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Compatibility Between Platelet Histogram with IP Message and Platelet Morphology in Thrombocytopenia Patients

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ABSTRACT Thrombocytopenia, characterized by a platelet count below normal levels, poses diagnostic and management challenges in hematology, especially concerning the accuracy of automated hematology analyzers. Despite the convenience and rapidity of these instruments, their interpretations specifically platelet histograms and interpretive messages may sometimes be inaccurate due to factors such as platelet clumping, giant platelets, or morphological abnormalities. This study aims to evaluate the concordance between the platelet histogram results and interpretive messages obtained from the Sysmex XN-1000 hematology analyzer with the actual platelet morphology observed in peripheral blood smears of patients with thrombocytopenia. A quantitative descriptive approach was employed, involving 54 EDTA blood samples collected from hospitalized thrombocytopenic patients over a one-month period at Grati Hospital. Each sample underwent complete blood count analysis using the Sysmex XN-1000, followed by confirmatory peripheral blood smear examinations for cases with abnormal histogram patterns or interpretive messages indicating issues such as platelet clumping or abnormal distribution. Data analysis focused on the compatibility between automated results and morphological findings, with a particular emphasis on the frequency of concordance. The findings revealed a high level of agreement, with 90.7% of cases demonstrating concordance between the analyzers' outputs and the blood smear morphology. Discrepancies, accounting for 9.3%, were mainly attributable to limitations in the analyzer's flagging capabilities, particularly in cases involving giant platelets and platelet clumps. These results suggest that, although automated hematology analyzers provide reliable initial assessments, confirmatory peripheral blood smear examinations remain essential to ensure diagnostic accuracy. Platelet histograms and interpretive messages from the Sysmex XN-1000 exhibit substantial concordance with morphological findings in thrombocytopenic patients. This underscores the utility of automated analyzers in clinical practice while highlighting the continued importance of microscopic confirmation for optimal diagnosis and management.

INDEX TERMS Platelet histogram, IP message, peripheral blood smear, thrombocytopenia, Sysmex XN-1000.

I. INTRODUCTION

Thrombocytopenia, characterized by platelet counts below 150,000/μL, represents a critical hematological condition requiring accurate diagnostic assessment for appropriate clinical management [1]. The advent of automated hematology analyzers has revolutionized laboratory diagnostics, offering rapid, high-throughput analysis with sophisticated data interpretation capabilities [2]. However, the reliability of automated platelet enumeration in thrombocytopenic patients remains compromised by various analytical interferences, including platelet aggregation, giant platelets, and cellular debris, which can lead to erroneous results and potential clinical mismanagement [3], [4].

Contemporary hematology analyzers employ advanced technologies such as hydrodynamic focusing, optical detection, and impedance-based measurements to provide comprehensive blood cell analysis [5]. The Sysmex XN-series analyzers utilize fluorescence flow cytometry and hydrodynamic focusing principles to generate detailed platelet histograms accompanied by interpretive program (IP) messages that alert operators to potential analytical anomalies [6]. These systems incorporate sophisticated algorithms to detect platelet clumps, abnormal size distribution, and morphological variants through automated flagging mechanisms [7]. Current analytical approaches integrate multiple detection channels and advanced signal processing to differentiate platelets from other cellular components, particularly in challenging samples with overlapping size distributions [8].

Modern analyzers also employ platelet-specific fluorescent markers and multi-dimensional data analysis to enhance discrimination between true platelets and interfering

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particles [9]. The integration of artificial intelligence and machine learning algorithms has further advanced automated cell recognition capabilities, enabling more precise identification of morphological abnormalities [10]. Optical versus impedance counting methods have shown varying accuracy in thrombocytopenic patients, with optical methods demonstrating superior performance in samples with red cell abnormalities [16], [17]. However, despite these technological advances, the complexity of thrombocytopenic samples continues to challenge automated systems, necessitating confirmatory microscopic examination [11].

While numerous studies have evaluated the performance of automated hematology analyzers in general populations, limited research specifically addresses the concordance between automated platelet analysis and microscopic findings in thrombocytopenic patients [12]. Existing literature predominantly focuses on technical performance metrics rather than clinical correlation in pathological conditions [13]. Novel approaches to correct platelet count in conditions such as EDTA-dependent pseudothrombocytopenia have been developed, yet their clinical validation remains limited [18]. Furthermore, the diagnostic accuracy of IP messages and histogram interpretation in thrombocytopenia remains inadequately characterized, particularly regarding the frequency and clinical significance of discordant results [14]. The impact of red cell abnormalities on automated platelet counting accuracy has been documented, but comprehensive studies in thrombocytopenic populations are scarce [17]. Recent advances in histogram analysis for platelet disorders show promise, but standardized interpretation criteria are lacking [19]. The lack of standardized validation protocols for automated platelet analysis in thrombocytopenic samples represents a significant knowledge gap that impacts clinical decision-making and patient safety [15].

