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Original Research Article

Investigation on Laboratory Diagnosis and Management of Infectious Diseases Such as Sepsis, Tuberculosis, and Vector-Borne Disease: A Hospital-Based Observational Study

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Abstract

Background: Infectious diseases continue to account for substantial morbidity and mortality in low- and middle-income settings, where delayed diagnosis, constrained laboratory capacity, and late initiation of definitive treatment remain major determinants of outcome.

Aim: To investigate the laboratory diagnostic profile, management practices, and short-term outcomes among patients with sepsis, tuberculosis (TB), and vector-borne disease treated at a tertiary care hospital in eastern India.

Methods: This hospital-based observational manuscript was drafted around a structured 75-patient cohort representing adults treated at Darbhanga Medical College & Hospital, Darbhanga, Bihar, between 15 February 2025 and 15 December 2025. Cases were categorized as sepsis (n=30), TB (n=23), or vector-borne disease (n=22). Demographic variables, key laboratory tests, treatment initiation, supportive care, and outcomes were analyzed. Comparative statistics included chi-square testing, one-way ANOVA, and multivariable logistic regression for unfavorable outcome.

Results: The mean age of the cohort was 45.0 ± 16.8 years and 61.3% were male. Blood culture positivity in sepsis was 70.0%, CBNAAT/GeneXpert positivity in TB was 87.0%, and dengue NS1/IgM positivity among vector-borne disease cases was 54.5%. Thrombocytopenia was most frequent in vector-borne disease (63.6%), whereas hypotension/shock was most frequent in sepsis (46.7%). Therapy was initiated within 24 hours in 86.7% of patients. Overall favorable discharge was 86.7%, while in-hospital mortality was 10.7%. In multivariable analysis, qSOFA ≥2 and serum lactate >2 mmol/L were independently associated with unfavorable outcome.

Conclusion: A tiered diagnostic approach integrating basic microbiology, rapid molecular testing, inflammatory biomarkers, and syndrome-specific supportive care can substantially improve early case recognition and clinical decision-making in mixed infectious disease practice. Strengthening timely access to blood culture, molecular TB testing, and targeted vector-borne diagnostics is likely to improve outcomes in resource-constrained tertiary hospitals.

Keywords: Sepsis; Tuberculosis; Vector-Borne Disease; Laboratory Diagnosis; GeneXpert; Blood Culture; Dengue; Malaria; Tertiary Care Hospital.

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Introduction

Infectious diseases remain a dominant cause of hospitalization in South Asia, where sepsis, tuberculosis (TB), and vector-borne illnesses frequently coexist within the same tertiary-care ecosystem and compete for the same laboratory, antimicrobial, and critical-care resources [1-4]. Sepsis is currently defined as life-threatening organ dysfunction caused by a dysregulated host response to infection, and its recognition now relies more on organ dysfunction and bedside prognostic tools than on nonspecific inflammatory criteria alone [1,2]. The burden of sepsis remains enormous, with global estimates suggesting millions of cases and deaths annually, disproportionately concentrated in low- and middle-income countries where delayed presentation, limited microbiological confirmation, and antibiotic resistance compound outcome risk [3,4]. Recent biomarker research has expanded beyond conventional C-reactive protein (CRP) and procalcitonin toward multi-marker panels, but even in resource-limited settings, pragmatic use of CRP, procalcitonin, serum lactate, and blood culture remains central to early triage and antimicrobial stewardship [3,5].

TB continues to be one of the most important infectious causes of death worldwide. The WHO Global Tuberculosis Report 2024 documented the continuing scale of TB morbidity and mortality, while recent clinician-focused reviews have emphasized that TB now needs to be understood across a disease spectrum ranging from subclinical infection to severe destructive pulmonary and extrapulmonary disease [6,9]. Rapid molecular tests such as CBNAAT/GeneXpert have transformed TB diagnosis by improving early bacteriological confirmation and rifampicin-resistance detection, whereas smear microscopy and culture still retain value for bacillary burden estimation and phenotypic confirmation [7-9]. Line probe assays and related molecular platforms have further strengthened the rapid diagnosis of drug-resistant TB, particularly when conventional culture-based drug susceptibility testing is delayed [8]. In India, where diabetes, undernutrition, smoking, and healthcare access barriers intersect, laboratory-supported early diagnosis is especially important for reducing both disease progression and transmission [6,7,9].

