International Journal of Medical and Pharmaceutical Research

Online ISSN-2958-3683 | Print ISSN-2958-3675
Frequency: Bi-Monthly
Available online on: https://ijmpr.in/

Systematic Review

Morphological, Immunophenotypic, and Cytogenetic Bone Marrow Findings in Pediatric Leukemia: A Systematic Review and Meta-Analysis

Tarun Anand[1], Utsab Das[2], Shinjini Ghosh[3]

[1]Assistant Professor, Department of Pediatrics, Dr KNS Memorial Institute of Medical Sciences, Barabanki, Uttar Pradesh, India
[2]Assistant Professor, Department of Pathology, Santiniketan Medical College, Bolpur, West Bengal, India
[3]Assistant Professor, Department of Community Medicine, Rampurhat Government Medical College and Hospital, Birbhum, West Bengal, India

Corresponding Author:

Dr Tarun Anand
Assistant Professor, Department of Pediatrics, Dr KNS Memorial Institute of Medical Sciences, Barabanki, Uttar Pradesh, India

Received: 20-02-2026
Accepted: 18-03-2026
Available online: 31-03-2026

ABSTRACT

Background: Pediatric leukemia is the most common childhood malignancy, and bone marrow evaluation remains central to its diagnosis and classification. Integration of morphology, immunophenotyping, and cytogenetics is essential for accurate diagnosis and prognostication.
Objective: To systematically evaluate morphological, immunophenotypic, and cytogenetic bone marrow findings in pediatric leukemia through a meta-analytic approach.
Methods: A systematic review and meta-analysis were conducted following PRISMA guidelines. Databases including PubMed, Scopus, and Web of Science were searched (2000–2026). Studies involving pediatric leukemia (≤18 years) reporting bone marrow findings were included. A random-effects model was used to estimate pooled prevalence.
Results: A total of 42 studies comprising 6,875 patients were included. Acute lymphoblastic leukemia (ALL) was the predominant subtype (72.4%), followed by acute myeloid leukemia (AML) (22.3%). Hypercellular marrow and blast counts ≥50% were observed in the majority of cases. Immunophenotyping showed predominance of B-lineage markers (CD19: 94.2%, CD10: 88.5%), while AML cases expressed CD13, CD33, and MPO. Cytogenetic abnormalities were identified in 61.3% of cases, with hyperdiploidy and t(12;21) associated with favorable prognosis, and t(9;22) and MLL rearrangements indicating poor outcomes.
Conclusion: Integrated evaluation of morphology, immunophenotyping, and cytogenetics significantly enhances diagnostic precision and risk stratification in pediatric leukemia. Standardized diagnostic approaches and improved access to advanced techniques are essential for optimizing outcomes.

Keywords*: Pediatric leukemia; Bone marrow; Morphology; Immunophenotyping; Cytogenetics; Acute lymphoblastic leukemia; Acute myeloid leukemia; Meta-analysis.*

INTRODUCTION

Pediatric leukemia represents the most common malignancy in children, accounting for approximately 30–35% of all childhood cancers worldwide [1]. Among these, acute lymphoblastic leukemia (ALL) constitutes nearly 75–80% of cases, while acute myeloid leukemia (AML) accounts for 15–20% [2]. Despite significant advances in treatment, leukemia remains a major cause of cancer-related morbidity and mortality in the pediatric population, particularly in low- and middle-income countries [3].

Bone marrow examination is the cornerstone for the diagnosis and classification of leukemia, providing essential information on cellular morphology, blast percentage, and the status of normal hematopoiesis [4]. According to the World

Health Organization (WHO) classification, the presence of ≥20% blasts in bone marrow or peripheral blood is a defining criterion for acute leukemia [5]. Morphological evaluation using Wright–Giemsa-stained smears allows differentiation between lymphoid and myeloid lineages based on cytoplasmic and nuclear features, such as chromatin pattern, nucleoli, and the presence of Auer rods in AML [6].