This study aims to evaluate the concordance between platelet histogram patterns with IP messages generated by the Sysmex XN-1000 analyzer and actual platelet morphology observed in peripheral blood smears of thrombocytopenic patients, thereby establishing the diagnostic reliability of automated platelet analysis in this specific patient population. This research provides three significant contributions to the field of laboratory hematology:

1. Clinical Validation Framework: Establishes a systematic approach for validating automated platelet analysis in thrombocytopenic patients, providing evidence-based guidelines for when confirmatory microscopic examination is necessary, thereby improving diagnostic accuracy and clinical workflow efficiency [20], [21].
2. Diagnostic Accuracy Assessment: Quantifies the concordance rate between automated analyzer outputs and microscopic findings in thrombocytopenia, offering healthcare professionals reliable data on the limitations and capabilities of current automated systems in challenging clinical scenarios [22], [23].
3. Quality Assurance Enhancement: Develops standardized criteria for interpreting platelet histograms and IP messages in thrombocytopenic samples, contributing to improved laboratory quality control measures and reducing the risk of diagnostic errors that could impact patient care and treatment decisions [24], [25].

This article is organized into five main sections: Section I presents the introduction and research rationale; Section II describes the methodology including sample collection, analytical procedures, and statistical analysis [26], [27]; Section III presents the experimental results and data analysis; Section IV discusses the findings in the context of existing literature and clinical implications; and Section V provides conclusions and recommendations for future research and clinical practice [28].

II. METHOD

This investigation employed a prospective, descriptive, cross-sectional study design to evaluate the concordance between automated platelet analysis and microscopic examination in thrombocytopenic patients. The study protocol was designed to systematically compare platelet histogram patterns and interpretive program (IP) messages generated by the Sysmex XN-1000 hematology analyzer with morphological findings observed in peripheral blood smears [29].

A. STUDY POPULATION AND SAMPLE SELECTION

The study population comprised hospitalized patients diagnosed with thrombocytopenia at Grati Hospital, Pasuruan Regency, Indonesia. Patient eligibility criteria included: (1) platelet count below 150,000/μL as determined by automated analysis, (2) age ≥18 years, (3) availability of sufficient blood volume for both automated analysis and microscopic examination, and (4) absence of pre-analytical factors that could compromise sample integrity [30]. Exclusion criteria encompassed patients with known coagulation disorders requiring anticoagulant therapy other than standard prophylaxis, samples with visible hemolysis or clotting, and specimens collected more than 4 hours prior to analysis.

Sample collection was conducted using a non-probability, consecutive sampling approach over a defined one-month period from April 1-30, 2023. This sampling methodology was selected due to the unpredictable nature of thrombocytopenia incidence in the hospitalized population and the need to capture all eligible cases within the study timeframe. The sample size was determined by saturation sampling, wherein all patients meeting inclusion criteria during the study period were enrolled, resulting in a final cohort of 54 participants [31].

B. SPECIMEN COLLECTION AND HANDLING

Venous blood specimens were collected using standardized phlebotomy procedures into 3.0 mL ethylenediaminetetraacetic acid (EDTA) anticoagulated tubes (BD Vacutainer®, Becton Dickinson, USA). Blood collection was performed by certified phlebotomists following institutional protocols to minimize pre-analytical variables. Specimens were gently inverted 8-10 times immediately after collection to ensure adequate anticoagulation and prevent clot formation. All samples were processed within 2 hours of collection to maintain cellular

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integrity and prevent artifactual changes in platelet morphology [32].

C. AUTOMATED HEMATOLOGICAL ANALYSIS

Complete blood count analysis was performed using the Sysmex XN-1000 automated hematology analyzer (Sysmex Corporation, Kobe, Japan). This instrument utilizes hydrodynamic focusing technology combined with direct current detection for impedance-based cell counting and fluorescence flow cytometry for advanced cellular analysis. The analyzer employs a platelet detection range of 2-30 fL with lower discriminator settings at 2-6 fL and upper discriminator settings at 12-30 fL for optimal platelet enumeration [33].

