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Accelerating bacteraemia management with molecular-AI versus molecular-phenotypic AI antimicrobial recommendations: A prospective study in a resource-limited setting

04. Diagnostic microbiology
04j. Artificial intelligence based tools and digital health

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Background

Background: Bloodstream infections require rapid targeted therapy to reduce mortality. Artificial intelligence clinical decision support systems (AI-CDSS) based on molecular data have demonstrated substantial agreement with clinician-selected therapy and high perceived clinical utility in bacteraemia management, supporting their real-world validity (1,2). However, discordance between molecular-AI and molecular–phenotypic AI recommendations appears to be driven by resistance mechanisms not detected through current molecular assays, a gap that remains insufficiently characterised in resource-limited settings.

Methods

Methods: We conducted a prospective observational study including 237 consecutive bloodstream infection episodes (September 2023–October 2024) in Lima, Peru. All cases underwent parallel rapid molecular testing (FilmArray BCID or Xpert MRSA/SA BC) and conventional culture with MALDI-TOF identification plus phenotypic antimicrobial susceptibility testing (AST). Therapeutic recommendations were generated sequentially: (1) OneChoice® AI using only molecular diagnostic results (pathogen identification and resistance genes); and (2) OneChoice Fusion® AI integrating both molecular results and phenotypic susceptibility results. Primary outcomes were diagnostic turnaround time reduction, diagnostic concordance (identification and resistance detection), and therapeutic concordance between OneChoice and OneChoice Fusion recommendations.

Results

Results: Molecular testing reduced diagnostic turnaround time by 33.2±14.2 hours versus conventional methods (62.7% reduction; $p<0.001$). Concordance between molecular and conventional methods was 94.5% for pathogen identification and 89.5% for antimicrobial resistance. Therapeutic concordance between OneChoice® (molecular-AI) and OneChoice Fusion® (molecular and phenotypic-AI) was 81.4% (95% CI: 75.9–85.8%). Resistance detection discordance was the sole independent predictor of therapeutic discordance (adjusted OR 7.70, 95% CI: 3.61–17.49; $P<0.001$). Most discordant cases involved phenotypic resistance mechanisms not detected by molecular testing—predominantly AmpC and other non-targeted resistance pathways.

Conclusions

Conclusions: OneChoice molecular-AI recommendations aligned with final molecular and phenotypic-AI-optimised therapy in more than 80% of bloodstream infections, enabling accurate, pathogen-directed therapy over 30 hours earlier than conventional workflows. Discordance was driven mainly by resistance mechanisms not detected molecularly, underscoring the need for phenotypic confirmation in settings with high antimicrobial resistance. Sequential deployment of molecular-AI followed by phenotypic-AI optimisation represents a feasible, stewardship-aligned strategy, particularly relevant in resource-limited environments.

