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Molecular Confirmation of HIV-1, HBV, and HCV in ELISA-Reactive Sudanese Blood Donors: qPCR and Endpoint PCR Characterization of Occult-Compatible HBV Profiles

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Abstract:

Background: *In conflict-affected blood services, reactive serological screening requires traceable molecular follow-up to distinguish current viraemia from unresolved or non-specific reactivity. This study evaluated paired qPCR/RT-qPCR and endpoint RT-PCR/PCR in initially ELISA-reactive Sudanese donor specimens.*

Methods: *The complete accessible cohort comprised 90 archived, traceable donor specimens reactive by ELISA for at least one transfusion-transmitted infection marker. All specimens underwent paired molecular testing for HIV-1, HBV and HCV. Composite molecular positivity was defined as reproducible target-specific detection by at least one method. Overall and virus-specific agreement, documented adjudication of discordant results, and two selected low-level HBV profiles were evaluated.*

Results: *Composite molecular positivity was identified in 67/90 donors (74.4%; 95% CI 64.6–82.3): 28 HCV, 22 HBV and 17 HIV-1, with no coinfections. qPCR detected 66 specimens and endpoint RT-PCR/PCR detected 63; 62 were concordant-positive, four were qPCR-only, one was endpoint-only and 23 were negative by both. The four qPCR-only results comprised two HBV, one HCV and one HIV-1 specimen; the endpoint-only result was HIV-1. All five discordant results were retained after documented repeat testing or expected-size band confirmation. Aggregate agreement was 94.4% (κ=0.863; exact McNemar p=0.375). Virus-specific κ values were 0.938 for HBV, 0.974 for HCV and 0.924 for HIV-1. Two selected HBV-positive specimens were repeat-HBsAg-non-reactive and anti-HBc-reactive, with Ct values of 36.99 and 36.83 and estimated loads of 14.2 and 15.3 IU/mL.*

Conclusions: *Molecular evidence was present in approximately three-quarters of this ELISA-reactive cohort. The verified discordance pattern indicates that qPCR's net numerical advantage arose from HBV and HCV, whereas HIV-1 method totals were equal. The selected low-level HBV cases support a predefined algorithm for late, HBsAg-non-reactive and occult-compatible results. Because no independent reference standard was used, sensitivity, specificity and method equivalence were not estimated.*

Keywords: blood donors; transfusion-transmitted infections; composite molecular positivity; HIV-1; hepatitis B virus; hepatitis C virus; occult-compatible HBV; qPCR; endpoint RT-PCR/PCR; Sudan

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INTRODUCTION

Blood safety depends on layered controls that include donor selection, quality-assured serological screening, molecular testing, controlled component release and haemovigilance. The World Health Organization recommends screening every donation for HIV, HBV, HCV and syphilis, but a reactive screening signal is not equivalent to proven active infection. Molecular testing is particularly valuable when infection is in the preseroconversion window period, serological reactivity is weak or non-specific, or HBV DNA persists despite undetectable HBsAg (World Health Organization 2010; 2017).

HIV-1 and HCV RNA may become detectable before antibody or antigen markers are reliably reactive, whereas HBV may be present during early infection or as low-level occult infection. In HBV-endemic populations, anti-HBc can enrich the probability of previous exposure but cannot independently establish current viraemia. Reliable interpretation therefore requires repeat testing, reproducible nucleic-acid detection, acceptable controls and, where feasible, an alternative molecular target (Gerlich 2013; Raimondo et al. 2019; Im et al. 2022).

Sudanese studies have demonstrated low-level HBV DNA, circulation of HBV genotypes D and E and substantial heterogeneity in occult-HBV estimates (Mahgoub et al. 2011; Mahmoud et al. 2013; Eltom et al. 2020). Comparatively little Sudanese evidence has assessed HIV-1, HBV and HCV simultaneously in one completely paired ELISA-reactive cohort using two amplification approaches. The Sudan conflict further disrupted the original Khartoum-centred pathway, requiring specimen and record retrieval through functioning blood-service facilities in River Nile, Northern and Eastern Sudan.

The objectives were to determine complete-cohort composite molecular positivity, describe the mutually exclusive distribution of HIV-1, HBV and HCV, quantify aggregate and virus-specific paired agreement, document resolution of discordant specimens and characterise selected low-level HBV profiles.