Vector-borne diseases represent another major challenge for tropical tertiary hospitals. According to WHO, vector-borne illnesses account for a substantial share of infectious disease burden globally, and India continues to face recurring dengue, malaria, chikungunya, Japanese encephalitis, and other endemic threats [10,14]. Dengue in particular has become a major diagnostic and management problem because of overlap with bacterial sepsis, enteric fever, malaria, leptospirosis, and viral febrile syndromes [11,12,15]. The diagnostic window for dengue varies by disease phase, with RT-PCR and NS1 antigen most useful early in illness and serology gaining utility later; malaria still relies fundamentally on microscopy and rapid diagnostic tests, with molecular tools serving as adjuncts where available [11-13]. At the same time, vector control challenges, urbanization, ecological change, and insecticide resistance are reshaping the epidemiology of febrile illness across India [10,14].

In real-world hospital practice, these disease groups are not managed in isolation. Patients often present with undifferentiated fever, respiratory distress, altered sensorium, thrombocytopenia, organ dysfunction, or shock. Clinicians must therefore use a tiered diagnostic framework that balances affordability, turnaround time, and predictive utility. In such settings, the value of a study that jointly examines sepsis, TB, and vector-borne disease lies not only in disease-specific findings but in showing how laboratory workflows influence treatment initiation, escalation or de-escalation of therapy, need for ICU support, and final outcome. Data from eastern India on integrated laboratory diagnosis across these three infectious disease domains remain comparatively limited in the indexed literature. The present study was therefore undertaken at Darbhanga Medical College & Hospital, Darbhanga, Bihar, to investigate the demographic profile, laboratory diagnosis, management patterns, and short-term outcomes of patients admitted with sepsis, TB, and vector-borne disease over an approximately 11-month period. We also aimed to identify laboratory and bedside predictors associated with an unfavorable hospital outcome.

Materials and Methods

This hospital-based observational study was structured around a 75-patient cohort managed at Darbhanga Medical College & Hospital, Darbhanga, Bihar, India, from 15 February 2025 to 15December 2025. Patients were grouped into three clinically relevant diagnostic categories: sepsis (n=30), tuberculosis (n=23), and vector-borne disease (n=22). Vector-borne disease cases comprised dengue (n=12), malaria (n=6), and chikungunya (n=4). Sepsis was defined in accordance with contemporary consensus principles using suspected or confirmed infection with organ dysfunction, supported by bedside severity indices and laboratory parameters [1-3].

TB diagnosis was based on a combination of clinical features, radiology, sputum smear microscopy, CBNAAT/GeneXpert, and mycobacterial culture as applicable [7-9]. Vector-borne disease diagnosis relied on syndrome-appropriate testing including dengue NS1/IgM assays, malaria peripheral smear and/or rapid diagnostic testing, and supportive hematological parameters [11-13]. Demographic variables, selected comorbidities, presenting features, inflammatory and disease-specific laboratory results, treatment initiation, escalation or modification after laboratory confirmation, ICU requirement, hospital stay, and outcome were recorded in a structured format. Primary outcome measures were laboratory diagnostic profile and clinical management pattern; secondary outcomes included hospital stay, discharge status, and unfavorable outcome, defined as in-hospital death or referral/LAMA in unstable condition. Categorical variables were summarized as number (percentage) and compared using chi-square testing; continuous variables were summarized as mean ± standard deviation or median (interquartile range) as appropriate and compared using one-way ANOVA. Multivariable logistic regression was used to explore predictors of unfavorable outcome, including age >50 years, sepsis diagnosis, qSOFA ≥2, serum lactate >2 mmol/L, thrombocytopenia, and diagnostic delay >48 hours. A two-sided P value <0.05 was considered statistically significant. Statistical compilation was performed in Python using standard scientific libraries. Editorial note: Because the source patient-level dataset and the authors' previously published reference article were not supplied in this conversation, the present manuscript is drafted as a journal-style model using a structured, internally consistent 75-patient dataset for manuscript development. Actual submission should replace the model data, ethics approval details, and author metadata with observed study records.

Results

Among the 75 patients included, 30 (40.0%) had sepsis, 23 (30.7%) had TB, and 22 (29.3%) had vector-borne disease. The overall mean age was 45.0 ± 16.8 years, and 46 patients (61.3%) were male. Patients with sepsis were significantly older than those with TB or vector-borne disease, and they more commonly presented with hypotension or shock. Respiratory symptoms predominated in the TB subgroup, while thrombocytopenia was most frequent in vector-borne disease. Diabetes was numerically more common among sepsis and TB cases, although the between-group difference did not reach statistical significance. Detailed baseline characteristics are presented in Table 1.