Table 1. Patient demographics and baseline characteristics

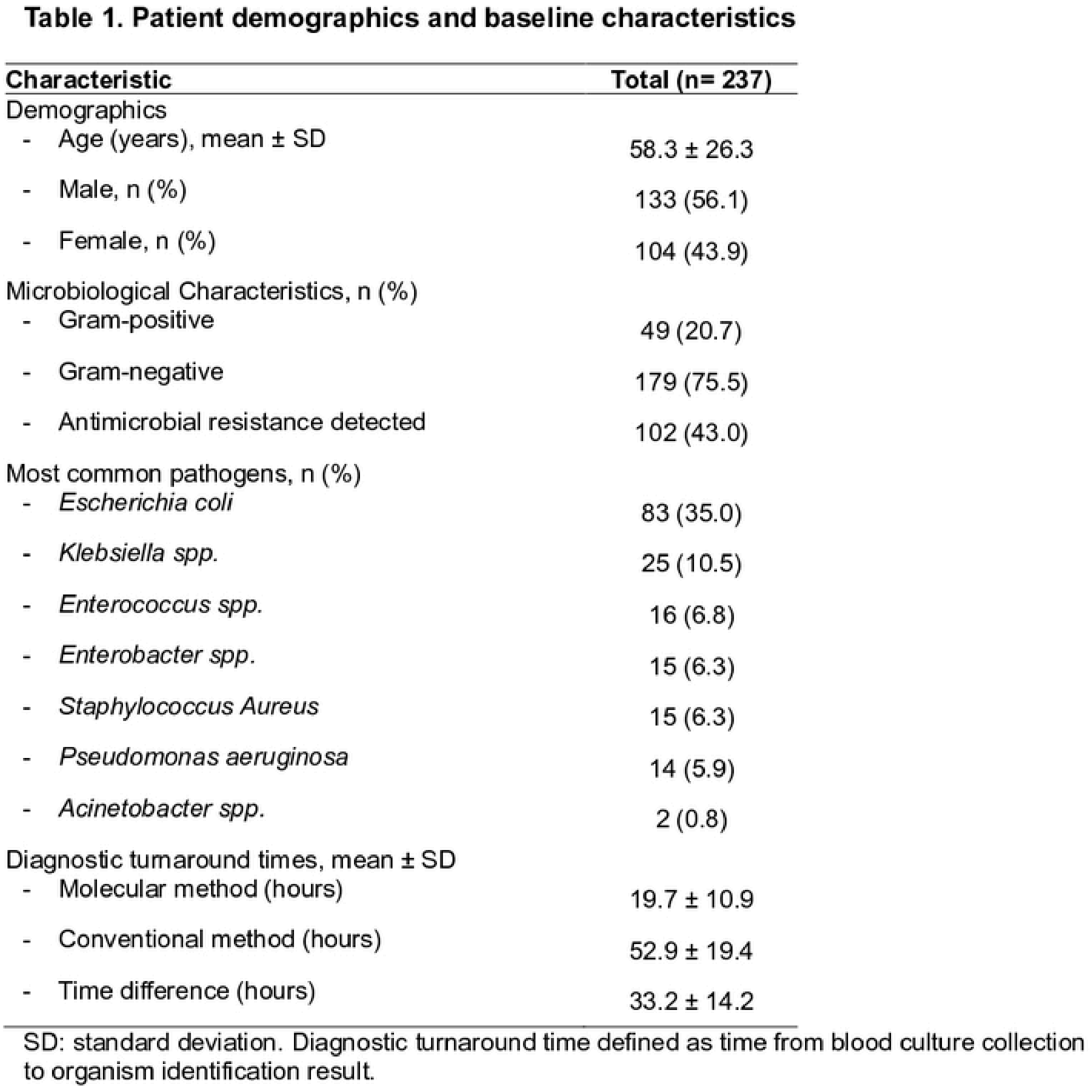

Table 1. Patient demographics and baseline characteristics

Characteristic	Total (n= 237)
Demographics	
- Age (years), mean ± SD	58.3 ± 26.3
- Male, n (%)	133 (56.1)
- Female, n (%)	104 (43.9)
Microbiological Characteristics, n (%)	
- Gram-positive	49 (20.7)
- Gram-negative	179 (75.5)
- Antimicrobial resistance detected	102 (43.0)
Most common pathogens, n (%)	
- *Escherichia coli*	83 (35.0)
- *Klebsiella spp.*	25 (10.5)
- *Enterococcus spp.*	16 (6.8)
- *Enterobacter spp.*	15 (6.3)
- *Staphylococcus Aureus*	15 (6.3)
- *Pseudomonas aeruginosa*	14 (5.9)
- *Acinetobacter spp.*	2 (0.8)
Diagnostic turnaround times, mean ± SD	
- Molecular method (hours)	19.7 ± 10.9
- Conventional method (hours)	52.9 ± 19.4
- Time difference (hours)	33.2 ± 14.2

SD: standard deviation. Diagnostic turnaround time defined as time from blood culture collection to organism identification result.

Fig 1: Cumulative distribution functions: Molecular vs conventional diagnostic methods

Fig 1: Cumulative distribution functions: Molecular vs conventional diagnostic methods (N=237)

Cumulative probability plots showing proportion of cases achieving diagnostic results as a function of time. Green curve = molecular diagnostics (FilmArray/Xpert), median 16.4 hours. Red curve = conventional culture/phenotypic AST, median 47.5 hours. Horizontal dashed line indicates 50th percentile (median). Vertical dashed lines mark respective medians. The rightward shift of the conventional curve relative to molecular curve illustrates substantial time delay. At 20 hours, ~60% of molecular diagnostics are complete vs ~5% of conventional methods. At 48 hours, 95% molecular complete vs ~55% conventional. Wilcoxon signed-rank test *P*<0.001.