MATERIALS AND METHODS

Study design, cohort and retrieval

A laboratory-based analytical paired method-comparison study was implemented under the protocol approved for the Central National Laboratory for Blood Transfusion (STAK), Khartoum State. The complete protocol-defined accessible cohort comprised 90 archived donor specimens reactive by routine ELISA for at least one transfusion-transmitted infection marker and retaining traceable identifiers. Following conflict-related disruption, all specimens and linked records were traced through functioning pathways in River Nile, Northern and Eastern Sudan and entered a central molecular workflow.

Eligibility, serology and specimen handling

Eligibility required initial ELISA reactivity, a reconciled donation/specimen code, adequate archived plasma, linked source documentation and valid paired molecular results. All 90 specimens met these criteria. Detailed repeat HBsAg, anti-HBc, anti-HCV and HIV-1/2 plus p24 data were available for a predefined 10-specimen characterisation subset only. Plasma was accepted when identifiers and available storage/transport

documentation did not indicate major pre-analytical compromise and was stored at approximately −70 °C until extraction.

Molecular testing, adjudication and data integrity

Probe-based qPCR was used for HBV DNA and reverse-transcribed HIV-1 and HCV targets. Endpoint testing used reverse transcription for RNA targets, direct PCR for HBV and agarose-gel detection. Runs required acceptable positive, negative and internal-control performance. Composite molecular positivity was defined as reproducible, quality-controlled, target-specific detection by at least one method; this definition was not an independent gold standard.

Discordant results underwent curve or gel review, repeat extraction from a separate aliquot, repeat amplification and second-target assessment where feasible. The raw dataset was preserved unchanged; documented transcription, coding and linkage corrections were maintained in a corrected working dataset, from which the final analysis dataset was generated. Ninety unique donor identifiers were reconciled against donor/ELISA records, extraction sheets, qPCR instrument files, amplification curves, endpoint run sheets, original gel images, repeat-testing records and final SPSS classifications.

Statistical analysis

Categorical results were summarised as counts and percentages with Wilson 95% confidence intervals. qPCR and endpoint results were cross-tabulated overall and separately for HBV, HCV and HIV-1. Observed agreement and Cohen's kappa quantified agreement beyond chance, and exact McNemar tests assessed directional discordance. Because the composite outcome was derived from the two methods being compared, sensitivity and specificity were not calculated. The detailed 10-specimen serological subset was analysed descriptively.

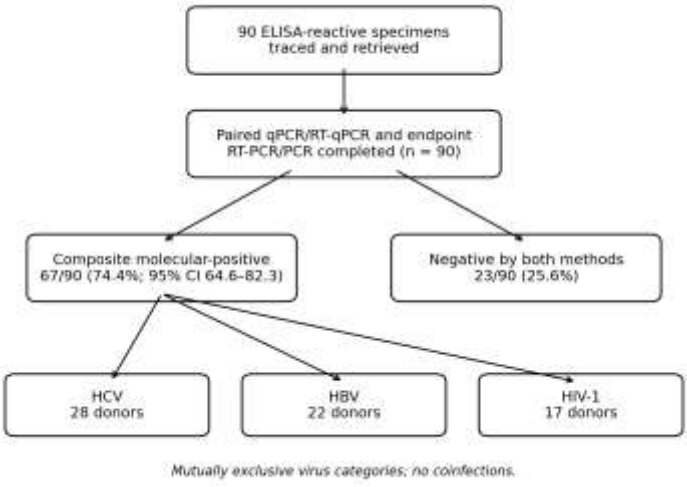

Figure 1. Conflict-adapted cohort retrieval, complete paired molecular testing and mutually exclusive composite classification.

RESULTS

Cohort disposition and composite molecular positivity.

All 90 initially ELISA-reactive donor specimens were traced, retrieved and tested by both molecular approaches. Composite molecular positivity was present in 67/90 unique donors (74.4%; 95% CI 64.6–82.3), whereas 23/90 (25.6%) were negative by both methods. The final virus categories were mutually exclusive because no coinfections were identified.

Table 1. Cohort disposition and complete molecular outcomes (n = 90).

