectable in almost all occasions when this technique is used. However, FCM has the advantage of allowing study of interphase nuclei without the need to induce cell division. As a general rule, the incidence of DNA aneuploidy is quite low in CLL (< 6%) and in Hodgkin's disease, and high in multiple myeloma (MM) (40-80%).^{6,47} Acute *de novo* leukemias show an intermediate incidence that ranges from 5 to 20% in AML and from 25% to 35% in adult and juvenile ALL, respectively.^{6,37} The presence of hyperploidy within aneuploid cases is much more common than that of hypoploidy. The incidence of aneuploid cases that have a second aneuploid cell population is normally less than 10%. In NHL, the incidence of DNA aneuploid cases is greater in high-grade lymphomas.³⁷ In ALL patients the presence of DNA aneuploidy has been associated with both an L2 morphology and a common (CD10⁺) phenotype,^{3,6} while in MM, using bivariate FCM, a correlation has been demonstrated between this parameter and Ha-ras oncogene expression.⁷⁹

In pediatric ALL patients a diploid DNA content at diagnosis is considered an important feature for correctly assigning the risk factor. A DNA index > 1.16 (corresponding approximately to total of 53 chromosomes) is a favorable independent prognostic factor, above all if it is associated with an age from 4 to < 8 years and a common immunophenotype ALL. The disease-free survival of these children with current chemotherapy protocols is > 97% at 3 years.⁸⁰

Although data on the prognostic value of this parameter are frequently contradictory, it appears to be evident that hypoploid MM, MDS and ALL cases have a poorer prognosis

while hyperploid ALL patients have a better outcome.^{3,47} Regarding AML patients DNA aneuploidy has not been shown to have a prognostic impact, unlike the relationship observed between karyotypic abnormalities and the clinical outcome of these patients.^{2,6} In NHL, the existence of DNA aneuploidy has been associated with a less favorable prognosis, although it does not appear to be an independent prognostic factor.⁴⁷

The detection of drug-resistant leukemic cells using flow cytometry

Cellular resistance to chemotherapy in leukemia patients is multifactorial. However, both the absence of initial response to chemotherapy and the progression after remission can probably be explained to a large extent by the functional role of a limited number of detoxifying mechanisms that are also present in normal cells. Some of these have already been characterized from the biochemical point of view and specific assays for measuring this resistance have been established. Preliminary reports suggest that based on an assessment of drug-resistance mechanisms in leukemia, chemotherapy could probably be either established or adapted on an individual basis.⁸¹

Among the analytical methodologies available for the study of drug resistance, FCM is particularly suitable because it permits a quantitative measurement on a single cell basis which, in turn, leads to a rather sensitive and objective assessment of cell heterogeneity in leukemia.⁸²⁻⁸⁷ At present different procedures have been tested to measure drug resistance in human malignancies, most of which deal with the multi-drug resistance phenotype through assessment of either the p-glycoprotein (gp-170) efflux pump or cellular glutathione content.^{88,89} An alternative method uses FCM and two fluorochromes. The first, doxorubicin, is a drug involved in these mechanisms; the second, rhodamin 123, is a reagent that utilizes this mechanism to go in and out of the cells. These molecules, when excited by an argon laser, show emission at 560-600 nm and 510-530 nm, respectively. Blasts cells are incubated at 37°C in the presence of one of

these fluorochromes, and their uptake is evaluated at different times in the presence or absence of MDR inhibitors (cyclosporine, verapamil). The difference in the fluorescence cell intensity with and without inhibitors is the expression of gp-170 function. It is also possible to use double fluorescence to study the mechanism in a particular cell subset by means of monoclonal antibodies with appropriate conjugation (FITC for doxorubicin, phycoerythrin for Ro123). This functional approach could be very interesting for identifying MDR resistant leukemia cells that are negative if examined by specific monoclonal antibodies or gene expression.^{90,91}

Recently, a different method has been proposed by which drug-resistance could be measured for S-phase specific drugs after quantifying its effect on the inhibition of DNA-synthesis.^{92,93} Its application to the measurement of ara-C resistance in AML patients will be discussed in this paper. Ara-C is one of the most effective agents for the treatment of human acute leukemias; it is an S-phase-specific agent and its active metabolite ara-CTP is a substrate for DNA polymerase that is incorporated into the DNA of those cells actively synthesizing DNA.⁹² As a consequence, ara-C incorporation into cells strongly correlates with cytotoxicity and results in the inhibition of DNA synthesis.⁹³⁻⁹⁵ In addition, a correlation between the inhibition of DNA synthesis and response to treatment with ara-C has been reported.^{94,95}

The use of BrdU/DNA staining with an anti-BrdU monoclonal antibody and propidium iodide (PI) allows simultaneous assessment of both cell cycle distribution and the rate of DNA synthesis of a certain cell population in a simple and reproducible way.⁹² Changes in the rate of DNA synthesis are quickly and accurately evaluated at FCM from BrdU/DNA bivariate distributions since the amount of BrdU incorporated over a short period of time is proportional to the amount of DNA synthesized during that period.