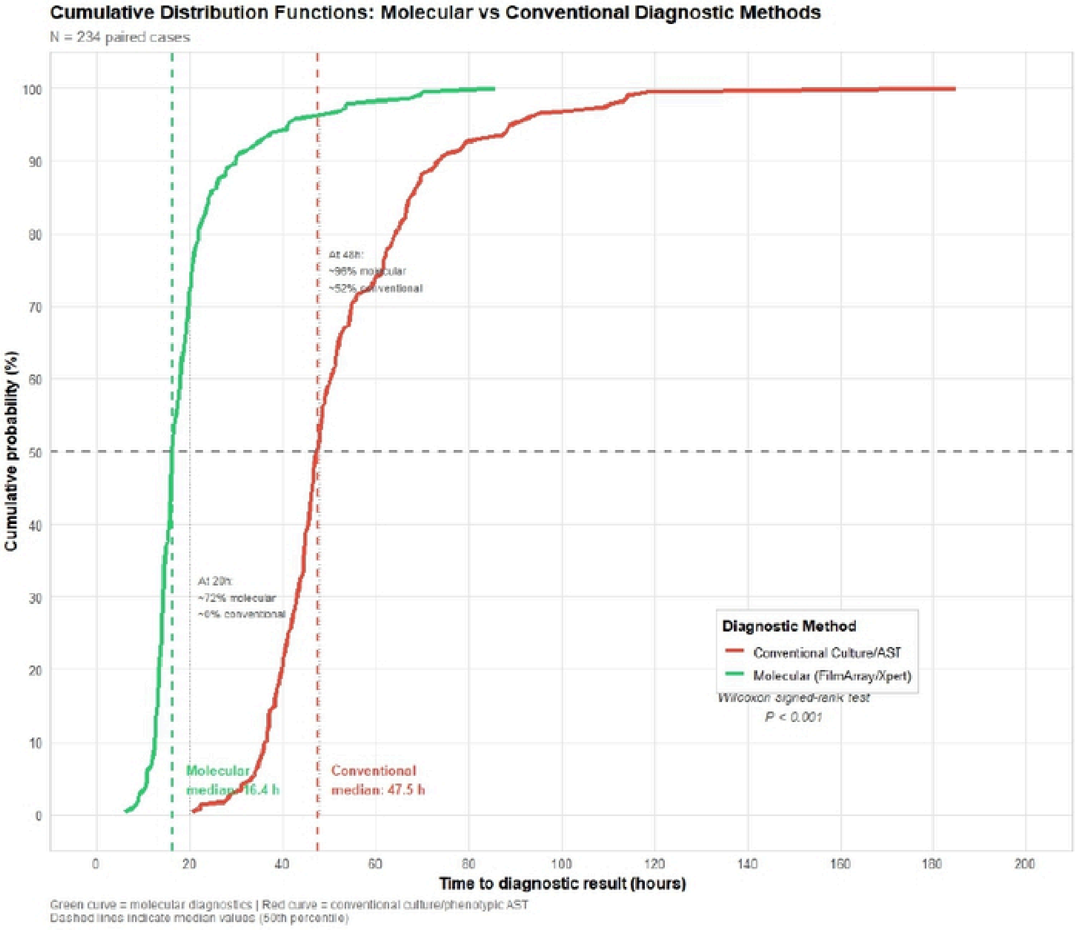

Table 2: Therapeutic concordance by clinical subgroups

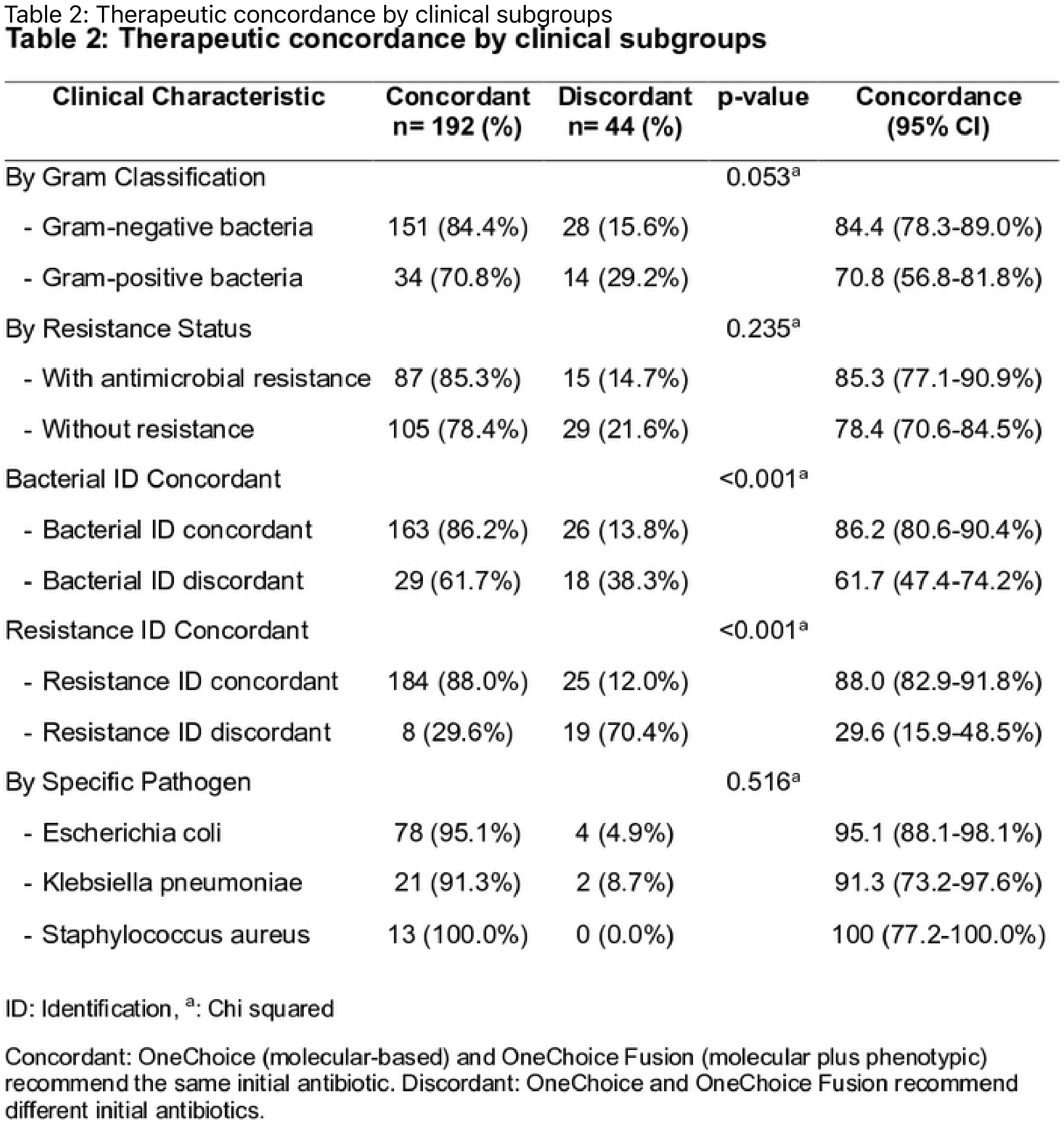

Table 2: Therapeutic concordance by clinical subgroups

Clinical Characteristic	Concordant n= 192 (%)	Discordant n= 44 (%)	p-value	Concordance (95% CI)
By Gram Classification			0.053^{a}	
- Gram-negative bacteria	151 (84.4%)	28 (15.6%)		84.4 (78.3-89.0%)
- Gram-positive bacteria	34 (70.8%)	14 (29.2%)		70.8 (56.8-81.8%)
By Resistance Status			0.235^{a}	
- With antimicrobial resistance	87 (85.3%)	15 (14.7%)		85.3 (77.1-90.9%)
- Without resistance	105 (78.4%)	29 (21.6%)		78.4 (70.6-84.5%)
Bacterial ID Concordant			<0.001^{a}	
- Bacterial ID concordant	163 (86.2%)	26 (13.8%)		86.2 (80.6-90.4%)
- Bacterial ID discordant	29 (61.7%)	18 (38.3%)		61.7 (47.4-74.2%)
Resistance ID Concordant			<0.001^{a}	
- Resistance ID concordant	184 (88.0%)	25 (12.0%)		88.0 (82.9-91.8%)
- Resistance ID discordant	8 (29.6%)	19 (70.4%)		29.6 (15.9-48.5%)
By Specific Pathogen			0.516^{a}	
- Escherichia coli	78 (95.1%)	4 (4.9%)		95.1 (88.1-98.1%)
- Klebsiella pneumoniae	21 (91.3%)	2 (8.7%)		91.3 (73.2-97.6%)
- Staphylococcus aureus	13 (100.0%)	0 (0.0%)		100 (77.2-100.0%)

ID: Identification, ^{a}: Chi squared

Concordant: OneChoice (molecular-based) and OneChoice Fusion (molecular plus phenotypic) recommend the same initial antibiotic. Discordant: OneChoice and OneChoice Fusion recommend different initial antibiotics.

Keyword 1
AI, digital health and data science
Keyword 2
Antibiotic stewardship (AMS)
Keyword 3 (Please provide your suggestion)
Molecular and rapid diagnostics

References, 300 characters, including spaces (if exceeding 300 characters please provide DOI number only) :

1. https://doi.org/10.3390/life15111756 2. https://doi.org/10.3390/met15101123

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Conflicts of interest

Do any of the authors have conflicts of interest related to the studies presented in this abstract?
Yes