Analytical quantity	Finding	Interpretation
ELISA-reactive specimens traced and retrieved	90/90 (100.0%)	Complete conflict-adapted cohort
Specimens tested by both methods	90/90 (100.0%)	Complete paired testing
Composite molecular-positive	67/90 (74.4%)	95% Wilson CI 64.6–82.3
Negative by both methods	23/90 (25.6%)	No target detected by either method
HCV	28/90 (31.1%)	41.8% of composite-positive donors
HBV	22/90 (24.4%)	32.8% of composite-positive donors
HIV-1	17/90 (18.9%)	25.4% of composite-positive donors
Coinfections	0/90	Mutually exclusive categories

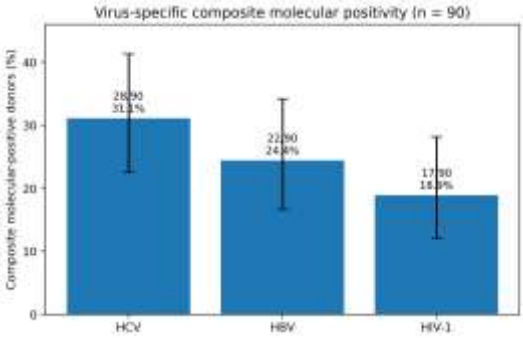

Figure 2. Virus-specific composite molecular-positivity proportions with Wilson 95% confidence intervals.

Aggregate and virus-specific paired agreement

qPCR detected 66/90 specimens and endpoint RT-PCR/PCR detected 63/90. Sixty-two were concordant-positive, four were qPCR-positive/endpoint-negative, one was qPCR-negative/endpoint-positive and 23 were concordant-negative. Aggregate observed agreement was 94.4%, κ was 0.863 and exact McNemar p was 0.375.

Table 2. Aggregate paired agreement between qPCR and endpoint RT-PCR/PCR (n = 90).

qPCR status	Endpoint positive	Endpoint negative	Total	Interpretation
qPCR positive	62	4	66	62 concordant-positive; 4 qPCR-only
qPCR negative	1	23	24	1 endpoint-only; 23 concordant-negative
Total	63	27	90	Agreement 94.4%; κ=0.863; p=0.375

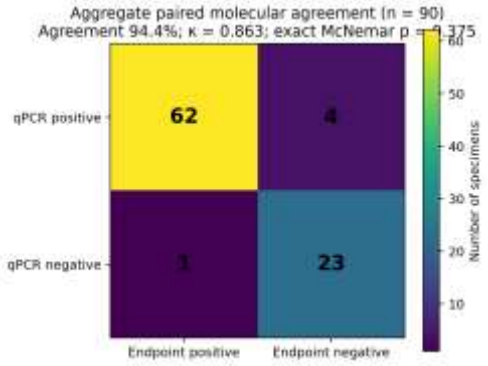

Figure 3. Aggregate paired molecular agreement matrix.

Virus-specific analysis located the aggregate discordance. HBV contained two qPCR-only results, HCV one qPCR-only result, and HIV-1 one qPCR-only plus one endpoint-only result. Thus, qPCR's net numerical advantage was attributable to HBV and HCV, whereas HIV-1 method totals were equal.

Table 3. Virus-specific paired agreement (n = 90 for each target).

Virus	Both positive	qPCR only	Endpoint only	Both negative	Agreement	κ	Exact McNemar p
HBV	20	2	0	68	97.8%	0.938	0.500
HCV	27	1	0	62	98.9%	0.974	1.000
HIV-1	15	1	1	73	97.8%	0.924	1.000

Discordant-specimen adjudication

All five discordant specimens were retained only after documented repeat or orthogonal evidence. The four qPCR-only specimens remained reproducibly qPCR-positive; the endpoint-only HIV-1 specimen remained endpoint-positive with a band at the expected size.

Table 4. Repeat testing and final classification of discordant specimens.

Donor ID	Target	Initial qPCR	Initial endpoint	Repeat/adjudication evidence	Final classification
STAK25-014	HBV	Positive	Negative	Repeat qPCR positive; repeat endpoint negative	qPCR-only positive
STAK25-027	HBV	Positive	Negative	Repeat qPCR positive; repeat endpoint negative	qPCR-only positive
STAK25-033	HCV	Positive	Negative	Repeat qPCR positive; Ct within validated range	qPCR-only positive
STAK25-058	HIV-1	Positive	Negative	Repeat qPCR positive; internal control valid	qPCR-only positive
STAK25-071	HIV-1	Negative	Positive	Repeat endpoint positive; expected-size band	Endpoint-only positive

Selected low-level HBV profiles

Detailed ancillary serology was available for 10 specimens, including two of the 22 HBV-positive donors. Both selected specimens were repeat-HBsAg-non-reactive, anti-HBc-reactive and concordantly positive by qPCR and endpoint PCR. Their late Ct values and

estimated HBV DNA concentrations below 20 IU/mL supported probable or operationally occult-compatible profiles. Sanger genotyping was attempted but unsuccessful, consistent with insufficient template for longer amplicons.