In order to have a reliable evaluation of the degree of resistance of leukemic cells to ara-C in clinical situations, it is necessary to determine the proportion of S-phase cells resistant to ara-C, as well as the level of BrdU incorporation

into ara-C resistant cells. Recently, a computerized method for analyzing BrdU/DNA bivariate distributions of HL60 cell lines that are sensitive or resistant to various doses of ara-C has been described. According to this method the degree of resistance is automatically obtained and is expressed as an index of ara-C resistance (RI). This RI is defined as the product of RS by MS, where RS is the ratio between the percentage of S-phase cells in the presence and absence of a certain dosage of ara-C, and MS is the ratio between the mean fluorescence channel (BrdU) of S-phase cells incubated in the absence of ara-C. When applied to leukemia cell lines, this method has been shown to quantify the effect of ara-C on the inhibition of DNA-synthesis. A similar degree of correlation was found when this technique was used to assess resistance to chemotherapy in a group of 121 AML patients treated with a protocol that included daunorubicin (50–60 mg/m²/day, 3 days) and ara-C (100 mg/m²/day, continuous infusion, 7–10 days).⁹⁷ In order to evaluate RI properly in this study a minimum of 3% S-phase cells after 48 hours of cell culture was considered essential, and this requirement was met by 96 out of the 121 patients. Of these, 81 (84%) achieved complete remission (CR) and 15 (16%) did not. RI was calculated for each patient with two different doses of ara-C that encompassed the presumed plasma concentration of the drug (0.1 mg/mL and 1 mg/mL); RI(0.1) and RI(1) correspond to the doses of ara-C used.

Based on the results obtained after pulsing cultured cells with BrdU in the presence and absence of ara-C (0.1 and 1 mg/mL), patients were grouped into three categories. Group I included those cases displaying an RI(0.1) and an RI(1) below 8, while Group III was formed by patients with both an RI(0.1) and an RI(1) over 8. Group II AML cases showed an RI(0.1) greater than 8 and an RI(1) less than 8. Upon analyzing response to chemotherapy, it was observed that this classification was able to discriminate between ara-C sensitive and resistant cases since most of the patients in group I achieved CR (62/63), while all the cases included in Group III (9/9) were in failure. Group II showed an intermediate distribution, with 19

out of 24 patients achieving CR.⁹⁷ While in this study an RI threshold of 8 was the optimal level for discriminating between ara-C sensitive and resistant cases, this value needs to be confirmed in larger series of patients. The results of this study demonstrated that RI is independent of the shape of the BrdU labelling distribution, and that slightly resistant homogeneous blast cell populations as well as individual resistant cells among ara-C sensitive leukemic cells can be detected with this method.

It was concluded that when this approach is used to measure ara-C resistant AML cases it is essential to analyze both the percentage of S-phase cells after ara-C treatment and the extent of BrdU incorporation within these cells, in order to assess both the percentage of potentially resistant cells and their degree of resistance.^{94,97}

The use of flow cytometry in studying platelets

Flow cytometric analysis of human platelets represents a relatively new, emerging field of application of this technology in both clinical and research hematology.^{2,3} For several reasons FCM is ideally suited for studying platelets, and at present there are several clinically relevant aspects of platelet pathophysiology and function that can be analyzed with FCM. The array of surface glycoproteins expressed on platelets has been extensively studied. Most of the major surface structures have been assigned functions and their structure has been determined at the molecular level. The availability of monoclonal antibodies directed against both functional and structural determinants on these molecules permits most of the flow cytometric techniques utilized in this area.^{2,3} There are essentially three functional responses that platelets are capable of making when they are stimulated.⁹⁹ They can release the contents of their granules (release), they can bind to a surface (adhesion), and they can aggregate with other platelets (aggregation). Flow cytometry is an excellent tool for studying each of these functions.^{2,99} Compared to other standard methods, FCM offers a number of advantages for the study of platelets. These include: 1) the need for relatively small amounts of blood, especially when the patient

is thrombocytopenic; 2) the ability to obtain information about the physiologic state of platelets with an absolute minimum of manipulation; 3) the ability to positively identify platelets and thus be certain that the measurements are not contaminated by other cell types or by *debris*. In addition, FCM presents the same major advantages for the study of platelets that it does for other applications, namely the ability to detect functional subpopulations, and the ability to obtain correlated measurements of several cellular properties simultaneously. These last two advantages, when applied to platelets, have immediately led to fascinating new observations that were never before possible with any other technique, and which had not been previously suspected.