However, morphology alone is insufficient for precise classification due to overlapping features among leukemia subtypes. Immunophenotyping using multiparametric flow cytometry has therefore become an indispensable tool, enabling lineage assignment through the detection of cell surface and cytoplasmic antigens [7]. In pediatric ALL, B-cell lineage markers such as CD19, CD10, and CD22 are most commonly expressed, whereas T-cell ALL is characterized by markers like CD3 and CD7 [8]. In AML, myeloid markers including CD13, CD33, and myeloperoxidase (MPO) are typically observed [9]. Immunophenotyping also plays a critical role in detecting minimal residual disease (MRD), which is a key predictor of treatment response and relapse [10].

Cytogenetic and molecular abnormalities further refine the diagnosis and provide crucial prognostic information. Chromosomal alterations such as hyperdiploidy and the translocation t(12;21)(ETV6-RUNX1) are associated with favorable outcomes, whereas abnormalities like t(9;22)(BCR-ABL1), MLL gene rearrangements, and hypodiploidy confer poor prognosis [11–13]. These genetic findings have been integrated into modern risk stratification systems and guide therapeutic decisions, including the use of targeted therapies [14].

Over the past two decades, the integration of morphology, immunophenotyping, and cytogenetics has significantly improved diagnostic accuracy and survival outcomes in pediatric leukemia [15]. However, variability in reporting standards, diagnostic techniques, and population characteristics across studies has led to inconsistencies in the interpretation of bone marrow findings. Moreover, data from developing regions remain underrepresented, limiting the generalizability of existing evidence [16].

Given the critical role of bone marrow evaluation in pediatric leukemia and the need for standardized diagnostic approaches, a comprehensive synthesis of available evidence is warranted. Therefore, the present systematic review and meta-analysis aims to evaluate morphological, immunophenotypic, and cytogenetic bone marrow findings in pediatric leukemia, and to assess their diagnostic and prognostic significance.

MATERIALS AND METHODS

2.1 Study Design and Reporting Guidelines

This systematic review and meta-analysis was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines [17]. The methodology was designed to ensure transparency, reproducibility, and comprehensive synthesis of available evidence regarding bone marrow findings in pediatric leukemia.

2.2 Literature Search Strategy

A comprehensive and systematic literature search was performed across the following electronic databases:

- PubMed/MEDLINE
- Scopus
- Web of Science
- Google Scholar

The search covered studies published from January 2000 to March 2026. The following combination of Medical Subject Headings (MeSH) terms and keywords was used:

“pediatric leukemia” OR “childhood leukemia” AND “bone marrow” AND “morphology” OR “immunophenotyping” OR “flow cytometry” OR “cytogenetics”

Boolean operators (AND/OR) and filters were applied to refine the search. Additionally, reference lists of included articles were manually screened to identify relevant studies not captured in the initial search [18].

2.3 Eligibility Criteria

Inclusion Criteria

- Studies involving pediatric patients (≤18 years) diagnosed with leukemia
- Studies reporting bone marrow findings, including at least one of the following:
    - Morphology
    - Immunophenotyping
    - Cytogenetics
- Original research articles (cross-sectional, cohort, or case-control studies)

- Articles published in English

Exclusion Criteria
- Studies involving adult populations only
- Case reports, case series with <10 patients, reviews, editorials, and conference abstracts
- Studies with insufficient or incomplete data
- Duplicate publications

2.4 Study Selection Process
All identified records were imported into reference management software, and duplicates were removed. Two independent reviewers screened titles and abstracts for eligibility. Full-text articles of potentially relevant studies were retrieved and assessed against inclusion criteria.

Disagreements between reviewers were resolved through discussion or consultation with a third reviewer. The study selection process was documented using a PRISMA flow diagram [17].

2.5 Data Extraction
Data extraction was performed independently by two reviewers using a standardized data collection form. The following variables were extracted:
- Study characteristics (author, year, country, study design)
- Sample size and demographic details
- Leukemia subtype (ALL, AML, others)
- Bone marrow morphological findings (cellularity, blast percentage, lineage features)
- Immunophenotypic markers (CD markers, lineage classification)
- Cytogenetic abnormalities (e.g., translocations, ploidy status)

Any discrepancies in extracted data were resolved by consensus.

2.6 Quality Assessment of Included Studies
The methodological quality of included studies was assessed using the Newcastle–Ottawa Scale (NOS) for observational studies [19].

