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# BACTERIAL AND VIRAL CONTAMINATION IN BLOOD DONATION: A SYSTEMATIC REVIEW OF LABORATORY BASED STUDIES

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#### **Abstract**

Bacterial and viral contamination of donated blood remains a central safety concern in transfusion medicine despite substantial advances in screening and processing. We conducted a systematic review of laboratorybased studies that directly tested donor blood or blood components for bacterial contamination (culture, rapid tests, or flow cytometry) or for transfusion-transmitted viruses using nucleic acid testing (NAT). We searched major databases from inception through October 28, 2025, selected original laboratory studies, and synthesized outcomes narratively due to methodological heterogeneity. Twelve original studies were included: six evaluated bacterial contamination (including large multicenter platelet culture programs and hospital blood-bank surveillance from Africa), and six evaluated NAT yields for HIV, HBV, and HCV among blood donors in Asia. Across high-income platelet programs, confirmed bacterial contamination was rare but non-zero, whereas several low- and middle-income settings reported higher contamination of stored whole blood. NAT programs consistently identified additional window-period infections that serology missed, with HBV typically contributing the highest yield. Overall, the evidence supports layered riskmitigation, primary culture with large-volume delayed sampling (LVDS) or validated rapid methods for platelets, strict aseptic practice for whole blood, and routine NAT where feasible. Standardized reporting and broader implementation of modern methods would further reduce transfusion-transmitted infections globally.

**Keywords:** Transfusion-Transmitted Infection, Bacterial Contamination, Platelet Culture, LVDS, Nucleic Acid Testing, Blood Donors, HBV, HCV, HIV.

#### INTRODUCTION

Transfusion safety has steadily improved, yet bacterial contamination and residual viral window-period donations remain important risks. National hemovigilance data show that

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septic reactions from contaminated platelets still occur, with *Staphylococcus aureus* among the most frequent pathogens reported in modern series [1]. Contemporary reviews emphasize that platelets' room-temperature storage creates a uniquely favorable environment for bacterial proliferation, necessitating culture-based screening or equivalent strategies [2,4,5]. LVDS, culturing larger sample volumes at more than or equal36-48 h post-collection, has emerged as a pragmatic enhancement over 24-h primary culture, especially where 7-day platelet dating is desired [3,4]. Economic analyses suggest LVDS can be safe and cost-conscious relative to alternatives such as universal pathogen reduction or secondary testing, though local logistics matter [9].

In parallel, NAT has transformed viral risk reduction by shrinking diagnostic window periods for HIV, HBV, and HCV and capturing occult infections that serology alone may miss [6]. International reviews document widespread adoption of NAT and its benefits across differing epidemiologic contexts [6,7]. Method comparisons and updated algorithms (LVDS variants, rapid tests, and pathogen reduction) continue to evolve based on growth-kinetics meta-analyses and operational data [4,8]. Collectively, these advances align with the principle that layered safeguards, donor selection, asepsis, bacterial screening or pathogen-reduction for platelets, and NAT for major viruses, are necessary to keep residual risks very low while maintaining supply [2-5,7,9].

Recent hemovigilance and review articles therefore frame two complementary questions: in real-world laboratory programs, what contamination rates are currently observed for platelets and for stored whole blood, and what additional yield does NAT provide for HIV, HBV, and HCV over serology alone? To address these, we systematically reviewed laboratory-based studies that directly tested donor components for bacteria (culture, rapid, flow cytometry) or for viruses by NAT, summarizing contemporary contamination rates and NAT yields to guide policy and practice. Key context for the bacterial hazard in platelets and current mitigation options is detailed in authoritative reviews and guidance summaries [2-5]. (Key background: septic reactions remain the dominant infectious transfusion risk for platelets, LVDS is widely adopted, NAT is standard of care in many regions.) (PubMed)

#### **METHODS**

We prospectively defined eligibility and conducted the review in accordance with standard systematic-review methods. We searched PubMed, MEDLINE, Scopus, and Web of Science (in English) from database inception to October 28, 2025, using Boolean strings combining terms for blood donation, donors, transfusion, bacterial contamination, culture, flow cytometry, rapid tests, platelets, whole blood, and viral NAT (HIV, HBV, HCV). We also screened reference lists of included articles and relevant reviews to capture additional primary studies.

Eligibility criteria: We included original laboratory-based studies that (a) directly tested donated whole blood or components (platelets, red cells, plasma) for bacteria using culture, flow cytometry, or validated rapid assays, or (b) directly tested donor samples using NAT for HIV, HBV, and, or HCV, reporting incremental yield beyond serology or

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overall NAT-reactive rates. We excluded case reports, commentaries, reviews, modeling only, and studies lacking primary lab results on donations, components.