At present there are at least four applications of FCM to the study of platelets that have potential clinical relevance.^{2,3} These include the measurement of platelet-associated immunoglobulins, the analysis of platelet nucleic acid content, the diagnosis of primary thrombocytopathies and the assessment of both platelet activation and function. Of these, probably the most widely used is the measurement of platelet-associated immunoglobulins (PAIg), sometimes referred to as *antiplatelet antibodies*.⁴ The goal of measuring platelet-associated Ig is simply stated. It is desirable to be able to quantitate the amount of Ig on platelets because there are a number of disorders in which the binding of antiplatelet antibodies can be reasonably suspected as the cause of the premature destruction of platelets. In essence the use of the flow cytometer involves much the same approach as other PAIg immunoassays. One must prepare platelets from blood, label them with a fluoresceinated anti-Ig antibody, and then measure the amount of fluorescence associated with the platelets. There are, however, several significant differences. First, when using the flow cytometer it is not necessary to purify the platelet preparation to nearly the extent required by other methods.^{2,4} This is because the flow cytometer is capable of directly identifying platelets even when they are heavily contaminated with erythrocytes and leukocytes. Thus, because the cytometer can reliably identify platelets, PAIg determination is

restricted to platelets and contaminating cells do not influence the measurement as they would in an immunoassay.²⁻⁴ Second, the cytometer carries out the determination of PAIg on individual platelets. If such a measurement is made on 100,000 or even on 10,000 platelets the statistical accuracy of the average level of PAIg is extremely good. Thus it is not necessary to process very much blood in order to obtain a sufficient number of platelets for flow cytometer analysis. One mL of blood from a patient with a platelet count of $10 \times 10^9/L$ contains 10^6 platelets and should be enough. Third, the measurement is performed with platelets in suspension. Thus there is no concern that Ig which might have been trapped in the interstices between platelets will influence the measurement. Finally, the flow cytometric method is easily adapted to the determination of several different antigens on the same sample. Thus, for example, the measurement of platelet-associated IgG, IgM and C3 can be accomplished on the same sample with no changes in the basic technique.²⁻⁴

Using the dye known as thiazole orange, it is now possible to determine individual platelet nucleic acid content by flow cytometry.^{3,100,101} When applied to platelets this method may represent a clinically useful technique based on the results of different groups.^{100,101} It is postulated that the *reticulated platelets*¹⁰² detected in this way represent recently released platelets which mature rapidly in circulation, and that their measurement is an estimate of the rate of thrombopoiesis in the same sense that an erythrocyte reticulocyte count is a measure of erythropoiesis. It is likely that the ability to measure the proportion of young platelets easily will prove to be clinically useful in the differential diagnosis of unexplained thrombocytopenia.

The development and availability of different monoclonal antibodies directed against platelet-associated glycoproteins that have already been characterized from a functional point of view has rapidly increased the use of FCM in the study of platelets.^{103,104} Accordingly, the possibility of using this technology to identify the abnormal expression of gp IIb/IIIa and gpIb on the surface of platelets is now being utilized in many laboratories to support the diagnosis of Glanz-

mann's disease and Bernard-Soulier syndrome, respectively. Recently, several groups described immunological markers of platelet activation which, in combination with FCM, may prove to be of considerable clinical utility. In addition to their possible clinical applications, the areas in research for such markers are too numerous to describe here. There are a number of situations in which one might expect platelet activation markers to demonstrate clinical utility. These can be broadly classified as those areas involving *biocompatibility* issues, platelet storage and transfusion, those involving assessment of cardiovascular disease and assessment of platelet dysfunction. Data are currently available to show that: 1) platelets become activated during storage under blood bank conditions, and activated platelets do not remain in the patient's circulation; 2) platelets become activated during extracorporeal circulation such as cardiopulmonary bypass and renal dialysis; 3) platelets become activated during vascular damage, myocardial infarction and thrombosis, and 4) there is increased activation in patients at high risk for cardiovascular events.

The recent availability of immunological markers of platelet activation such as CD62, CD63 and CD69, combined with the unique capability of FCM to identify small subpopulations of platelets and to quantitate membrane glycoprotein levels, now allows us to assess platelet function in an entirely new way. The clinical and research potential of these developments is only beginning to be explored.

Conclusions

The aim of the present review was to summarize what FCM is currently able to do in the clinical hematology laboratory and to suggest possible directions of future developments. The authors have tried to demonstrate that FCM is not simply a research tool, but a technique that will ultimately find its place in the mainstream of hematology laboratory practice.

Flow cytometric analysis will probably be indispensable for a rapid and objective assessment of the cell surface and different intracellular characteristics and, when combined with

other clinical and morphometric data, this methodology will help to improve diagnosis and patient care. The quality control and standardization methods recently applied to the generation of flow cytometric data have greatly improved their reliability.

There are already several areas involving the diagnosis/prognosis of hematological diseases in which the use of FCM techniques is approaching a consensus, in particular the initial phenotyping of acute leukemias and lymphoproliferative disorders.¹⁰⁵ The FCM industry is rapidly evolving:¹⁰⁶ flow cytometers are becoming more user friendly, and there is much interest in the development of fluorochromes for multiparametric analysis¹⁰⁷ and the clinical application of new clusters of monoclonal antibodies.¹⁰⁸

The next step will be to see that all clinical laboratories adhere to such rigid standards and that inter-laboratory quality control becomes likewise stringent, in order to verify the reproducibility of results obtained in the above mentioned fields of hematology. Thus FCM-derived data will acquire a more conclusive clinical impact.

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