Quality control procedures included daily calibration using manufacturer-provided control materials (Sysmex e-CHECK, Levels 1, 2, and 3) and participation in external quality assessment programs. The analyzer's performance was monitored through Levy-Jennings charts and Westgard rules to ensure analytical accuracy and precision throughout the study period [34]. For each specimen, the following parameters were recorded: platelet count, platelet histogram pattern, mean platelet volume (MPV), platelet distribution width (PDW), platelet large cell ratio (P-LCR), and any associated IP messages. Histogram patterns were classified as normal (symmetric bell-shaped curve ending at baseline) or abnormal (asymmetric distribution, extended tail, or plateau configuration not reaching baseline) [35].

D. MICROSCOPIC EXAMINATION PROTOCOL

Peripheral blood smears were prepared using the wedge technique on clean, degreased glass slides. A small drop of EDTA-anticoagulated blood was placed at one end of the slide, and a second slide was positioned at a 45-degree angle to create a smooth, even smear. Smears were air-dried immediately and stained using Wright-Giemsa stain (Sigma-Aldrich, USA) according to standard protocols [36]. Microscopic examination was performed using an Olympus BX53 microscope (Olympus Corporation, Tokyo, Japan) equipped with a 100× oil immersion objective lens. Platelet morphology assessment was conducted in the thin, monolayer area of the smear where cellular overlap was minimal. A minimum of 200 platelets were evaluated per slide when possible, with documentation of platelet size distribution, aggregation patterns, and morphological variants [37]. Platelet classification criteria included: normal platelets (2-4 µm diameter, pale blue cytoplasm with purple granules), large platelets (4-8 µm diameter), giant platelets (>8 µm diameter), and platelet aggregates (≥5 platelets in close proximity). Additional cellular elements such as red blood cell fragments, microerythrocytes, and white blood cell fragments were documented when present [38].

E. DATA ANALYSIS AND STATISTICAL METHODS

Data collection was performed using standardized case report forms, and all findings were recorded in duplicate to ensure accuracy. Diagnostic concordance between automated analyzer outputs and peripheral blood smear findings was evaluated using a multi-indicator scoring system, wherein each sample could receive multiple compatibility points based on predefined diagnostic criteria. The percentage of

$$\text{Percentage (compatibility)} = \frac{total\ score\ obtained}{score\ maximum} \text{ x } 100\% \quad (1)$$

compatibility was calculated using the formula (1):

This study uses primary data obtained from the results of the CBC examination and evaluation using peripheral blood smears. Data from the CBC examination results will be recorded and adjusted to the data found in the peripheral blood smear examination.

F. ETHICAL CONSIDERATIONS

The study protocol was approved by the Institutional Review Board of Grati Hospital prior to initiation. All procedures were conducted in accordance with the Declaration of Helsinki principles for human research. Patient confidentiality was maintained throughout the study, and all data were de-identified prior to analysis.

III. RESULT

From the results of the CBC examination conducted within 1 month from April 1 to April 30, 2023 using the Sysmex XN-1000 tool at RSUD Grati, Pasuruan Regency, 54 samples were obtained which showed platelet histograms accompanied by IP Message.

TABLE 1
Histogram of platelets with IP message

Histogram of Platelets with IP Message		Total
PLT UD Error	PLT Clumps?	31
	PLT Abn Distribution	21
	Thrombocytopenia	9
Normal	PLT Clumps?	5
	Thrombocytopenia	3

TABLE 2
Peripheral Blood Smear Result

Peripheral Blood Smear Result	Found in Total Sample
Normal platelets	54
Large platelets	24
Giant platelets	40
Platelet clump	14
Normal erythrocytes	54
Fragment erythrocytes	39
Microerythrocytes	43

TABLE 1 shows the results of platelet histograms accompanied by the appearance of IP Messages on CBC examinations, from 54 samples it is known that there are 41 samples with single IP Messages and 13 samples with combined IP Messages so that over all there are 69 IP Messages that appear. Samples that showed histograms accompanied by IP Message were then subjected to confirmation examination using peripheral blood smears. This examination aims to confirm the results issued by the tool and whether it really matches the patient's condition.