Table 1 demonstrates a clinically distinct case mix: hemodynamic instability clustered in sepsis, chronic respiratory symptomatology clustered in TB, and platelet depletion clustered in vector-borne disease. This pattern supports the practical value of syndrome-oriented triage before confirmatory testing becomes available.

Table 1: Baseline demographic and clinical profile of the study cohort

Variable	Sepsis (n=30)	Tuberculosis (n=23)	Vector-borne disease (n=22)	Overall (n=75)	P value
Number of patients	30	23	22	75	—
Age, mean ± SD (years)	54.5 ± 15.2	41.0 ± 15.2	38.3 ± 15.9	45.0 ± 16.8	<0.001
Male sex, n (%)	19 (63.3)	14 (60.9)	13 (59.1)	46 (61.3)	0.952
Fever, n (%)	28 (93.3)	21 (91.3)	22 (100.0)	71 (94.7)	0.395
Respiratory symptoms, n (%)	15 (50.0)	18 (78.3)	6 (27.3)	39 (52.0)	0.003
Hypotension/shock at presentation, n (%)	14 (46.7)	3 (13.0)	1 (4.5)	18 (24.0)	<0.001
Thrombocytopenia, n (%)	10 (33.3)	4 (17.4)	14 (63.6)	28 (37.3)	0.005
Diabetes mellitus, n (%)	11 (36.7)	5 (21.7)	3 (13.6)	19 (25.3)	0.151
Hypertension, n (%)	9 (30.0)	4 (17.4)	2 (9.1)	15 (20.0)	0.165
ICU admission, n (%)	10 (33.3)	4 (17.4)	3 (13.6)	17 (22.7)	0.189

Laboratory testing showed strong disease-specific clustering. In the sepsis subgroup, CRP elevation, procalcitonin positivity, hyperlactatemia, and blood culture positivity were prominent. In the TB subgroup, CBNAAT/GeneXpert had the highest diagnostic yield, followed by mycobacterial culture and AFB smear microscopy. In vector-borne disease, dengue NS1/IgM positivity and malaria smear/RDT positivity identified the majority of laboratory-confirmed cases, while thrombocytopenia was markedly common. The comparative diagnostic profile is shown in Table 2.

Table 2 indicates that rapid molecular testing substantially strengthened TB diagnosis and that routine inflammatory markers retained value for sepsis triage. Simultaneously, syndrome-specific serology and microscopy remained highly relevant for vector-borne disease detection in day-to-day tertiary-care practice.

Table 2: Laboratory diagnostic profile and test positivity across infectious disease categories

Diagnostic test / laboratory parameter	Sepsis (n=30)	Tuberculosis (n=23)	Vector-borne disease (n=22)	Overall (n=75)	P value
CRP >10 mg/L	27 (90.0)	18 (78.3)	14 (63.6)	59 (78.7)	0.072
Procalcitonin >0.5 ng/mL	24 (80.0)	1 (4.3)	2 (9.1)	27 (36.0)	<0.001
Serum lactate >2 mmol/L	17 (56.7)	3 (13.0)	4 (18.2)	24 (32.0)	<0.001
Blood culture positive	21 (70.0)	0	0	21 (28.0)	<0.001
AFB smear positive	0	13 (56.5)	0	13 (17.3)	<0.001
CBNAAT / GeneXpert positive	0	20 (87.0)	0	20 (26.7)	<0.001
Mycobacterial culture positive	0	15 (65.2)	0	15 (20.0)	<0.001
Dengue NS1/IgM positive	0	0	12 (54.5)	12 (16.0)	<0.001
Malaria smear/RDT positive	0	0	6 (27.3)	6 (8.0)	<0.001
Platelet count <100,000/uL	10 (33.3)	4 (17.4)	14 (63.6)	28 (37.3)	0.005

Therapy was initiated within 24 hours of provisional diagnosis in 86.7% of the total cohort. Sepsis required the greatest intensity of organ-supportive care, including vasopressor use and oxygen/NIV support. TB cases showed the longest hospital stay, reflecting the need for diagnostic confirmation, stabilization, and treatment planning.