Table 5. Molecular and serological profiles of two selected low-level HBV-positive specimens.

Sample	Repeat HBsAg	Anti-HBc	qPCR Ct	HBV DNA (IU/mL)	Classification
STAK25-002	Non-reactive	Reactive	36.99	14.2	Probable/operationally occult-compatible HBV
STAK25-005	Non-reactive	Reactive	36.83	15.3	Probable/operationally occult-compatible HBV

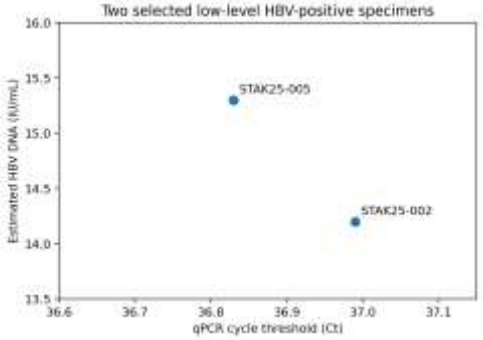

Figure 4. qPCR Ct values and estimated HBV DNA concentrations in the two selected low-level specimens.

DISCUSSION

The completed cohort demonstrates substantial molecular evidence among initially ELISA-reactive blood donations. Of the 90 specimens subjected to paired molecular testing, 67 (74.4%) were classified as composite molecular-positive for HIV-1, HBV, or HCV, while 23 (25.6%) were negative by both molecular methods. This proportion should be interpreted specifically as the molecular follow-up yield within an enriched screening-reactive cohort and not as a national prevalence estimate for Sudanese blood donors. The double-negative specimens may represent non-specific ELISA reactivity, resolved infection without detectable viraemia, nucleic-acid degradation during storage or transport, viral concentrations below the analytical detection limits, or sequence variation affecting primer or probe binding. These possibilities highlight the importance of a structured donor-resolution pathway incorporating repeat testing and appropriate confirmatory procedures rather than automatically classifying such specimens as either true infection or laboratory error.

The distribution of the **67 composite molecular-positive donors—28 HCV, 22 HBV, and 17 HIV-1, with no identified coinfections—**extends Sudanese molecular evidence beyond the predominantly HBV-focused literature. HCV was numerically the most frequent molecular target in this selected cohort, although previous Sudanese donor studies have commonly reported HBV markers as predominant. This apparent difference is biologically and methodologically plausible because the present cohort was selected on

the basis of initial ELISA reactivity rather than random donor sampling. Furthermore, molecular positivity reflects detectable viraemia and is influenced by infection stage, viral load, the original screening marker, specimen integrity, and assay inclusivity. The observed distribution therefore characterizes this selected ELISA-reactive cohort and should not be interpreted as evidence that HCV is more prevalent than HBV among Sudanese blood donors generally (Ahmed et al. 2020; Vermeulen et al. 2009).

The verified virus-specific agreement matrices provide a more informative assessment of assay performance than the aggregate 66 qPCR-positive versus 63 endpoint-positive results alone. Overall, 62 specimens were concordant-positive, four were qPCR-only, one was endpoint-only, and 23 were negative by both methods, producing 94.4% agreement and κ=0.863. Virus-specific analysis showed similarly strong agreement for HBV (κ=0.938), HCV (κ=0.974), and HIV-1 (κ=0.924). Importantly, qPCR's net numerical gain arose from two additional HBV and one additional HCV specimen. HIV-1 produced one discordant result in each direction and therefore identical overall detection totals between the two methods. These findings suggest a modest detection advantage for qPCR for HBV and HCV while demonstrating strong overall concordance. However, the limited number of discordant pairs and absence of an independent reference standard prevent interpretation in terms of formal sensitivity, superiority, non-inferiority, or analytical equivalence.

The five discordant specimens were retained as composite molecular-positive only after documented repeat or orthogonal evidence. This distinction strengthens the validity of the final classification. The 62 concordant-positive specimens provide the strongest cross-method molecular evidence, whereas the four qPCR-only specimens and single endpoint-only specimen represent adjudicated positive results within the predefined composite algorithm. Transparent reporting of these discordant cases is particularly important because they account for the difference between the concordant-positive count and the final total of 67 molecular-positive donors. This approach is consistent with the principle that transfusion molecular testing should integrate screening, repeat testing, discriminatory assays, and confirmation within a documented laboratory workflow rather than rely on an isolated amplification signal (Candotti and Allain 2013).