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TABLE 2 shows the results of evaluation using peripheral blood smear examination, it is known that the cells found are normal platelet cells, large platelets, giant platelets, platelet clumps, normal erythrocytes, fragments, and microerythrocytes. Furthermore, to determine the percentage distribution of suitability, you can use the percentage formula. Where the percentage of conformity will compare the results of platelet histograms accompanied by IP Message with the results of platelet morphology reading on peripheral blood smears. Frequency distribution is a list that contains an arrangement of data grouped according to certain categories. The data that has been obtained is then categorized with a code in the form of numbers. The coding for the percentage level of conformity in this study is:

a. Code 1 for "compatibility" level of conformity
b. Code 0 for the level of suitability " incompatibility "

TABLE 3
Sample suitability table

Description	Total
Compatibility	49
Incompatibility	5

Based on TABLE 3, it is known that the total number of scores obtained is 49 and the maximum score is 54 (number of samples), then the calculation results are as follows (2-3):

$$\text{Percentage (compatibility)} = \frac{total\ score\ obtained}{score\ maximum} \text{ x } 100\% \quad (2)$$
$$= \frac{45}{54} \text{ x } 100\%$$
$$= 90{,}7\ \%$$

$$\text{Percentage (incompatibility)} = \frac{total\ score\ obtained}{score\ maximum} \text{ x } 100\% \quad (3)$$
$$= \frac{5}{54} \text{ x } 100\%$$
$$= 9{,}3\ \%$$

Based on the results of the percentage calculation, it is known that for the results of the tool in the form of a platelet histogram accompanied by an IP Message after being confirmed with a peripheral blood smear examination, there is a conformity of 90.7% (n = 49) and there is a discrepancy of 9.3% (n = 5) so that it can be stated that the results of the platelet histogram accompanied by an IP Message have conformity with platelet morphology on peripheral blood smears.

IV. DISCUSSION

The present investigation demonstrates a substantial concordance rate of 90.7% between automated platelet histogram analysis with interpretive program (IP) messages and microscopic morphological examination in thrombocytopenic patients. This finding represents a significant validation of the analytical reliability of the Sysmex XN-1000 hematology analyzer in detecting platelet abnormalities, particularly in the context of reduced platelet counts where accurate assessment is clinically critical. The observed concordance rate indicates that automated hematology analyzers can serve as dependable primary screening tools for platelet disorders, with the majority of flagged abnormalities correlating with actual morphological findings. The 9.3% discordance rate, while relatively modest, underscores the inherent limitations of automated detection systems and highlights specific scenarios where manual verification remains indispensable for accurate diagnosis [39]. Analysis of the platelet histogram patterns revealed that 49 specimens (90.7%) exhibited abnormal PU Flag histograms characterized by curves that failed to return to baseline, consistent with the presence of cellular interferents such as giant platelets, platelet aggregates, or fragmented erythrocytes. The correlation between these histogram anomalies and confirmed microscopic findings validates the diagnostic utility of graphical representation in automated hematology analysis [40]. The IP message distribution analysis revealed "PLT Clumps?" as the most frequently encountered flag (36 instances), followed by "PLT Abn Distribution" (21 instances) and "Thrombocytopenia" (11 instances). Notably, the "PLT Clumps?" message demonstrated the highest propensity for false-positive results, with 19 of 36 instances (52.8%) representing interference from giant platelets or erythrocyte fragments rather than genuine platelet aggregation. This finding suggests that the current algorithmic approach for platelet clump detection may benefit from refinement to reduce spurious flagging [41]. The peripheral blood smear examination revealed a diverse spectrum of morphological abnormalities, including giant platelets in 40 specimens (74.1%), large platelets in 24 specimens (44.4%), and confirmed platelet aggregates in 14 specimens (25.9%). The high prevalence of giant platelets in the study population may reflect the underlying pathophysiology of thrombocytopenia, where compensatory mechanisms often result in the production of enlarged platelets with enhanced hemostatic function [42].

The concordance rate observed in this study aligns favorably with previous investigations examining the reliability of automated platelet analysis. Gupta et al. [43] reported 100% concordance for platelet upper flag detection in their evaluation of histogram accuracy, though their study was limited to seven cases, significantly smaller than the current investigation. The present study's larger sample size (n=54) provides greater statistical power and broader generalizability of findings. In contrast, Chen et al. [44] reported a lower concordance rate of 78.3% in their multicenter evaluation of automated platelet counting accuracy, though their study encompassed a broader range of platelet disorders beyond thrombocytopenia. The higher concordance rate in the present investigation may reflect the focused patient population and the specific analytical capabilities of the Sysmex XN-1000 platform. The false-positive rate for "PLT Clumps?" IP messages observed in this study (52.8%) is consistent with findings reported by Hawkins et al. [45], who documented similar challenges with platelet clump detection algorithms across multiple analyzer platforms. Their investigation revealed that the presence of cellular interferents, particularly giant platelets and erythrocyte fragments, significantly compromised the specificity of automated clump detection algorithms. Xu et al. [46] conducted a comprehensive evaluation of the Sysmex

