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Clinical utility of FilmArray BCID and resistance gene detection in bacteraemia: Five-year retrospective analysis from Lima, Peru

04. Diagnostic microbiology
04d. Molecular diagnostics (incl POCT and syndromic testing)

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Background

Bacteraemia causes significant mortality worldwide, with outcomes critically dependent on timely pathogen identification and antimicrobial resistance detection. Conventional blood culture methods require 48-72 hours for results, mandating empirical therapy that proves inappropriate in 20-30% of cases. The FilmArray Blood Culture Identification (BCID) panel promises rapid molecular diagnosis, but real-world validation data from high-resistance Latin American settings remain limited.

Methods

We conducted a retrospective observational study of 803 bacteraemia episodes processed between october 2019 and march 2024 in a private reference laboratory in Lima, Peru. All positive blood cultures underwent both FilmArray BCID testing and conventional workflows, including subculture, MALDI-TOF identification, and phenotypic susceptibility testing (Vitek 2.0). Primary outcomes included: (1) time-to-identification differences; (2) concordance between molecular and conventional organism identification; and (3) predictive performance of resistance genes—*CTX-M* (extended-spectrum β-lactamases), *mecA* (methicillin resistance), *vanA/vanB* (vancomycin resistance), and carbapenemase genes (*KPC*, *NDM*, *VIM*, *OXA*, *IMP*)—for phenotypic resistance. Results were stratified by Gram stain and organism type to assess diagnostic performance across clinically relevant subgroups.

Results

The cohort included 75.8% Gram-negative bacteria, with *Escherichia coli* (26.8%), *Pseudomonas aeruginosa* (10.7%), and *Klebsiella pneumoniae* (8.5%) predominating. FilmArray BCID reduced time to identification by 30.1 hours versus conventional methods (24.8±18.5 vs 55.4±24.4 hours; 54.4% reduction, P<0.001). Overall concordance was 70%, with excellent performance for Gram-negative organisms (80.1%) but poor concordance for Gram-positive organisms (37.2%, P<0.001). Among 182 episodes with resistance gene analysis, *CTX-M* demonstrated high specificity (97.8-98.8%) and positive predictive value (97.0-98.0%) for cephalosporin resistance, with 88.2% accuracy for ceftazidime. *VanA/vanB* showed 100% sensitivity and 95.7% accuracy for vancomycin resistance in *Enterococcus* species. *MecA* perfectly predicted methicillin resistance in *Staphylococcus aureus*. Carbapenemase genes were detected in 3.1% of cases.

Conclusions

FilmArray BCID provides >30-hour acceleration in pathogen identification with excellent performance for Gram-negative organisms and highly specific resistance gene prediction, enabling earlier pathogen-directed therapy and stronger antimicrobial stewardship in high-resistance settings. Persistent limitations in Gram-positive identification reinforce the need for complementary culture-based methods.

Time to definitive pathogen identification comparing FilmArray Blood Culture Identification (BCID) panel versus conventional culture with MALDI-TOF mass spectrometry