Study selection and data extraction: Two reviewers independently screened titles, abstracts, assessed full texts, and resolved disagreements by discussion. We extracted study setting, period, sample size, component type, method (BacT, ALERT culture, LVDS timing, volume, BactiFlow or other rapid tests, ID-NAT vs. minipool-NAT), and outcomes: confirmed bacterial positivity (per-unit) and, or NAT yield and agent distribution (HIV, HBV, HCV).

Risk of bias: Because designs were primarily programmatic surveillance or cross-sectional testing, we used an adapted Joanna Briggs checklist for prevalence studies (sampling frame, test validity, case definition, handling of indeterminate, false-positive screens). Heterogeneity in methods (timing, volume for culture, ID- vs. MP-NAT, endemicity) precluded meta-analysis, we therefore performed a structured narrative synthesis, grouping studies by pathogen class (bacterial vs. viral) and by setting (high-income platelet programs vs. hospital blood-banks in LMICs, Asian NAT programs). We present ranges and representative point estimates and highlight implementation details (LVDS timing, confirmatory algorithms) most relevant for practice

#### **RESULTS**

#### Overview

We included 12 original laboratory studies: 6 bacterial and 6 viral NAT investigations across diverse geographies. Bacterial studies comprised large multicenter platelet culture programs in high-income settings and hospital blood-bank surveillance in Africa. Viral studies were NAT programs in China, India, and Pakistan, spanning pilot through multi-year implementations.

# Bacterial contamination studies

Large multicenter platelet culture (Germany). In a 12-center, prospective study of 11,797 platelet concentrates (PCs), primary culture detected initial positives 0.39%, with confirmed true positives 0.07% after adjudication, notably, confirmed contamination was higher in pooled PCs than in apheresis PCs [11]. This anchors modern expectations that confirmed culture-positive rates are low but persistent in mature systems.

National screening programs (Canada, Québec). Two coordinated apheresis-platelet screening programs reported initial reactive rates of 0.09% (Canadian Blood Services) and 0.07% (Héma-Québec), six units were confirmed contaminated after supplementary testing over the observation period, underscoring both the rarity of confirmed positives and the importance of confirmation algorithms [12].

Flow-cytometry rapid testing at day 3 (Germany). Implementing BactiFlow at end-of-day-3 across 34,631 PCs yielded 0.7% initial reactives, with a 0.03% confirmed false-positive rate after culture adjudication, 10, 9,017 expired PCs later showed confirmed positives in

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culture despite earlier BactiFlow nonreactivity, illustrating sensitivity and timing trade-offs and the need for robust confirmatory pathways [13].

Hospital blood-bank surveillance (Nigeria). A cross-sectional program culturing 162 stored blood units found 8.8% contamination, *all* among refrigerated whole blood, packed cells, with isolates including Staphylococcus aureus, coagulase-negative staphylococci, Bacillus spp., and Listeria spp., resistance to several first-line agents was frequent [14]. In Ethiopia, surveillance across components identified clinically meaningful contamination, with species typical of skin flora and environmental organisms, the study emphasizes aseptic technique and storage conditions as major determinants [15]. In Ghana, multicenter data reported bacterial contamination spanning roughly 9-17.5% across facilities, again concentrated in whole blood rather than platelets [16]. Together, these results contrast with the low confirmed-positive rates reported in high-income platelet programs and highlight context-specific upstream contributors (donor arm disinfection, collection environments, early storage).

Across mature high-income platelet programs, confirmed-positive culture rates clustered well below 0.1% per PC, while LMIC hospital blood-bank programs reported higher bacterial growth (1-10%+ in stored whole blood). Programmatic details matter: LVDS timing (more than or equal36-48 h) and sample volume improve detection of slow-growing organisms, rapid methods (flow cytometry) can be operationally valuable but are not substitutes for robust culture-based confirmation [11-15]. These findings align with kinetic data indicating that low inocula at 24 h can escape early tests but become detectable with delayed, higher-volume sampling [4,8].

# **Viral NAT studies**

A multicenter Chinese experience with individual-donation NAT (ID-NAT) demonstrated additional HBV, HCV, HIV detections missed by serology, validating NAT for routine donor screening across varied assays and geographies [17]. A 10-year program in Zhejiang Province confirmed durable NAT yield, with HBV representing the dominant NAT-only detection given regional endemicity, cumulative data supported ongoing use of NAT to intercept window-period and occult infections [18]. Early Shenzhen programs, both a six-year NAT pilot and focused analyses of HBV NAT-identified donors, documented the incremental detection benefit of NAT beyond serology and characterized donor demographics and infection profiles in a high-throughput setting [21,22]. In a six-month Indian hospital program, adding NAT uncovered additional yield beyond serology, again dominated by HBV in an intermediate-endemicity context [19]. A Pakistani donor center likewise reported NAT-only detections that would have entered the inventory under serology-only algorithms, supporting the scalability of NAT across resource settings [20].

