



Clinical Lab Intelligence

September 3, 2026

Hematology and transfusion: morphology, genotyping, and evidence-based escalation

Five practice-facing studies show where automated correction helps, where it stops, and when phenotype must yield to molecular resolution.

READING KEY Finding = what the source established. Why it matters = practical or educational relevance. Limits = what should not be overclaimed.	ADVANCE-PREPARED ISSUE Dated for this issue and assembled from verified 2026 sources available by September 2.
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Core developments

01 Objective limits for automated platelet-clump correction

Gong et al. | JALM | July 22, 2026 | Peer reviewed, open access | [SOURCE](#)

Finding. The Mindray BC-6800 Plus CDR mode agreed closely with impedance counts in normal specimens and corrected several spurious-count patterns. For platelet aggregation, fewer than 162 aggregates and a PLT-OF minus PLT-I difference above $115 \times 10^9/L$ best identified correctable cases.

Why it matters. This offers a teachable, quantitative reflex pathway that may reduce recollections while preserving smear review and citrate recollection for severe aggregation.

Limits / cautions. Platform-specific, modest sample size, and limited interferent types; thresholds need local verification before direct reporting.

02 Thirty years of hemoglobinopathy diagnosis changed with migration and screening

Molina-Arrebola et al. | Laboratory Medicine | August 4, 2026 | Peer reviewed; access may require subscription | [SOURCE](#)

Finding. A southern Spain laboratory identified 5,340 hemoglobinopathies from 1996-2025. Diagnoses increased more than fivefold, especially after systematic HPLC screening began in 2008; migrant patients accounted for 83.8% of cases and a broader variant spectrum.

Why it matters. Laboratory menus, reference algorithms, and educator case banks must evolve with the served population. Equity here means building capacity for the variants actually encountered, without treating ancestry labels as diagnostic shortcuts.

Limits / cautions. Single regional, retrospective experience; detection trends reflect both demography and changing methods.

03 Long-read sequencing resolved a complex alpha-thalassemia structural variant

Li et al. | Laboratory Medicine | August 10, 2026 | Peer-reviewed case study; access may require subscription | [SOURCE](#)

Finding. Gap-PCR produced an unclear pattern and MLPA suggested heterozygous -alpha3.7, while third-generation sequencing resolved a Hong Kong alpha-alpha/-alpha4.2 genotype by identifying the deletion, duplication, and phase.

Why it matters. For unexplained genotype-phenotype discordance, laboratories need an escalation rule that considers assay blind spots, structural complexity, phase, and the clinical cost of an incorrect reproductive-risk interpretation.

Limits / cautions. One family/case; long-read cost, informatics, and validation requirements remain substantial.

04 DAT-positive anemia in newly diagnosed multiple myeloma

Zheng et al. | Laboratory Medicine | August 4, 2026 | Peer reviewed; access may require subscription | [SOURCE](#)

Finding. In 77 newly diagnosed patients, 52 were DAT positive. DAT-positive cases were enriched for IgG M-protein and showed different chemistry and lymphocyte-subset patterns, including higher CD8-related measures.

Why it matters. The study supports coordinated interpretation among hematology, chemistry, flow cytometry, and transfusion services when a positive DAT appears in plasma-cell disease.

Limits / cautions. Retrospective single-center association; DAT positivity did not establish immune hemolysis or causality.

05 Turning visual PRP collection judgment into a trainable protocol

Shi et al. | Laboratory Medicine | August 6, 2026 | Peer reviewed; access may require subscription | [SOURCE](#)

Finding. In 35 automated autologous platelet-rich plasma collections, a visual-feedback protocol produced a median platelet concentration of $1,500 \times 10^9/L$ and low leukocyte contamination, although 37.1% exceeded a proposed residual RBC threshold.

Why it matters. This is a supervision case about converting tacit expertise into documented adjustment rules, measurable product specifications, and competency assessment.

Limits / cautions. Small retrospective series and subjective visual criteria; prospective machine-vision validation is still needed.

Unexpected Connections & Leads

Established evidence is separated from the proposed collaboration or research lead.

ABO genotyping can protect organ allocation when serology is ambiguous

Lemp et al. | Human Immunology | August 26, 2026; HRSA/OPTN guidance | [SOURCE](#)

Established. Across more than 44,000 deceased donors, 4% of serologic typings were indeterminate; genotyping of 471 donors resolved many difficult cases. HRSA guidance recognizes DNA testing as an adjunct when transfusion or discrepant reactions undermine serology.

Collaboration lead. Blood banks, HLA laboratories, organ-procurement organizations, and molecular laboratories could predefine rapid referral triggers and interoperable discrepancy documentation.

Next question. What turnaround, staffing, and governance model makes genotyping actionable before allocation rather than retrospective?

Boundary. Genotyping is an adjunct, not a substitute for required independent samples and complete serologic review.

Fibrinogen may carry nonlinear prognostic information after stroke

Zheng et al. | Laboratory Medicine | August 13, 2026 | [SOURCE](#)

Established. A secondary analysis of 21,459 ischemic-stroke records found a U-shaped association between fibrinogen and poststroke epilepsy, with an inflection near 2.9 g/L.

Collaboration lead. Coagulation laboratories, neurologists, and data scientists could test whether nonlinear laboratory features improve poststroke risk models beyond conventional thresholds.

Next question. Does fibrinogen add predictive value after accounting for stroke severity, infection, treatment, and repeated measurements?

Boundary. Retrospective association from a shared database; not causal and not ready for clinical decision limits.

References

Every source cited in this issue is listed below with a full, clickable direct link.

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