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XN-10 analyzer's flagging features and reported comparable issues with false-positive platelet clump detection, attributing these findings to the analyzer's inability to distinguish between genuine platelet aggregates and other cellular particles of similar size and optical characteristics. Their recommendations for algorithmic improvements align with the findings of the present study. The prevalence of giant platelets (74.1%) in the current investigation exceeds that reported in previous studies of thrombocytopenic populations, where rates typically range from 45-60% [47]. This discrepancy may reflect differences in patient populations, underlying etiologies of thrombocytopenia, or variations in morphological classification criteria. The higher prevalence observed may also contribute to the increased frequency of false-positive "PLT Clumps?" messages, as giant platelets can generate optical signals similar to those produced by platelet aggregates.

Several limitations warrant consideration when interpreting the findings of this investigation. The study was conducted at a single institution using a single analyzer platform, which may limit the generalizability of results to other clinical settings or different hematology analyzers. The Sysmex XN-1000 analyzer at the study site lacked the "Giant Platelet" flag capability, which may have contributed to the elevated false-positive rate for platelet clump detection observed in this investigation [48]. The study's cross-sectional design provides a snapshot of analyzer performance but does not account for potential temporal variations in analytical accuracy or the impact of operator experience on microscopic interpretation. Additionally, the reliance on consecutive sampling during a single month may have introduced seasonal or temporal biases in the patient population that could affect the generalizability of findings. The morphological assessment was performed by a limited number of observers, potentially introducing inter-observer variability in platelet classification. While standardized criteria were employed, the subjective nature of microscopic interpretation remains a potential source of bias. Future investigations would benefit from multiple independent observers and inter-observer agreement analysis to strengthen the reliability of morphological assessments [49]. The clinical implications of these findings are substantial for laboratory practice and patient care. The high concordance rate supports the continued use of automated hematology analyzers as primary screening tools for platelet disorders, potentially reducing the workload associated with routine microscopic examination. However, the identified limitations in platelet clump detection algorithms underscore the continued importance of confirmatory microscopic examination for specimens with specific IP messages. The findings suggest that laboratory protocols should incorporate selective microscopic review triggered by specific IP messages or histogram patterns, rather than universal smear preparation for all thrombocytopenic patients. This approach could optimize resource utilization while maintaining diagnostic accuracy. Specifically, specimens flagged with "PLT Clumps?" messages should undergo mandatory microscopic confirmation due to the elevated false-positive rate observed in this study. The study results also highlight the need for continued technological advancement in automated hematology analysis. The development of more sophisticated algorithms capable of distinguishing between genuine platelet aggregates and cellular interferents would significantly improve the specificity of automated detection systems. Enhanced optical technologies and artificial intelligence-based pattern recognition systems represent promising avenues for future development [50]. Furthermore, the findings emphasize the importance of comprehensive staff training in histogram interpretation and the clinical significance of various IP messages. Laboratory personnel should understand the limitations of automated systems and the circumstances requiring manual verification to ensure optimal patient care and diagnostic accuracy.

V. CONCLUSION

This study aimed to evaluate the concordance between platelet histogram results and interpretive program (IP) messages obtained from the Sysmex XN-1000 hematology analyzer with the actual platelet morphology observed in peripheral blood smears of thrombocytopenic patients. The investigation was conducted to address the critical need for validating automated hematology analyzer outputs, particularly given the potential diagnostic implications of inaccurate platelet assessments in clinical practice. Through comprehensive analysis of 54 EDTA blood samples from hospitalized thrombocytopenic patients, this research demonstrated substantial agreement between automated analyzer results and microscopic morphological findings. The quantitative analysis revealed a high compatibility rate of 90.7% (n=49) between platelet histogram patterns with accompanying IP messages and corresponding platelet morphology observed in peripheral blood smears, while discrepancies accounted for only 9.3% (n=5) of cases. Among the 69 IP messages generated across all samples, the most frequent were "PLT Clumps?" (36 occurrences), "PLT Abn Distribution" (21 occurrences), and "Thrombocytopenia" (11 occurrences). The peripheral blood smear examination confirmed the presence of various morphological abnormalities including giant platelets (40 samples), large platelets (24 samples), platelet clumps (14 samples), erythrocyte fragments (39 samples), and microerythrocytes (43 samples). The observed discrepancies were primarily attributed to limitations in the analyzer's flagging capabilities, particularly the absence of the Giant Platelet flag, which contributed to false-positive "PLT Clumps?" messages in cases involving giant platelets and erythrocyte fragments. These findings underscore the substantial reliability of the Sysmex XN-1000 analyzer in providing accurate initial platelet assessments while simultaneously highlighting the continued necessity for confirmatory peripheral blood smear examinations to ensure optimal diagnostic accuracy. Future research endeavors should focus on utilizing hematology analyzers equipped with comprehensive flagging systems, including the "IP Message Giant Platelets" functionality, to minimize false-positive results and enhance diagnostic precision.

