Identification of selected primary bloodstream infection pathogens in patients attending Kisii level five and Homa Bay county hospitals [version 2; peer review: 1 approved with reservations, 1 not approved]

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Abstract

Background: Bloodstream infection (BSI) contributes to a substantial proportion of mortality in sub-Saharan Africa and is marked by the presence of bacterial and/or fungal microorganisms in the blood. Because BSI can be life threatening, it requires a timely, reliable and accurate diagnosis. This study retrospectively analyzed data of identified BSI pathogens and compared the performance of the different diagnostic technologies used in terms of accuracy, sensitivity, turnaround time (TAT) and cost.

Methods: Currently, culture followed by analytical profile index biochemical strips (API), (BioMerieux) are used as the conventional standard diagnostics in Kenyan public hospitals and labs. We compared the results of this standard to that of the BioFire FilmArray (FA) (BioFire Diagnostics) and MicroScan WalkAway-40 plus System (MS) (Beckman Coulter) used in diagnosis of BSI. The FA technology was able to identify 150/152 bacterial and yeast isolates with an overall accuracy of 99.04% (95% CI: 96.59-99.88%), sensitivity of 98.68% (95% CI: 95.33-99.84%), mean TAT of 8 hours 40 minutes per eight samples and running cost per sample of USD 140.11. The MS identified 150/152 isolates with an overall accuracy of 98.56% (95% CI: 95.86-99.70%), sensitivity of 98.68% (95% CI: 95.30-99.84%), mean TAT per sample was 42 hours and running cost per sample of USD 28.05. API detected 150/152 isolates, with an overall accuracy of 99.04% (95%
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CI: 96.59-99.88%), sensitivity of 98.68% (95% CI: 95.33-99.84%) and the mean TAT per sample was 53 and 103 hours for bacterial and yeast samples, respectively, with a running cost per sample of USD 28.05.

Conclusions: The findings in this paper suggest that the FA and MS platforms should be able to perform adequately in Kenya referral hospitals and medical clinics as a rapid diagnostic tool.

Keywords
Bloodstream infection, FilmArray, MicroScan, Resistance genes
Introduction

Bacteremia accounts for a large number of hospital admissions and results in high morbidity and mortality\(^1\). In sub-Saharan Africa, there is limited information on bloodstream infections (BSI)\(^2,3\), which can be partly attributed to the paucity of studies conducted in developing countries lacking high throughput BSI diagnostic technology. The availability of such equipment would facilitate widespread BSI detection in patients, help close this critical knowledge gap, and potentially save lives\(^4,5\).

Blood culture and analytical profile index (API, BioMerieux) strip analysis has been the conventional standard for bacteremia diagnosis in many hospitals throughout the world, including Kenya\(^6\). Using this technique has been a challenge because it is a labor-intensive process that requires experienced laboratory technologists and has a reportedly lower level of accuracy than other techniques such as conventional cultures\(^7-9\). To address this issue, diagnostic platforms such as the BioFire FilmArray (FA) and MicroScan WalkAway 40 plus (MS) are now widely used in Europe and the United States\(^2,9\).

The FA is a sophisticated closed-automated polymerase chain reaction (PCR) system that utilizes specific commercial pouches such as FA blood culture ID panel to identify BSI causative agents and antimicrobial resistance markers within 1 hour of a positive blood culture\(^2\). This platform can identify 24 causative agents of BSI (eight gram-positives, 11 gram-negatives, and give yeast species) and three antimicrobial resistance genes: mecA for methicillin, vanA/B for vancomycin and bld\(\text{S}_{256}\) for carbapenem by nested multiplex PCR\(^2-8\). The MS system can provide identification of bacteria within 16 to 20 hours, phenotypic antimicrobial profile (AST) and extended-spectrum beta lactamase (ESBL) using negative combo panel type 66 for gram negatives and positive combo panel type 39 for gram positives\(^8,10\) and identification of yeast within 4 hours using a rapid yeast panel (Beckman Coulter, United States).

The use of conventional methods requires considerably long turnaround time (TAT) from 12–72 hours. In potentially life-threatening cases of BSI, the microbial cause of infection must be identified as quickly as possible to ensure proper treatment and management of the disease. The newly employed methods FA\(^2\) and MS\(^9\) have never been used before in Kisii and Homa Bay hospitals.

In this paper, we compared the accuracy, sensitivity, turnaround time (TAT) and cost of new technologies against the conventional API strip technique based on past data from blood culture isolates. Based on our findings, we will identify whether these automated platforms would be capable of providing a rapid diagnosis of BSI in Kenya hospitals.

Methods

Study sites

Stored blood culture samples received from Kisii Teaching and Referral Hospital and Homa Bay County Referral hospital were analyzed at Microbiology Hub Kericho. These collection sites were selected because they do not have the capacity to identify BSI pathogens to the species level. Kisii Teaching and Referral Hospital is a public hospital located in Kitutu Chache Constituency, Kisii County. It is located in Kisii town Central Business, District Hospital Road, and serves a population of over 1 million. Homa Bay County Referral Hospital is a government health center located in Homa Bay Township Sub-location, Homa-Bay Location, Asego Division, and Rangwe Constituency in Homa Bay County. It has a population of over 1 million. The common diseases in these areas are malaria, upper respiratory tract infections, typhoid, pneumonia, tuberculosis and HIV\(^11\).