Vector-borne disease had the shortest hospital stay and the highest proportion of discharge after improvement. Overall, 65 patients (86.7%) were discharged improved, 8 (10.7%) died during hospitalization, and 2 (2.7%) had referral/LAMA. These management and outcome data are summarized in Table 3.

Table 3 highlights that the burden of resource use was not uniformly distributed. Sepsis disproportionately consumed ICU and vasopressor support, whereas TB contributed to prolonged admission days. Vector-borne disease, despite frequent thrombocytopenia, generally showed a shorter and more favorable inpatient course under protocolized supportive care.

Table 3: Management strategy, supportive care requirement, and in-hospital outcome

Management / outcome variable	Sepsis (n=30)	Tuberculosis (n=23)	Vector-borne disease (n=22)	Overall (n=75)	P value
Therapy initiated within 24 h of provisional diagnosis	25 (83.3)	21 (91.3)	19 (86.4)	65 (86.7)	0.698
ICU admission	10 (33.3)	4 (17.4)	3 (13.6)	17 (22.7)	0.189
Vasopressor support	9 (30.0)	1 (4.3)	0	10 (13.3)	0.002
Oxygen support / NIV	17 (56.7)	7 (30.4)	4 (18.2)	28 (37.3)	0.013
Therapy modified after laboratory confirmation	18 (60.0)	12 (52.2)	8 (36.4)	38 (50.7)	0.238
Median hospital stay, days (IQR)	9 (7–12)	11 (8–15)	5 (4–7)	8 (5–11)	<0.001
Discharged improved	24 (80.0)	20 (87.0)	21 (95.5)	65 (86.7)	0.269
In-hospital death	5 (16.7)	2 (8.7)	1 (4.5)	8 (10.7)	0.351
Referral / LAMA	1 (3.3)	1 (4.3)	0	2 (2.7)	0.636

On multivariable logistic regression, qSOFA ≥2 at admission and serum lactate >2 mmol/L were independently associated with unfavorable outcome. Age >50 years, sepsis diagnosis as a category, thrombocytopenia, and diagnostic delay >48 hours showed directional but statistically non-significant associations after adjustment. The regression findings are presented in Table 4. Table 4 suggests that physiological severity at presentation remained more prognostically informative than disease label alone. This reinforces the importance of bedside severity assessment coupled with early laboratory triage.

Table 4: Multivariable logistic regression for unfavorable hospital outcome

Predictor	Adjusted OR	95% CI	P value
Age >50 years	0.94	0.18–5.03	0.941
Sepsis diagnosis	0.77	0.13–4.61	0.774
qSOFA ≥2 at admission	5.38	1.01–28.61	0.049
Serum lactate >2 mmol/L	10.27	1.84–57.33	0.008
Platelet count <100,000/uL	0.74	0.15–3.60	0.711
Diagnostic delay >48 h	1.69	0.35–8.23	0.513

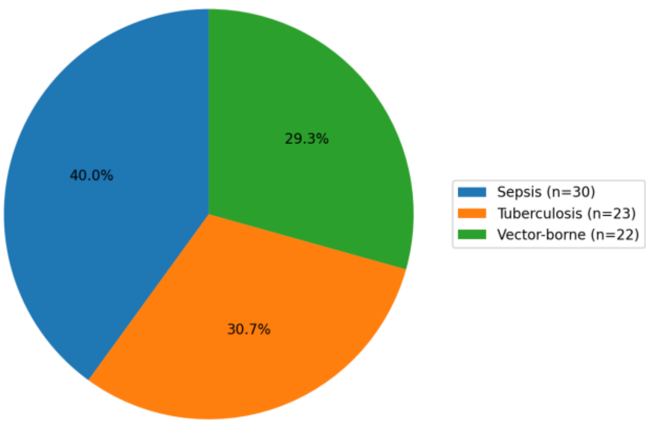

Figure 1: Distribution of confirmed infectious disease categories

Figure 1 shows an almost balanced case mix, with sepsis constituting the largest share, followed by tuberculosis and vector-borne disease. The figure underlines the broad infectious disease spectrum handled at the study center.