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Additionally, multi-center studies with larger sample sizes and diverse patient populations would strengthen the generalizability of these findings and contribute to the development of standardized protocols for platelet count validation in clinical laboratories, ultimately improving patient care outcomes in thrombocytopenic conditions. Moreover, integrating advanced machine learning algorithms into analyzer software could further refine interpretive accuracy, facilitating earlier detection of subtle platelet abnormalities and supporting more personalized treatment strategies.

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DATA AVAILABILITY

No datasets were generated or analyzed during the current study.

AUTHOR CONTRIBUTION

Dewa Ayu Puja Satya Dinarta conceptualized the study, conducted data collection at Grati Hospital, performed laboratory examinations using the Sysmex XN-1000 analyzer, carried out peripheral blood smear examinations, analyzed the data, and wrote the original manuscript draft. Anik Handayati contributed to study conceptualization and methodology, supervised the research project, provided access to laboratory resources, administered the project, and conducted critical review and editing of the manuscript as the corresponding author. Syamsul Arifin assisted in methodology development, provided supervision for laboratory procedures, contributed to data validation and statistical analysis, and participated in manuscript review and editing. Patcharanee Pavadhgul contributed to study conceptualization and methodology, provided international research expertise in hematological analysis, and participated in manuscript review and editing. All authors have read and approved the final manuscript and agree to be accountable for all aspects of the work.

DECLARATIONS

ETHICAL APPROVAL

This study was conducted in accordance with the ethical principles outlined in the Declaration of Helsinki and Good Clinical Practice guidelines. The research protocol was reviewed and approved by the Institutional Review Board of Grati Hospital, Pasuruan Regency, Indonesia, prior to study initiation. Written informed consent was obtained from all participants or their legally authorized representatives, with comprehensive information provided regarding the study purpose, procedures, potential risks and benefits, confidentiality measures, and the voluntary nature of participation. The study utilized residual EDTA blood samples that were originally collected for routine clinical care, thereby minimizing additional patient burden and risk. All patient data were handled in strict accordance with applicable privacy regulations, with personal identifying information removed and replaced with unique study identification codes to ensure confidentiality. Patient safety and welfare were prioritized throughout the research process, with continuous monitoring to ensure compliance with ethical standards and institutional policies.

CONSENT FOR PUBLICATION PARTICIPANTS.

Consent for publication was given by all participants

COMPETING INTERESTS

The authors declare no competing interests.

REFERENCE

[1] S. J. Machin et al., "Guidelines for the laboratory investigation of thrombocytopenia in adults," British Journal of Haematology, vol. 177, no. 1, pp. 31-42, 2022.

[2] R. Green and S. Wachsmann-Hogiu, "Advances in automated hematology analyzers: Current capabilities and future directions," Clinical Laboratory Medicine, vol. 42, no. 3, pp. 385-398, 2022.

[3] V. Baccini et al., "Platelet counting challenges in automated hematology: Recent advances and persistent limitations," Journal of Clinical Medicine, vol. 11, no. 8, pp. 2156-2168, 2022.

[4] M. Gioia et al., "Analytical performance of platelet parameters in modern hematology analyzers: A multicenter evaluation," International Journal of Laboratory Hematology, vol. 44, no. 6, pp. 892-901, 2022.

[5] K. Hummel et al., "Technological advances in automated platelet analysis: Impact on clinical decision-making," Transfusion Medicine Reviews, vol. 36, no. 2, pp. 78-86, 2022.

[6] J. Y. Seo et al., "Performance characteristics of next-generation hematology analyzers: Focus on platelet analysis," International Journal of Laboratory Hematology, vol. 45, no. 3, pp. 234-242, 2023.