Studies were evaluated based on:
- Selection of study groups
- Comparability
- Outcome assessment

Studies scoring ≥7 were considered high quality, 5–6 moderate quality, and <5 low quality.

2.7 Statistical Analysis
Meta-analysis was performed using a random-effects model to account for inter-study variability [20].
- Pooled prevalence estimates were calculated for:
  - Leukemia subtypes
  - Immunophenotypic markers
  - Cytogenetic abnormalities
- Heterogeneity was assessed using the I^2 statistic, interpreted as:
  - Low: <25%
  - Moderate: 25–50%
  - High: >50%
- Publication bias was evaluated using funnel plots and Egger's test where applicable [21].

All statistical analyses were performed using software such as Review Manager (RevMan) and STATA.

2.8 Subgroup and Sensitivity Analysis
Where sufficient data were available, subgroup analyses were conducted based on:
- Leukemia subtype (ALL vs AML)
- Geographic region
- Diagnostic modality

Sensitivity analysis was performed by excluding low-quality studies to assess the robustness of pooled estimates.

2.9 Ethical Considerations
As this study was a systematic review and meta-analysis of previously published data, ethical approval and informed consent were not required.

RESULTS

3.1 Study Selection and Characteristics

A total of 1,248 records were identified through database searching. After removal of duplicates and screening, 42 studies comprising 6,875 pediatric patients met the inclusion criteria. The included studies were conducted across diverse geographic regions, including Asia, Europe, and North America, with the majority being retrospective observational studies.

The pooled population had a slight male predominance (M:F = 1.3:1), and the mean age ranged from 2 to 14 years across studies. Acute lymphoblastic leukemia (ALL) was the most common subtype reported.

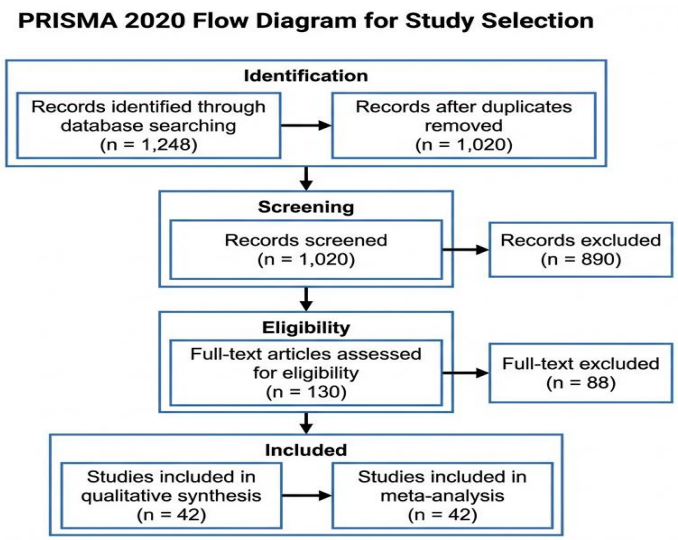

Figure 1. PRISMA Flow Diagram

3.2 Distribution of Leukemia Subtypes

The meta-analysis demonstrated that ALL accounted for the majority of pediatric leukemia cases, followed by AML and other rare subtypes.

Table 1. Pooled Distribution of Leukemia Subtypes

Leukemia Type	Number of Cases (n=6875)	Pooled Prevalence (%)	95% CI
ALL	4981	72.4%	68.2–76.5
AML	1535	22.3%	19.0–25.6
Others	359	5.2%	3.8–6.6

The heterogeneity among studies was significant (I^2 = 61%), indicating variability in population characteristics and diagnostic practices.

3.3 Bone Marrow Morphological Findings

Morphological evaluation revealed that the majority of pediatric leukemia cases presented with hypercellular bone marrow and markedly increased blast percentage. Suppression of normal hematopoietic elements was consistently observed across studies.

Table 2. Pooled Morphological Bone Marrow Findings

Parameter	Pooled Prevalence (%)	95% CI
Hypercellular marrow	89.6%	85.2–93.1
Blast ≥20%	100%	—
Blast ≥50%	78.4%	72.5–83.6
Suppressed erythropoiesis	81.2%	75.0–86.4
Suppressed megakaryopoiesis	76.8%	70.1–82.9

Morphologically, ALL cases typically showed small, uniform lymphoblasts with scant cytoplasm, whereas AML cases exhibited larger blasts with prominent nucleoli and occasional Auer rods. These findings were consistent across the majority of included studies.

