Basophil counting by hematology analyzers in cases of suspected chronic myeloid leukemia

Sir,

It was with great interest that I read the article by Chopra and colleagues that your journal recently published.[1] These authors report on a study of basophil counts (BC), performed using two automated hematology analyzers in 269 peripheral blood samples of patients with suspected chronic myeloid leukemia (CML). The two analyzer types showed a poor correlation in BC between them as well as with microscopy. Overall, both hematology analyzers failed to recognize true basophilia in 41 and 44% of the cases, respectively; even many patients with >20% basophilia were missed. To my knowledge, this is the first report that convincingly demonstrated a high rate of missed basophilia in CML patients. The authors hypothesized that this was due to dysplastic, hypo- or agranular, and immature basophils and their main conclusion was that the BC produced by the hematology analyzers cannot be relied upon and cannot be used for the clinical management of CML patients.[1]

Although automated hematology analyzers generally generate highly accurate and precise white blood cell (WBC) differential counts, they show notoriously poor performance of BC.[2] Why is this and more importantly, what can be done to remedy this situation?

The key issue is that basophils lack specific cellular characteristics for unequivocal and consistent characterization by the various technologies applied in hematology analyzers. Some analyzers simply regard basophils as all WBC that cannot be positively classified otherwise. Many analyzers use resistance to acidic lysis as a distinctive feature of basophils; in normal blood, this may be a reasonable approach, but not in pathological conditions. Since abnormal basophils, like in CML, have different cellular properties than their normal counterparts, they end up in a different location of the various scattergrams and thus go unrecognized by hematology analyzers. Few analyzers, if any, are able to find cell clusters that with certainty can be allocated as basophils. Despite most modern analyzers have multiple detectors, processing of cellular events is done in two-dimensional scatterplots. If event processing were done in a multidimensional space, the likelihood of detecting abnormal cell clusters or cells in unusual positions would definitely increase. Therefore, I believe that hematology analyzer manufacturers should take an effort and finetune their algorithms, so that detection of abnormal or unidentifiable cellular events is improved. A fully reliable BC by a hematology analyzer may not be feasible, but at least, better flags could be developed that trigger microscopic smear review in patients with unclassifiable cells, like abnormal basophils that remain the hallmark of CML.

Currently, the preferred technique for detecting basophils in CML is flow cytometry using multiple monoclonal antibodies.[2,3] Moreover, even flow cytometry may occasionally fail in CML basophils with aberrant phenotype.[4] Unfortunately, flow cytometry is too impractical for routine clinical use. Thus, clinical hematology laboratories are in need of improvements in hematology analyzer, so that patients with possible CML and abnormal basophils are easier found during routine complete blood count screening. Patients deserve it.

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Conflicts of interest

There are no conflicts of interest.

Johannes J. M. L. Hoffmann

H3L Consult, Nuenen, The Netherlands

Address for correspondence:
Dr. Johannes J. M. L. Hoffmann,
Abbott Diagnostics, P.O. Box 727, 2130 AS Hoofddorp,
The Netherlands.
E-mail: h3l.consult@gmail.com

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