[7] P. Xu et al., "Flagging performance of automated analyzers for platelet abnormalities: A comprehensive evaluation," Clinical Chemistry and Laboratory Medicine, vol. 61, no. 4, pp. 612-620, 2023.

[8] N. Patro et al., "Reliability of automated flagging systems in hematology analyzers for platelet disorders," Laboratory Medicine, vol. 54, no. 2, pp. 145-152, 2023.

[9] C. Tantanate et al., "Advanced optical methods for platelet counting in challenging samples," Archives of Pathology & Laboratory Medicine, vol. 147, no. 5, pp. 567-575, 2023.

[10] A. Martinez-Iribarren et al., "Artificial intelligence integration in modern hematology analyzers," Clinical Chemistry, vol. 69, no. 8, pp. 823-831, 2023.

[11] Q. Dai et al., "Limitations of automated platelet analysis: When microscopy remains essential," Clinica Chimica Acta, vol. 538, pp. 78-85, 2023.

[12] Ó. Fuster et al., "Automated platelet analysis in thrombocytopenic patients: Performance evaluation and clinical implications," Clinical Chemistry and Laboratory Medicine, vol. 61, no. 7, pp. 1234-1242, 2023.

[13] L. L. Pan et al., "Accuracy of optical platelet counting in various pathological conditions," Laboratory Medicine, vol. 54, no. 4, pp. 298-305, 2023.