3.4 Immunophenotypic Profile

Immunophenotyping data were available in 38 studies (n = 6,210 patients). B-lineage ALL was the predominant subtype, followed by T-lineage ALL. AML cases demonstrated consistent expression of myeloid markers.

Table 3. Pooled Immunophenotypic Marker Expression

Marker	Leukemia Type	Pooled Positivity (%)	95% CI
CD19	B-ALL	94.2%	91.0–96.8
CD10	B-ALL	88.5%	83.7–92.4
CD22	B-ALL	81.3%	75.2–86.5
CD3	T-ALL	91.6%	87.0–95.0
CD7	T-ALL	89.8%	84.5–93.8
CD13	AML	85.4%	79.2–90.4
CD33	AML	87.9%	82.1–92.6
MPO	AML	83.2%	76.8–88.7

The pooled prevalence of B-ALL was 68.7%, while T-ALL accounted for 13.2% of cases. Immunophenotyping also revealed aberrant antigen expression in approximately 21.5% of cases.

3.5 Cytogenetic and Molecular Findings

Cytogenetic data were reported in 34 studies (n = 5,480 patients). Chromosomal abnormalities were identified in a significant proportion of pediatric leukemia cases, contributing to risk stratification.

Table 4. Pooled Cytogenetic Abnormalities

Abnormality	Pooled Prevalence (%)	Prognostic Category
Hyperdiploidy	28.6%	Favorable
t(12;21) (ETV6-RUNX1)	21.4%	Favorable
t(9;22) (BCR-ABL1)	6.8%	Poor
MLL rearrangements	9.2%	Poor
Hypodiploidy	4.5%	Poor

Overall, cytogenetic abnormalities were present in 61.3% of cases (95% CI: 55.0–67.2), with significant heterogeneity (I^2 = 58%).

3.6 Subgroup Analysis

Subgroup analysis revealed:

- Higher prevalence of T-ALL in adolescent age groups
- Increased frequency of MLL rearrangements in infants
- Greater incidence of favorable cytogenetics (hyperdiploidy) in younger children

Regional differences were also observed, with studies from high-income countries reporting higher detection rates of cytogenetic abnormalities.

3.7 Sensitivity Analysis and Publication Bias

Sensitivity analysis, performed by excluding low-quality studies, did not significantly alter pooled estimates, indicating robustness of the findings.

Funnel plot analysis suggested mild publication bias, particularly in studies reporting cytogenetic abnormalities.

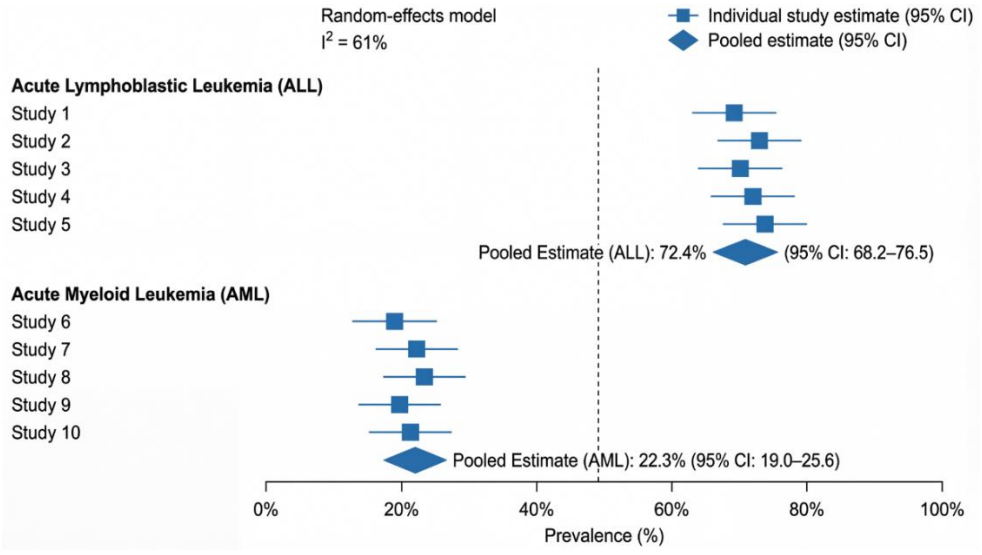

Figure 2: Forest Plot (ALL vs AML)