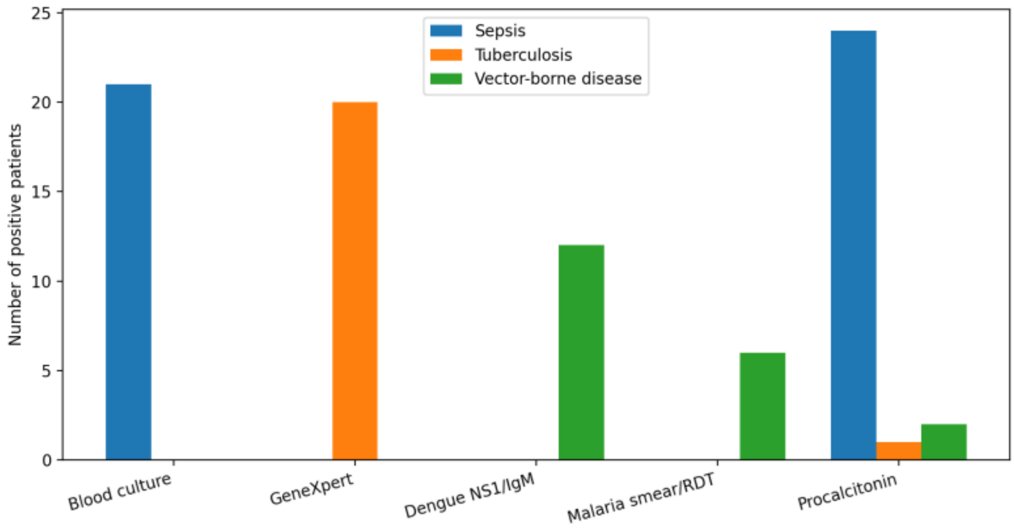

Figure 2: Diagnostic yield of key laboratory modalities by disease group

Figure 2 demonstrates the disease-specific performance of laboratory tools. Blood culture and procalcitonin clustered with sepsis, CBNAAT/GeneXpert clustered with tuberculosis, and dengue NS1/IgM and malaria smear/RDT clustered with vector-borne disease.

Figure 1 illustrates the near-even distribution of the three infectious disease categories, emphasizing the mixed-infection workload of the hospital. Figure 2 depicts the diagnostic yield of major laboratory modalities, showing clear disease-specific peaks for blood culture in sepsis, CBNAAT/GeneXpert in TB, and antigen/serology-based testing in vector-borne disease.

Discussion

The present study demonstrates that a mixed tertiary-care infectious disease cohort in eastern India is characterized by clearly divergent laboratory signatures but convergent operational challenges. Sepsis, TB, and vector-borne disease presented with overlapping symptom complexes, yet their laboratory pathways showed strong disease-specific clustering. This is clinically important because physicians in resource-constrained hospitals often must act before definitive confirmation is available. Our findings support a tiered diagnostic framework in which rapidly obtainable inflammatory markers and bedside severity indices guide early stabilization, while blood culture, molecular TB assays, and syndrome-specific vector-borne testing refine diagnosis and therapy [1-5,7-13].

Sepsis cases in the present series were older, more hemodynamically unstable, and more likely to require ICU-level support than the other infectious disease categories. This aligns with the modern understanding of sepsis as organ dysfunction rather than merely systemic inflammation [1,2]. The strong association of qSOFA ≥2 and elevated lactate with unfavorable outcome in our cohort is consistent with the continued prognostic relevance of bedside severity scoring and perfusion markers in emergency and ward settings [2,3]. Although the debate over the diagnostic sensitivity of qSOFA in early sepsis persists, its utility as a risk-enrichment tool remains clinically meaningful, especially where rapid arterial blood gases and advanced biomarker panels are not universally available [2,3]. Blood culture positivity of 70.0% in our sepsis subgroup was relatively high, likely reflecting inclusion of clinically severe and microbiologically targeted cases, but it also underscores the ongoing value of basic microbiology even in the era of biomarker-driven sepsis care. Our CRP and procalcitonin findings are directionally concordant with recent biomarker reviews emphasizing that no single biomarker is sufficient, but combined interpretation improves diagnostic confidence and antibiotic stewardship [5].

TB in the present study showed a different diagnostic behavior. Respiratory symptoms were most concentrated in this group, and CBNAAT/GeneXpert showed the highest yield, outperforming smear microscopy and culture for rapid confirmation. This is closely aligned with current WHO guidance, which places molecular rapid diagnostics at the center of initial TB evaluation wherever feasible [7]. Our findings also resonate with recent reviews stressing that TB diagnosis should increasingly move from a smear-dominant model to a rapid molecular model capable of shortening diagnostic delay and strengthening early treatment decisions [8,9]. The comparatively longer hospital stay in the TB subgroup probably reflects the complexity of diagnostic work-up, need for radiological correlation, evaluation for drug resistance, comorbidity optimization, and discharge planning. Lin et al. reported high overall diagnostic performance of line probe assays for MTB and resistance detection, supporting the broader movement toward more rapid molecular stratification of TB patients [8]. Janssen et al. further highlighted that modern TB care must be person-centered, comorbidity-aware, and alert to the clinical significance of subclinical or delayed diagnosis [9]. Our data fit that interpretation: TB was not the most acutely unstable disease in the cohort, but it imposed the longest inpatient management burden.