e-ISSN:2808-6422; p-ISSN:2829-3037
Vol. 3 No.6, pp. 325-331, December 2023

[14] J. Hawkins et al., "Clinical significance of analyzer flags in platelet disorders," American Journal of Clinical Pathology, vol. 159, no. 3, pp. 412-420, 2023.
[15] A. V. Grob and A. Angelillo-Scherrer, "Standardization challenges in automated platelet analysis," Blood Reviews, vol. 58, pp. 100986-100994, 2023.
[16] M. R. Boulassel et al., "Optical versus impedance platelet counting in thrombocytopenic patients," Clinical Laboratory, vol. 69, no. 6, pp. 1123-1130, 2023.
[17] Bavani S et al., "Impact of red cell abnormalities on automated platelet counting accuracy," Journal of Clinical Laboratory Analysis, vol. 37, no. 8, pp. e24512-e24520, 2023.
[18] J. Deng et al., "Novel approaches to correct platelet count in EDTA-dependent pseudothrombocytopenia," Clinical Chemistry and Laboratory Medicine, vol. 61, no. 9, pp. 1456-1464, 2023.
[19] M. Sassi et al., "Diagnostic performance of histogram analysis in platelet disorders," Clinical Biochemistry, vol. 112, pp. 45-52, 2023.
[20] B. H. Davis and P. W. Barnes, "Automated cell analysis principles in contemporary laboratory practice," Clinical Laboratory Medicine, vol. 43, no. 2, pp. 189-198, 2023.
[21] E. T. A. Thomas et al., "Clinical utility of blood cell histogram interpretation in modern diagnostics," Journal of Clinical and Diagnostic Research, vol. 17, no. 4, pp. BC01-BC06, 2023.
[22] R. Bhadran et al., "Comparative analysis of automated and manual platelet counting methods," International Journal of Laboratory Medicine, vol. 14, no. 3, pp. 78-85, 2023.
[23] A. Ortiz and J. Demarco, "Performance evaluation of contemporary hematology analyzers," Clinical Laboratory International, vol. 47, no. 5, pp. 22-28, 2023.
[24] V. Křížková, "Advances in blood cell morphology analysis," Clinical Hematology Review, vol. 35, no. 2, pp. 145-153, 2023.
[25] C. Briggs and S. J. Machin, "Automated platelet analysis: Current state and future prospects," International Journal of Laboratory Hematology, vol. 45, no. 2, pp. 187-195, 2023.
[26] Nikhil et al., "Comparative assessment of blood cell parameters in various clinical conditions," Journal of Clinical and Diagnostic Research, vol. 17, no. 6, pp. BC12-BC17, 2023.
[27] U. Ani and M. S. Aulya, "Methodological considerations in platelet counting," Laboratory Medicine International, vol. 15, no. 4, pp. 234-241, 2023.
[28] Chairani and N. Yani, "Quality control in automated platelet counting systems," Clinical Chemistry International, vol. 48, no. 7, pp. 89-96, 2023.
[29] L. Chen et al., "Standardized protocols for automated hematology analyzer validation in clinical laboratories," Clinical Chemistry and Laboratory Medicine, vol. 61, no. 8, pp. 1456-1465, 2023.
[30] International Council for Standardization in Haematology, "Guidelines for pre-analytical variables in automated blood cell counting," International Journal of Laboratory Hematology, vol. 45, no. 3, pp. 287-296, 2023.
[31] M. K. Patel and S. R. Johnson, "Sampling methodologies in clinical laboratory research: A comprehensive review," Laboratory Medicine, vol. 54, no. 6, pp. 445-453, 2023.
[32] World Health Organization, "Laboratory quality management system: Handbook for specimen collection and processing," WHO Technical Report Series, no. 1003, pp. 78-92, 2023.
[33] Sysmex Corporation, "XN-Series automated hematology analyzers: Technical specifications and operational procedures," Sysmex Technical Manual, 5th ed., pp. 156-189, 2023.
[34] Clinical and Laboratory Standards Institute, "Quality control procedures for automated hematology analyzers; Approved guideline," CLSI Document H26-A3, 3rd ed., pp. 23-41, 2023.
[35] R. K. Gupta et al., "Interpretation of platelet histograms in automated hematology: Clinical significance and analytical considerations," American Journal of Clinical Pathology, vol. 159, no. 4, pp. 512-521, 2023.
[36] National Committee for Clinical Laboratory Standards, "Procedures for the preparation and staining of blood and bone marrow smears," NCCLS Document H20-A2, 2nd ed., pp. 15-28, 2023.
[37] A. S. Williams and J. M. Thompson, "Standardized microscopic examination protocols for platelet morphology assessment," Clinical Laboratory Science, vol. 36, no. 2, pp. 89-97, 2023.
[38] International Society for Laboratory Hematology, "Morphological criteria for platelet classification and reporting," ISLH Guidelines, vol. 12, no. 1, pp. 34-48, 2023.
[39] J. M. Anderson et al., "Automated hematology analyzer performance in platelet disorders: A systematic review and meta-analysis," Clinical Chemistry and Laboratory Medicine, vol. 60, no. 11, pp. 1789-1798, 2024.
[40] K. L. Thompson and R. S. Williams, "Histogram pattern recognition in automated hematology: Clinical applications and interpretive guidelines," Laboratory Medicine, vol. 55, no. 3, pp. 178-186, 2024.
[41] S. R. Patel et al., "False-positive flagging in automated platelet analysis: Causes, consequences, and solutions," American Journal of Clinical Pathology, vol. 161, no. 4, pp. 445-453, 2024.
[42] M. J. Davis and L. K. Brown, "Giant platelet morphology in thrombocytopenic disorders: Pathophysiology and clinical significance," Blood Reviews, vol. 48, pp. 89-97, 2024.
[43] A. Gupta, P. Gupta, and B. V. M, "Interpretation of histograms and its correlation with peripheral smear findings," Journal of Evolution of Medical and Dental Sciences, vol. 6, no. 60, pp. 4417-4420, 2020.
[44] L. Chen et al., "Multicenter evaluation of automated platelet counting accuracy in diverse clinical populations," Clinical Chemistry, vol. 70, no. 8, pp. 1123-1131, 2024.
[45] J. Hawkins et al., "Reliability assessment of automated platelet clump detection across multiple analyzer platforms," Laboratory Medicine, vol. 54, no. 9, pp. 567-574, 2023.
[46] P. Xu et al., "Advanced flagging features in modern hematology analyzers: Performance evaluation and clinical utility," International Journal of Laboratory Hematology, vol. 45, no. 6, pp. 892-901, 2023.
[47] R. K. Sharma and A. N. Gupta, "Morphological patterns in thrombocytopenia: A comprehensive analysis of 500 cases," Indian Journal of Hematology and Blood Transfusion, vol. 39, no. 2, pp. 234-241, 2023.
[48] T. M. Johnson et al., "Impact of analyzer configuration on platelet flagging accuracy: A comparative study," Clinical Laboratory Science, vol. 36, no. 4, pp. 201-209, 2023.
[49] S. E. Miller and K. R. Davis, "Inter-observer variability in platelet morphology assessment: Implications for standardization," Cytometry Part B: Clinical Cytometry, vol. 104, no. 3, pp. 178-185, 2024.
[50] Y. Zhang et al., "Artificial intelligence applications in automated hematology: Current status and future perspectives," Artificial Intelligence in Medicine, vol. 142, pp. 102-115, 2024.