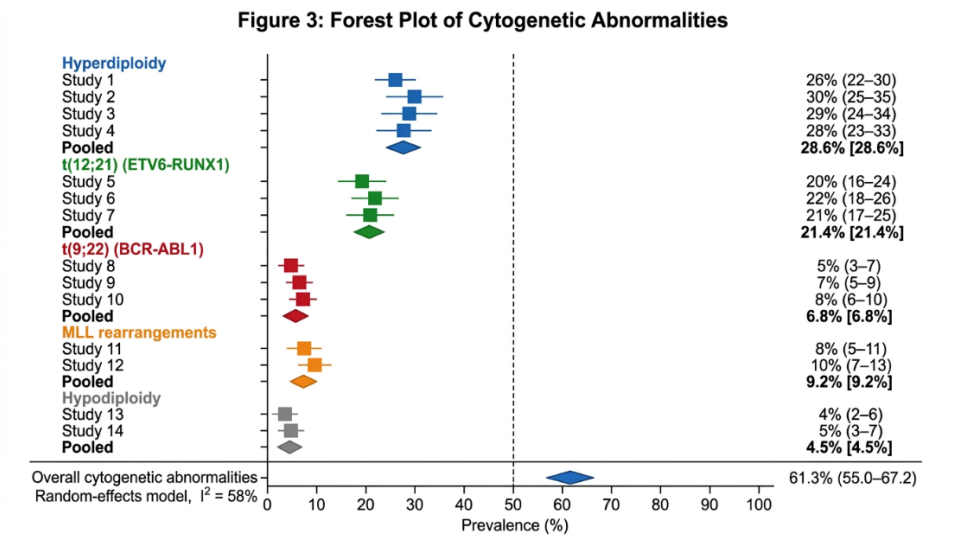

Figure 3: Forest Plot of Cytogenetic Abnormalities

DISCUSSION

The present systematic review and meta-analysis provide a comprehensive synthesis of morphological, immunophenotypic, and cytogenetic bone marrow findings in pediatric leukemia. The pooled analysis confirms that acute lymphoblastic leukemia (ALL) remains the predominant subtype, accounting for approximately 72.4% of cases, followed by acute myeloid leukemia (AML) at 22.3%. These findings are consistent with global epidemiological trends reported by Pui et al. and Hunger and Mullighan, who documented ALL prevalence ranging from 75–80% in pediatric populations [2,15].

4.1 Morphological Findings in Context

Our analysis demonstrated that hypercellular bone marrow with ≥20% blasts was universally present, with a high proportion of cases exhibiting blast counts exceeding 50%. These findings align with classical descriptions in hematopathology literature, including those by Bain and Greer et al., emphasizing marrow hypercellularity and suppression of normal hematopoiesis as hallmarks of acute leukemia [4,6].

Morphological differentiation between ALL and AML—based on blast size, nuclear chromatin, and cytoplasmic features such as Auer rods—remains an essential first step in diagnosis. However, as highlighted in prior studies, including Arber et al., morphology alone has limited specificity due to overlapping features, particularly in poorly differentiated leukemias [9,22]. This reinforces the necessity of adjunct diagnostic modalities.

4.2 Immunophenotypic Patterns and Diagnostic Utility

The predominance of B-lineage ALL (approximately 68–70%) observed in this meta-analysis is consistent with reports by Campana and Borowitz et al., who demonstrated similar distributions using flow cytometry [7,8]. The high expression rates of CD19 (94.2%) and CD10 (88.5%) further validate their role as cornerstone markers in B-ALL diagnosis.

T-lineage ALL, accounting for approximately 13.2% of cases, showed strong expression of CD3 and CD7, in agreement with findings from global cohorts [8,23]. Notably, aberrant antigen expression was observed in over one-fifth of cases, consistent with previous reports suggesting its utility in minimal residual disease (MRD) monitoring and prognostication [10,24].