The two selected low-level HBV profiles provide an additional blood-safety observation. Both specimens were repeat-HBsAg-non-reactive and anti-HBc-reactive, yet HBV DNA was reproducibly detected by molecular testing. Their late Ct values (36.99 and 36.83) and very low estimated viral loads (14.2 and 15.3 IU/mL) are compatible with low-level occult HBV profiles. Similar observations have been reported in Sudan, where very low HBV DNA concentrations may be detectable using short molecular targets but remain difficult to amplify across longer genomic regions required for successful genotyping (Mahgoub et al. 2011). The unsuccessful genotyping of these specimens is therefore biologically plausible in the context of extremely limited viral template. Nevertheless, because the viral loads approached the lower analytical range and intrahepatic HBV DNA was not assessed, these cases should conservatively be described as probable or operationally occult-compatible HBV infections, rather than definitively proven occult HBV infection (Gerlich 2013; Raimondo et al. 2019).

The study has several methodological strengths, including complete paired testing of all 90 specimens, reconciliation of one verified record for each donor, mutually exclusive classification of the 67 unique molecular-positive donors, virus-specific

agreement analysis, and documented adjudication of every discordant result. Explicit separation of complete-cohort findings from the 10-specimen ancillary subset also prevents detailed serological observations from being inappropriately generalized to the entire cohort. However, the ELISA-reactive sampling framework limits generalizability to the wider donor population. Other limitations include the absence of an independent molecular reference standard, incomplete full-cohort demographic and repeat-serological data, unavailable state-specific denominators, and unsuccessful genotyping of the two low-level HBV specimens.

Overall, these findings support a structured molecular follow-up strategy for ELISA-reactive blood donations in Sudan. qPCR/RT-qPCR and endpoint RT-PCR/PCR demonstrated strong agreement, with qPCR providing a modest additional detection yield confined to HBV and HCV. The adjudicated discordant specimens and low-level occult-compatible HBV profiles further emphasize the importance of repeat testing, rigorous quality control, and cautious interpretation of low-level molecular signals. The findings therefore support composite molecular confirmation and method agreement, but they should not be extrapolated to national prevalence or interpreted as evidence of formal diagnostic superiority of either molecular platform.

CONCLUSION

Among 90 initially ELISA-reactive donor specimens, composite molecular positivity for HIV-1, HBV or HCV was identified in 67 unique donors (74.4%). The mutually exclusive classifications comprised 28 HCV, 22 HBV and 17 HIV-1, with no coinfections. Aggregate agreement between qPCR and endpoint RT-PCR/PCR was 94.4% (κ=0.863), and virus-specific agreement exceeded 97% for every target. Documented repeat/adjudication evidence supported inclusion of the five discordant specimens. qPCR's net numerical advantage arose from HBV and HCV, while HIV-1 method totals were equal. Two selected HBV cases showed reproducible occult-compatible low-level profiles. These findings support a traceable molecular follow-up algorithm for ELISA-reactive donations, with explicit management of discordant and low-level results.

STATEMENTS AND DECLARATIONS

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Author contributions: Einass TajAlkhatm Abdalla Omar: investigation, laboratory work, data curation and original draft. Nadia Madani Mohamed Ahmad: conceptualisation, supervision and critical revision. Babikir Ahmad Mohamed: co-supervision, methodological review and critical revision. Mutaz Mohamed Ibrahim Ali: methodology, statistical and data-integrity verification, manuscript restructuring, visualisation and publication preparation.

Ethical approval and consent: Ethical approval was obtained from Karary University and administrative permission from STAK; informed consent was obtained under the approved protocol. Ethics approval reference: [insert official reference before submission].

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Competing interests: [All authors must confirm the final competing-interest declaration before submission].

Data availability: De-identified data and the audit evidence package may be made available by the corresponding author on reasonable request, subject to donor confidentiality and institutional authorisation.

Related-manuscript disclosure: A companion manuscript from the same thesis dataset focuses on operational performance, direct cost and implementation feasibility. The present paper focuses on virus-specific composite positivity, adjudication and low-level HBV profiles; overlapping cohort counts are reported only where necessary for scientific interpretation.

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