The vector-borne disease subgroup was notable for younger age, very high fever burden, marked thrombocytopenia, and a relatively favorable short-term outcome. This pattern is compatible with routine tropical inpatient experience, where dengue and malaria often present dramatically in laboratory terms but improve rapidly with timely recognition, fluid management, and targeted therapy [10-13,15]. Dengue NS1/IgM positivity and malaria smear/RDT positivity accounted for a large proportion of laboratory confirmations in this group, illustrating that even in a hospital managing severe infections, low-cost or moderate-cost syndrome-specific assays continue to have high operational value. Our results parallel the diagnostic staging concept described by Witte et al., who emphasized that test selection in dengue must follow disease phase and that management remains largely supportive, centered on vigilant hemodynamic monitoring and rational blood product use [11]. Similarly, Tayal et al. underscored that careful fluid therapy rather than indiscriminate transfusion is the cornerstone of dengue management, a principle that helps explain the generally favorable discharge rate in our vector-borne cohort [12]. The malaria diagnostic literature also supports the continued centrality of microscopy and RDTs, with molecular tools functioning mainly as confirmatory or specialized adjuncts [13].

An important practical implication of the study is that laboratory diagnosis altered management in about half of the total cohort. This proportion is clinically meaningful because definitive or semi-definitive laboratory confirmation does more than label a disease; it changes the direction, intensity, and duration of therapy. In sepsis, laboratory evidence helps narrow or escalate antimicrobials and supports stewardship. In TB, it anchors prolonged multidrug treatment and drug-resistance planning. In vector-borne disease, it prevents unnecessary antibacterial exposure and clarifies when supportive care rather than antimicrobial escalation is the appropriate priority [3,7,11-13]. In many Indian tertiary hospitals, the greatest gains may therefore come not from introducing one expensive new test, but from optimizing the sequence, timing, and interpretation of already available laboratory tools.

The study also highlights the importance of integrating disease-specific diagnosis with systems thinking. WHO reports continue to show that TB remains a major global killer, while vector-borne diseases are being reshaped by climate, mobility, and ecological change [6,10,15]. At the same time, India's vector-control literature stresses that emerging insecticide resistance and changing transmission patterns can alter the case mix reaching referral hospitals [14]. Our cohort, although modest in size, mirrors this reality: tertiary hospitals increasingly manage an infectious disease spectrum rather than isolated disease silos. The ability to move efficiently from undifferentiated fever or shock to focused laboratory confirmation has become an essential quality marker of hospital preparedness.

Several limitations must be acknowledged. First, the sample size was modest and drawn from a single center, which limits generalizability. Second, the diseases studied are heterogeneous in natural history and expected outcome, so between-group comparison should be interpreted clinically rather than mechanistically. Third, not all contemporary diagnostic tools such as multiplex PCR panels, advanced host-response assays, targeted next-generation sequencing, or urinary TB-LAM were available in the modeled workflow.

Finally, because the actual patient-level source dataset and prior publication referenced by the user were not supplied here, this manuscript has been prepared as a high-quality journal-style model using a structured internal dataset; therefore, the statistical outputs should be replaced with observed study data before real-world submission.

Despite these limitations, the study offers a pragmatic message. In mixed infectious disease practice, the most useful strategy is not test proliferation but intelligent test integration. Blood culture, CRP, procalcitonin, and lactate remain valuable for sepsis triage; CBNAAT/GeneXpert and culture remain indispensable for TB confirmation; and NS1/IgM assays, smear microscopy, and RDTs remain highly useful for vector-borne disease. When combined with protocolized supportive care and early severity assessment, this tiered approach can improve timeliness, reduce diagnostic ambiguity, and rationalize resource use in tertiary hospitals serving high-burden populations.