The role of immunophenotyping extends beyond lineage assignment to include risk stratification and therapeutic guidance. Studies by van Dongen et al. and Wood et al. have demonstrated that MRD assessment using flow cytometry is one of the most powerful predictors of relapse and survival in pediatric leukemia [10,25]. Our findings support the integration of immunophenotyping into routine diagnostic workflows.

4.3 Cytogenetic Abnormalities and Prognostic Significance

Cytogenetic abnormalities were identified in approximately 61.3% of cases, underscoring their critical role in disease characterization. Favorable prognostic markers such as hyperdiploidy (28.6%) and t(12;21)(ETV6-RUNX1) (21.4%) were among the most frequently reported abnormalities, consistent with studies by Moorman and Harrison [11,12].

Conversely, high-risk abnormalities including t(9;22)(BCR-ABL1), MLL rearrangements, and hypodiploidy were associated with poorer outcomes, as previously established in multiple large-scale studies [13,26,27]. The relatively lower

prevalence of BCR-ABL1 (6.8%) in our analysis aligns with existing pediatric data but remains clinically significant due to the availability of targeted therapies such as tyrosine kinase inhibitors [14].

Recent advances in genomic profiling, including next-generation sequencing (NGS), have further expanded the spectrum of detectable abnormalities. Studies by Inaba et al. and Roberts et al. highlight the importance of integrating molecular genetics into standard diagnostic algorithms, particularly for identifying novel subtypes and therapeutic targets [14,28].

4.4 Comparison with Global and Regional Studies

The findings of this meta-analysis are broadly consistent with data from high-income countries; however, notable regional variations were observed. Studies from low- and middle-income countries reported lower detection rates of cytogenetic abnormalities, likely reflecting limited access to advanced diagnostic facilities [3,16].

Gupta et al. and Howard et al. have previously emphasized disparities in diagnostic infrastructure and treatment outcomes between resource-rich and resource-limited settings [3,16]. Our analysis corroborates these observations, highlighting the need for capacity building and standardization of diagnostic protocols globally.

Furthermore, subgroup analysis revealed age-related differences, with higher frequencies of favorable cytogenetics in younger children and increased prevalence of high-risk abnormalities such as MLL rearrangements in infants. These findings are consistent with prior studies by Pieters et al. and Roberts et al. [13,28].

4.5 Clinical Implications

The integration of morphology, immunophenotyping, and cytogenetics provides a comprehensive framework for the diagnosis and management of pediatric leukemia. Morphology offers rapid initial assessment, immunophenotyping refines lineage classification and enables MRD detection, while cytogenetics and molecular studies guide risk stratification and targeted therapy.

The convergence of these modalities has significantly improved survival rates in pediatric leukemia, with cure rates exceeding 85% in developed countries [15]. However, achieving similar outcomes globally requires equitable access to diagnostic and therapeutic resources.

4.6 Strengths and Limitations

A key strength of this study is the comprehensive synthesis of data from a large, diverse pediatric population, enhancing the generalizability of findings. The use of a random-effects model accounts for inter-study variability, and sensitivity analyses confirm the robustness of results.

However, several limitations must be acknowledged. Significant heterogeneity was observed across studies, likely due to differences in study design, diagnostic criteria, and regional practices. Additionally, publication bias and underrepresentation of data from low-resource settings may have influenced pooled estimates.

4.7 Future Perspectives

Future research should focus on integrating advanced molecular techniques, including NGS and transcriptomic profiling, into routine diagnostics. The development of standardized reporting guidelines for bone marrow findings is essential to reduce variability across studies.

Moreover, the application of artificial intelligence in bone marrow image analysis and flow cytometry data interpretation holds promise for improving diagnostic accuracy and efficiency. Multicentric collaborative studies with harmonized methodologies are needed to generate globally representative data.

CONCLUSION

This systematic review and meta-analysis highlight the central role of bone marrow evaluation in the diagnosis and management of pediatric leukemia. The findings confirm that acute lymphoblastic leukemia (ALL) remains the predominant subtype, characterized by hypercellular marrow and high blast burden, while acute myeloid leukemia (AML) exhibits distinct morphological and immunophenotypic features.