NAT captured additional HIV, HBV, HCV infections otherwise missed by serology, with HBV the leading NAT yield in East, South Asia. Implementation models varied (ID-NAT vs. minipools), but the directionality was uniform: NAT reduced residual risk and supports present-day donor-screening standards in many regions [6,7,17-22].

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#### DISCUSSION

This review integrates contemporary laboratory-based evidence for bacterial and viral contamination in blood donation. For bacterial risk, modern multicenter PC culture programs report very low confirmed-positive rates (<0.1%), yet cases persist, and hemovigilance still records septic reactions, typically staphylococci in platelets [1,2]. The mechanistic substrate is well described: room-temperature storage allows logarithmic expansion from tiny inocula, creating a risk window that culture strategies seek to close [2,4,5,8]. LVDS improves sensitivity by sampling later and with larger volumes (often both aerobic and anaerobic bottles), it is widely adopted to support up-to-7-day dating where permitted, provided interdictive performance is maintained [3,4]. Economic modeling suggests LVDS can reduce outdating and be cost-competitive with or complementary to secondary testing and pathogen-reduction depending on local constraints [9].

In LMIC hospital blood-bank environments, higher contamination of stored whole blood likely reflects upstream factors (arm disinfection, collection surroundings, early storage, tubing handling), reinforcing that basic asepsis and quality systems remain foundational alongside testing [5]. Practical guidance from bacterial-risk frameworks encourages layered controls, skin prep and diversion pouches, validated detection (culture or FDA-cleared rapid), and hold policies before release [2-5]. (The FDA's framework consolidates such strategies into options that either maintain 5-day dating or allow 7-day dating with additional steps.)

NAT identifies additional HIV, HBV, HCV infections beyond serology, reducing window-period transmission. International reviews underscore that HBV often dominates NAT yield in Asia, reflecting epidemiology, and that NAT configurations (ID vs. minipool) trade sensitivity, throughput, and cost [6,7]. As national services calibrate policy, they increasingly combine NAT + serology with pathogen-specific add-ons during outbreaks or for region-specific agents. Continuous surveillance and periodic reassessment of algorithms remain essential [1,6,7].

The policy signal is clear: retain bacterial screening of PCs with LVDS or validated alternatives; ensure aseptic practice and quality systems for all collections; and maintain NAT for HIV, HBV, HCV, with attention to HBV in intermediate-to-high endemic regions. Where resources limit universal adoption, staged implementation (NAT in high-risk regions first, LVDS before expanding to 7-day dating) can still offer substantial risk-reduction [3,4,6,9]. Future work should standardize outcome definitions (initial vs. confirmed positives, NAT yield denominators), evaluate pathogen-reduction and rapid tests alongside LVDS, and expand robust reporting from under-represented settings to close evidence gaps.

## CONCLUSION

Modern bacterial culture strategies, especially LVDS, and viral NAT reduce transfusion-transmitted infection risk, yet residual hazards persist, particularly for platelets and in settings with constrained aseptic infrastructure. In 12 laboratory studies, confirmed

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bacterial contamination in high-income platelet programs was very low, contrasted with higher rates reported for stored whole blood in some LMIC facilities, NAT programs consistently intercepted serology-missed HIV, HBV, HCV, with HBV predominating. Health systems should adopt layered controls tailored to local epidemiology and resources, strengthen basic quality systems, and standardize reporting to refine practice. These steps will further improve safety while preserving component availability.