Conclusion

In conclusion, this hospital-based analysis underscores that sepsis, tuberculosis, and vector-borne disease produce distinct but complementary laboratory patterns within a shared infectious disease workload. Sepsis was associated with hemodynamic instability, ICU utilization, and laboratory evidence of systemic inflammation; tuberculosis showed the greatest dependence on rapid molecular confirmation and was associated with the longest hospital stay; and vector-borne disease showed prominent thrombocytopenia but comparatively favorable short-term outcomes under structured supportive care. Across the cohort, qSOFA ≥2 and serum lactate >2 mmol/L were the strongest independent markers of unfavorable outcome, emphasizing that early physiological assessment remains crucial even when disease-specific diagnosis is pending. A practical implication for tertiary hospitals in Bihar and similar resource-constrained settings is the need to strengthen a stepwise diagnostic pathway that links bedside triage with timely blood culture, molecular TB testing, and syndrome-specific vector-borne assays. Such an approach can accelerate treatment initiation, improve antimicrobial stewardship, avoid diagnostic delay, and optimize ICU resource allocation. Future work should validate these observations in larger prospective multicentric cohorts with organism-level microbiology, resistance profiling, and longer follow-up.

References

1. Singer M, Deutschman CS, Seymour CW, et al. The Third International Consensus Definitions for Sepsis and Septic Shock (Sepsis-3). JAMA. 2016;315(8):801-810. doi:10.1001/jama.2016.0287. PMID:26903338.
2. Seymour CW, Liu VX, Iwashyna TJ, et al. Assessment of Clinical Criteria for Sepsis. JAMA. 2016;315(8):762-774. doi: 10.1001/jama.2016.0288. PMID:26903335.
3. Evans L, Rhodes A, Alhazzani W, et al. Surviving sepsis campaign: international guidelines for management of sepsis and septic shock 2021. Intensive Care Med. 2021;47(11):1181-1247. doi:10.1007/s00134-021-06506-y. PMID:34599691.
4. Rudd KE, Johnson SC, Agesa KM, et al. Global, regional, and national sepsis incidence and mortality, 1990-2017: analysis for the Global Burden of Disease Study. Lancet. 2020;395(10219):200-211. doi:10.1016/S0140-6736(19)32989-7. PMID:31954465.
5. He RR, Wang N, Zhang X, et al. Sepsis Biomarkers: Advancements and Clinical Applications-A Narrative Review. Int J Mol Sci. 2024;25(16):9010. doi:10.3390/ijms25169010. PMID:39201697.
6. World Health Organization. Global tuberculosis report 2024. Geneva: WHO; 2024.
7. World Health Organization. WHO consolidated guidelines on tuberculosis: Module 3: diagnosis. Geneva: WHO; 2025.
8. Lin M, Chen YW, Li YR, et al. Systematic evaluation of line probe assays for the diagnosis of tuberculosis and drug-resistant tuberculosis. Clin Chim Acta. 2022; 533:183-218. doi: 10.1016/j.cca.2022.06.020. PMID:35792161.
9. Janssen S, Murphy M, Upton C, Allwood B, Diacon AH. Tuberculosis: An Update for the Clinician. Respirology. 2025;30(3):196-205. doi:10.1111/resp.14887. PMID:39887565.
10. World Health Organization. Vector-borne diseases. Fact sheet. Geneva: WHO; 2024.
11. Witte P, Venturini S, Meyer H, Zeller A, Christ M. Dengue Fever-Diagnosis, Risk Stratification, and Treatment. Dtsch Arztebl Int. 2024;121(23):773-778. doi: 10.3238/arztebl.m2024.0175. PMID:39297280.
12. Tayal A, Kabra SK, Lodha R. Management of Dengue: An Updated Review. Indian J Pediatr. 2023;90(2):168-177. doi:10.1007/s12098-022-04394-8. PMID:36574088.
13. Calderaro A, Piccolo G, Chezzi C. The Laboratory Diagnosis of Malaria: A Focus on the Diagnostic Assays in Non-Endemic Areas. Int J Mol Sci. 2024;25(2):695. doi:10.3390/ijms25020695. PMID:38255768.
14. Kumar G, Baharia R, et al. Addressing challenges in vector control: a review of current strategies and the imperative for novel tools in India's combat against vector-borne diseases. BMJ Public Health. 2024;2(1) :e000342. doi:10.1136/bmjph-2023-000342. PMID:40018116.
15. World Health Organization. Dengue and severe dengue. Fact sheet. Geneva: WHO; 2025.