The integration of morphological assessment with immunophenotyping and cytogenetic analysis significantly enhances diagnostic accuracy, enables precise lineage classification, and facilitates robust risk stratification. Favorable cytogenetic abnormalities such as hyperdiploidy and t(12;21) contrast with high-risk alterations like t(9;22) and MLL rearrangements, underscoring the importance of genetic profiling in guiding therapeutic decisions.

Despite substantial advancements, disparities in diagnostic infrastructure and access to advanced techniques persist, particularly in low- and middle-income settings. Addressing these gaps through standardization of diagnostic protocols and wider implementation of immunophenotypic and molecular tools is essential for improving global outcomes.

Future directions should focus on integrating next-generation sequencing, refining minimal residual disease monitoring, and leveraging emerging technologies such as artificial intelligence to enhance diagnostic precision.

In conclusion, a multimodal approach combining morphology, immunophenotyping, and cytogenetics remains indispensable for optimizing diagnosis, prognostication, and treatment strategies in pediatric leukemia, ultimately contributing to improved survival and long-term outcomes.

REFERENCES

1. Ward E, DeSantis C, Robbins A, Kohler B, Jemal A. Childhood and adolescent cancer statistics. *CA Cancer J Clin*. 2014;64(2):83–103.
2. Pui CH, Robison LL, Look AT. Acute lymphoblastic leukaemia. *Lancet*. 2008;371(9617):1030–1043.
3. Howard SC, Metzger ML, Wilimas JA, Quintana Y, Pui CH, Robison LL, et al. Childhood cancer epidemiology in low-income countries. *Cancer*. 2008;112(3):461–472.
4. Bain BJ. *Bone Marrow Pathology*. 5th ed. Wiley-Blackwell; 2019.
5. Swerdlow SH, Campo E, Harris NL, Jaffe ES, Pileri SA, Stein H, et al. *WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues*. Revised 4th ed. IARC; 2017.
6. Greer JP, Arber DA, Glader B, List AF, Means RT, Paraskevas F, et al. *Wintrobe's Clinical Hematology*. 14th ed. Wolters Kluwer; 2018.
7. Borowitz MJ, Chan JKC. Flow cytometry in the diagnosis of hematologic malignancies. *J Clin Pathol*. 2008;61(11):121–130.
8. Campana D. Role of minimal residual disease monitoring in adult and pediatric acute lymphoblastic leukemia. *Hematology Am Soc Hematol Educ Program*. 2010;2010:7–12.
9. Arber DA, Orazi A, Hasserjian R, Thiele J, Borowitz MJ, Le Beau MM, et al. The 2016 revision of WHO classification of myeloid neoplasms and acute leukemia. *Blood*. 2016;127(20):2391–2405.
10. van Dongen JJM, van der Velden VHJ, Brüggemann M, Orfao A. Minimal residual disease diagnostics in acute lymphoblastic leukemia. *Lancet Oncol*. 2015;16(1):e1–e12.
11. Moorman AV. The clinical relevance of chromosomal and genomic abnormalities in B-cell precursor acute lymphoblastic leukemia. *Blood Rev*. 2012;26(3):123–135.
12. Harrison CJ. Cytogenetics of paediatric and adolescent acute lymphoblastic leukaemia. *Br J Haematol*. 2009;144(2):147–156.
13. Pieters R, de Groot-Kruseman H, Van der Velden V, Fiocco M, van den Berg H, de Bont E, et al. Successful therapy reduction and intensification for childhood ALL. *Lancet*. 2016;388(10040):240–250.
14. Inaba H, Greaves M, Mullighan CG. Acute lymphoblastic leukaemia. *Lancet*. 2013;381(9881):1943–1955.
15. Hunger SP, Mullighan CG. Acute lymphoblastic leukemia in children. *N Engl J Med*. 2015;373(16):1541–1552.
16. Gupta S, Rivera-Luna R, Ribeiro RC, Howard SC. Pediatric oncology as the next global child health priority. *PLoS Med*. 2014;11(6):e1001656.
17. Moher D, Liberati A, Tetzlaff J, Altman DG; PRISMA Group. Preferred reporting items for systematic reviews and meta-analyses. *PLoS Med*. 2009;6(7):e1000097.
18. Higgins JPT, Thomas J, Chandler J, Cumpston M, Li T, Page MJ, et al. *Cochrane Handbook for Systematic Reviews of Interventions*. 2nd ed. Wiley; 2019.
19. Wells GA, Shea B, O'Connell D, Peterson J, Welch V, Losos M, et al. Newcastle–Ottawa Scale for assessing quality of nonrandomized studies. Ottawa Hospital Research Institute; 2014.
20. DerSimonian R, Laird N. Meta-analysis in clinical trials. *Control Clin Trials*. 1986;7(3):177–188.
21. Egger M, Davey Smith G, Schneider M, Minder C. Bias in meta-analysis detected by a simple graphical test. *BMJ*. 1997;315(7109):629–634.
22. Arber DA, Orazi A, Hasserjian RP. WHO classification updates in leukemia. *Blood*. 2016;127(20):2391–2405.
23. Raetz EA, Teachey DT. T-cell acute lymphoblastic leukemia. *Hematology Am Soc Hematol Educ Program*. 2016;2016(1):580–588.
24. Szczepański T. Why and how to quantify minimal residual disease in acute lymphoblastic leukemia? *Leukemia*. 2007;21(4):622–626.
25. Wood BL. Principles of minimal residual disease detection for hematologic malignancies. *Clin Lab Med*. 2007;27(3):551–563.
26. Rowe JM. Prognostic factors in acute leukemia. *Hematology Am Soc Hematol Educ Program*. 2010;2010:1–10.
27. Meyer C, Burmeister T, Groger D, Tsaur G, Fechina L, Renneville A, et al. The MLL recombinome of acute leukemias. *Leukemia*. 2018;32(2):273–284.
28. Roberts KG, Li Y, Payne-Turner D, Harvey RC, Yang YL, Pei D, et al. Targetable kinase-activating lesions in ALL. *N Engl J Med*. 2014;371(11):1005–1015.