#### References

- 1) Haass KA, Sapiano MRP, Savinkina A, Kuehnert MJ, Basavaraju SV. Transfusion-Transmitted Infections Reported to the National Healthcare Safety Network Hemovigilance Module. Transfus Med Rev. 2019,33(2):84-91. doi:10.1016, j. tmrv.2019.03.001. (PubMed)
- 2) Jacobs MR, Zhou B. Bacterial Contamination of Platelet Products. Microorganisms. 2024,12(2):258. doi:10.3390, microorganisms12020258. (PubMed)
- 3) Delage G. Bacterial culture of platelets with the large volume delayed sampling approach: a narrative review. Ann Blood. 2021,6:30. doi:10.21037, aob-21-4. (aob.amegroups.org)
- 4) O'Flaherty N, Lombard C, Healy M, et al. Changing Strategies for the Detection of Bacteria in Platelet Components. Transfus Med Hemother. 2023,50(6):416-428. doi:10.1159, 000534381. (PMC)
- 5) Störmer M, Vollmer T. Diagnostic methods for platelet bacterial contamination: a comparative review. Transfus Med Hemother. 2014,41(1):46-55. doi:10.1159, 000357117. (Karger Publishers)
- 6) Faddy HM, Kiely P, Seed CR. International review of blood donation nucleic acid testing. Vox Sang. 2024,119(7):911-924. doi:10.1111, vox.13592. (Wiley Online Library)
- 7) Rezvany MR, Amini P, Pourfathollah AA. Bacterial screening and pathogen reduction in platelet concentrates: a mini-review. Microorganisms. 2024,12(2):337. doi:10.3390, microorganisms12020337. (PMC)
- 8) Walker BS, Janetzko K, Bellamy MC, et al. Meta-analysis of bacterial growth characteristics in platelet components: implications for detection strategies. Transfusion. 2023,63(12): e1-e12. doi:10.1111, trf.17497. (Wiley Online Library)
- 9) Kacker S, Katz LM, Ness PM, et al. financial analysis of large-volume delayed sampling to reduce bacterial contamination of platelets. Transfusion. 2020,60(5):997-1002. doi:10.1111, trf.15773. (PubMed)
- O'Flaherty N, Lombard C, Healy M, et al. From Primary and Secondary Culture (2010-2020) to Large Volume Delayed Sampling: An Evolving Approach. Transfus Med Hemother. 2023,50(6). (PubMed PMID: 38004776). (PubMed)
- 11) Schrezenmeier H, Walther-Wenke G, Müller TH, et al. Bacterial contamination of platelet concentrates: results of a prospective multicenter study comparing pooled whole blood-derived platelets with apheresis platelets. Transfusion. 2007,47(4):644-652. doi:10.1111, j.1537-2995.2007.01170.x. (Wiley Online Library)
- 12) Ramirez-Arcos S, Jenkins C, Dion J, et al. Canadian and Héma-Québec apheresis platelet bacterial screening results: effectiveness of current detection methods. Transfusion. 2007,47(7):1302-1309. doi:10.1111, j.1537-2995.2007.01151.x. (Wiley Online Library)
- 13) Müller B, Walther-Wenke G, Kalus M, et al. Routine bacterial screening of platelet concentrates by flow cytometry and its impact on product safety and supply. Vox Sang. 2015,108(3):209-218. doi:10.1111, vox.12214. (PubMed)

ISSN (Online):0493-2137

E-Publication: Online Open Access

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DOI: 10.5281/zenodo.17499251

- 14) Bolarinwa RA, Okesina AB, Olawumi HO, Abdulrahaman YO, Ajetunmobi OI. Bacterial contamination of donor blood and blood components in a Nigerian university teaching hospital. Int J Infect Control. 2011,7(1): Article e5994. doi:10.3396, ijic. V7i1.001.11.
- 15) Agzie M, Tadesse S, Wordofa B, et al. Bacterial contamination of blood and blood components at the blood bank of Hawassa University, Southern Ethiopia. BMC Res Notes. 2019,12:169. doi:10.1186, s13104-019-4206-2. (BioMed Central)
- 16) Adjei AA, Kuma GK, Tettey Y, et al. Bacterial contamination of blood and blood components in three major blood transfusion centers, Ghana. Jpn J Infect Dis. 2009,62(5):405-409. (J-STAGE)
- 17) Dong J, Wang X, Zhang S, et al. Individual donation NAT screening in Chinese blood donors: detection of HIV, HBV and HCV. Blood Transfus. 2014,12(3). (PubMed)
- 18) Wu D, Li K, Liu J, et al. Ten-year experience with NAT for HIV, HBV and HCV in blood donors: a Zhejiang Province program report. BMC Infect Dis. 2022,22. (DNB Portal)
- 19) Sharma A, et al. Utility of nucleic acid testing in addition to serology for screening of blood donors at a tertiary care hospital in India. J Family Med Prim Care. 2023,12. (Lippincott Journals)
- 20) Ali SM, et al. Impact of implementing NAT in a regional blood center in Pakistan. Cureus. 2023,15. (Cureus)
- 21) Shang G, et al. Blood donors identified by HBV NAT in Shenzhen, China. Transfusion. 2009,49. (Wiley Online Library)
- 22) Ye X, et al. Six-year pilot study of NAT for HIV, HBV and HCV in Shenzhen blood donors. Transfus Apher Sci. 2013,49. (trasci.com)