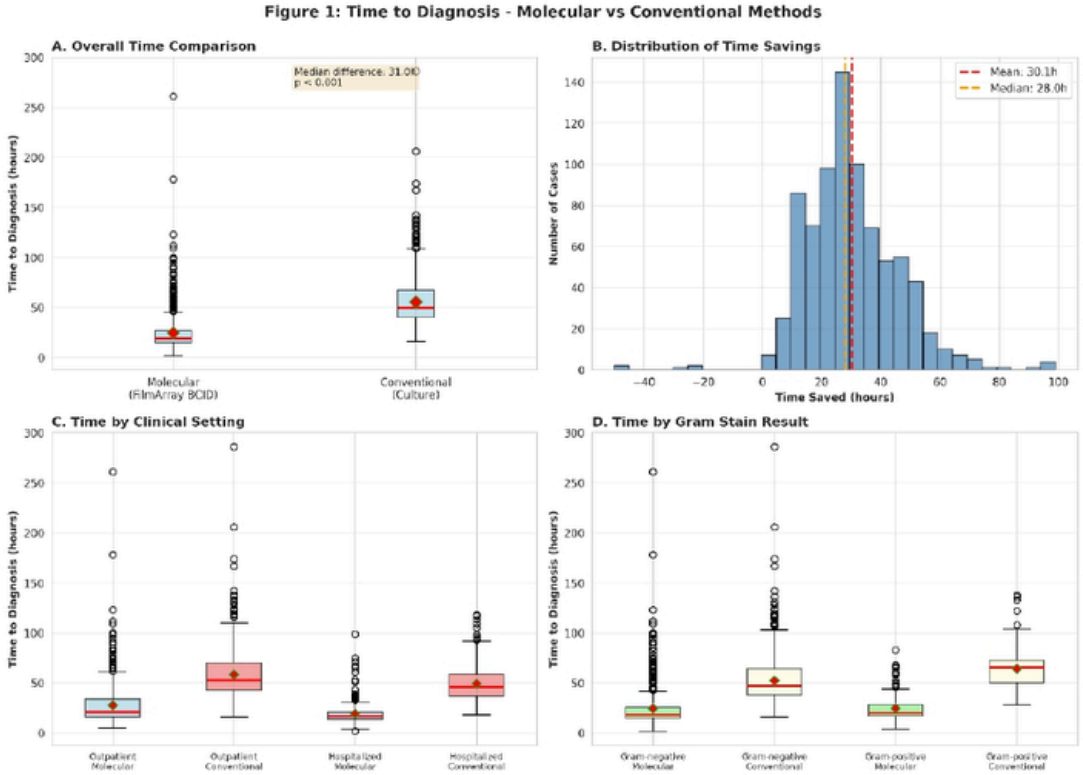

Figure 1: Time to definitive pathogen identification comparing FilmArray Blood Culture Identification (BCID) panel versus conventional culture with MALDI-TOF mass spectrometry across 803 bacteremia episodes. **(A)** Overall comparison showing molecular methods achieved significantly faster diagnosis (median 19.0 hours, mean 24.8±18.5 hours) compared to conventional culture (median 50.0 hours, mean 55.4±24.4 hours), representing 31.0 hours median time reduction ($p<0.001$, Wilcoxon signed-rank test). Box plots show median (red line), mean (red diamond), interquartile range (box), and data range (whiskers). **(B)** Frequency distribution of time savings demonstrates right-skewed distribution with mean 30.1 hours (red dashed line) and median 28.0 hours (orange dashed line) saved per episode, with majority of cases (>75%) showing 15-45 hours reduction. **(C)** Stratified analysis by clinical setting shows comparable time savings for outpatient (30.5 hours, N=520) and hospitalized (29.4 hours, N=283) patients, though hospitalized patients had shorter absolute processing times for both methods. **(D)** Analysis by Gram stain reveals greater time benefit for Gram-positive organisms (38.8 hours saved, N=187) compared to Gram-negative organisms (27.4 hours saved, N=609), reflecting slower conventional culture growth characteristics of Gram-positive bacteria. Grid lines indicate Y-axis scale; all statistical comparisons $p<0.001$.

Concordance analysis between FilmArray BCID and conventional culture with MALDI-TOF identification

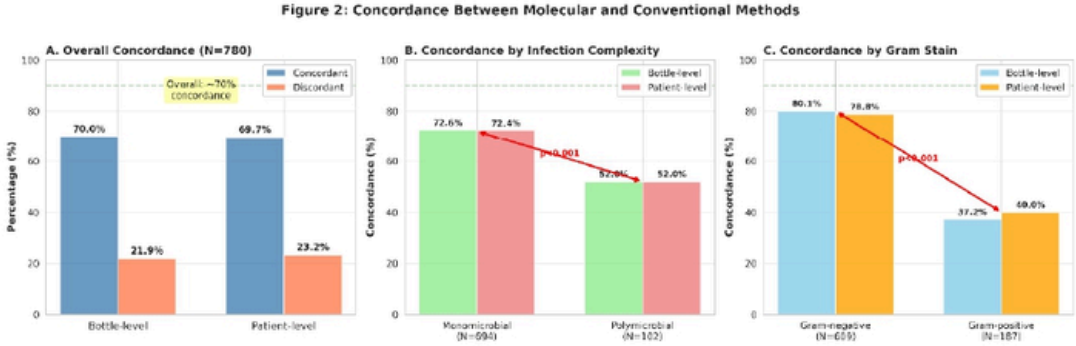

Figure 2. Concordance analysis between FilmArray BCID and conventional culture with MALDI-TOF identification across 780 bacteremia episodes with complete data from both methods. **(A)** Overall concordance was approximately 70% at both bottle-level (70.0% concordant, 21.9% discordant) and patient-level (69.7% concordant, 23.2% discordant), with 25.3% of cases requiring second microbiologist review for significant discrepancies. **(B)** Stratification by infection complexity demonstrated significantly higher concordance for monomicrobial infections (72.6% bottle-level, 72.4% patient-level, N=694) compared to polymicrobial infections (52.0% at both levels, N=102), reflecting FilmArray panel limitations in detecting all organisms present in mixed infections ($p<0.001$). **(C)** Concordance varied dramatically by Gram stain result, with excellent agreement for Gram-negative organisms (80.1% bottle-level, 78.8% patient-level, N=609) but substantially lower concordance for Gram-positive organisms (37.2% bottle-level, 40.0% patient-level, N=187, $p<0.001$), indicating challenges in Gram-positive identification due to greater species diversity, fastidious growth requirements, and limited FilmArray target coverage for clinically relevant Gram-positive bacteria. Green dashed lines indicate 90% concordance threshold; red arrows highlight statistically significant differences between groups. All comparisons used chi-square tests with $p<0.001$ considered significant.

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Molecular and rapid diagnostics
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Antimicrobial susceptibility testing
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Conflicts of interest

Do any of the authors have conflicts of interest related to the studies presented in this abstract?
No