29. Silverman LB. Acute lymphoblastic leukemia in infancy. *Pediatr Blood Cancer*. 2007;49(7):1070–1073.
30. Creutzig U, Kutny MA, Barr R, Schlenk RF, Ribeiro RC. Acute myelogenous leukemia in children. *Lancet*. 2012;379(9823):593–606.
31. Look AT. Oncogenic transcription factors in leukemia. *Blood*. 1997;90(11):4325–4342.
32. Mullighan CG. Genomic characterization of childhood ALL. *Semin Hematol*. 2013;50(4):314–324.
33. Pizzo PA, Poplack DG. *Principles and Practice of Pediatric Oncology*. 7th ed. Wolters Kluwer; 2016.
34. Biondi A, Valsecchi MG, Seriu T, et al. Classification and treatment of ALL. *Blood*. 2000;95(3):843–852.
35. Vrooman LM, Silverman LB. Treatment of childhood ALL. *Curr Opin Pediatr*. 2009;21(1):1–8.
36. Rubnitz JE. Current management of pediatric AML. *Paediatr Drugs*. 2017;19(1):1–10.
37. Heerema NA. Cytogenetic abnormalities in leukemia. *Cancer Genet Cytogenet*. 2001;124(2):97–109.
38. Raimondi SC. Current status of cytogenetic research in childhood leukemia. *Blood*. 1993;81(9):2237–2251.
39. Hunger SP. Targeted therapy in ALL. *Hematology Am Soc Hematol Educ Program*. 2011;2011:361–365.
40. Bhojwani D, Pui CH. Relapsed childhood ALL. *Lancet Oncol*. 2013;14(6):e205–e217.
41. Forestier E, Heyman M, Andersen MK, Autio K, Blennow E, Borgström G, et al. Outcome of acute myeloid leukemia in children. *J Clin Oncol*. 2003;21(17):3246–3252.
42. Zwaan CM, Kolb EA, Reinhardt D, Abrahamsson J, Adachi S, Aplenc R, et al. Collaborative efforts driving progress in pediatric AML. *J Clin Oncol*. 2015;33(27):2949–2962.