Study design

This study analyzed BSI isolates data tested using FA, MS technologies and culture followed by API strip analysis. A total of 152 isolates data (122 blood culture isolates and 30 control isolates) were analyzed. The study focused on the identification of BSI, accuracy, sensitivity, TAT as well as the cost of the items. Isolate analysis was performed at the Microbiology Hub Kericho (MHK), a United States Army Medical Research Directorate-Africa (USAMRD-A) facility working in collaboration with Kenya Medical Research Institute (KEMRI). The MHK performs surveillance and clinical research diagnosis of enteric pathogens causing acute diarrhea across Kenya in addition to screening blood culture samples for BSI agents.

Sample size determination

Formula \(n = Z^2 \times P (1-P)/d^2\), \(n = \) Sample size, Prevalence \((p) = 10.4\%\)

95% confidence interval \((z) = 1.96\)

Precision \(\pm 0.05\)

\(n = 1.96^2 \times 0.104(1-0.104)/0.05^2\)

Calculated sample size \(n = 143\) isolates.

The prevalence was taken from the study by Maze \textit{et al.} (2018)\(^12\) “The epidemiology of febrile illness in sub-Saharan Africa: implications for diagnosis and management”. The prevalence rate is based on East Africa data which is part of Kenya, the ranges in prevalence is between 10–20% in Kenya.

Blood culture

Blood samples were collected into BACTEC Plus Aerobic/F, Peds Plus Aerobic/F, Anaerobic/F and Lytic/10 Anaerobic/F vials (BD, United States) and incubated using the BacTec...
9050 instrument (BD, United States) for 5 days to account for slow-growing pathogens. A positive signal was indicated by an increased fluorescence caused by the carbon dioxide released by an organism reacting with the vial dye. Positive blood culture samples were removed and processed to identify the organism. Samples were processed directly using the FA without need for prior subculture. As for the MS and the API strip method, samples were first gram-stained and sub-cultured on MacConkey agar, Blood agar plate, Sabouraud Dextrose agar, Hektoen enteric agar and Tryptic soy agar (Becton Dickson).

**Microbial identification of the positive blood culture samples**

For identification by FA, samples were tested per the manufacturer’s instructions. First, the blood culture identification panel was inserted in the loading chamber, then hydration solution was added to the sample and then the panel was placed into the FA. The results were checked after 1 hour.

Pure colonies were used for the MS identification procedure. An inoculum of 0.5 McFarland standard equivalents was prepared by selecting 1 to 3 discrete colonies from pure culture on MacConkey agar (MAC) or blood agar plate (BAP) or Sabouraud dextrose agar (SDA) and suspended in 3 ml of the MS inoculum water (Beckman Coulter). From the solution, 100 μl was transferred and mixed with 25 ml of the MS inoculum water with pluronic and then poured into the sterile inoculator D set tray. The solution (140 μl) was transferred into a gram-negative or a gram-positive panel (Beckman Coulter), and then loaded into the MS and results checked after 18–24 hours and 4 hours for yeast organisms.

For manual biochemical analysis method, the API strips (BioMerieux, United States) and media (MacConkey agar, blood agar, Hektoen enteric agar, triple sugar iron and Sabouraud dextrose agar plates) were brought to room temperature. After this, 5 mL of deionized water was added to the tray along with the strips. The API ampules or equivalent suspension medium was inoculated with a single colony. The inoculation of wells for gram negative, gram positive and yeast organisms was done as per manufacturer’s instruction. The incubation box was closed and incubated at 36°C for 18–24 hours for bacterial while for the yeast it was incubated at 29°C for 48 to 72 hours. A positive signal was indicated by a colorimetric change that was interpreted using the API guidelines.

**Statistical analysis**

Overall accuracy was calculated as the (number of individual isolate identified using evaluated technique) / (total number of same isolates identified) x 100%).

**Results**

**The sensitivity and accuracy of the FA, MS, and API**

The overall accuracy and sensitivity of each platform is shown in Table 1. For the FA, the calculated specificity was 99.04% (95% CI, 96.59-99.88%). Out of the total 152 isolates identified, FA technology was able to correctly identify 150 isolates resulting in a calculated sensitivity of 98.68% (95% CI: 95.33-99.84%). Similar to the specificity computation for the FA instrument, the specificity of the MS instrument was determined based on the number of isolates correctly identified by the MS out of the total number of isolates correctly identified. This yielded a specificity of 98.56% (95% CI: 95.86-99.70%). The MS technology identified 149 true isolates, which produced a calculated sensitivity of 98.68% (95% CI: 95.30-99.84%).

| Parameter Evaluated | API         | FA          | MS          |
|---------------------|-------------|-------------|-------------|
| Specificity         | 99.04%      | 99.04%      | 98.56%      |
|                     | (96.59 - 99.88%) | (96.59 to 99.88%) | (95.86 - 99.70%) |
| Sensitivity         | 98.68%      | 98.68%      | 98.68%      |
|                     | (95.33% - 99.84%) | (95.33% to 99.84%) | (95.30% - 99.84%) |

FA, FilmArray; MS, MicroScan; API, Analytical Profile Index.
The API strip analysis identified 150 isolates with specificity of 99.04% (95% CI: 96.59-99.88%) with no significant difference in overall specificity to the FA and MS. The sensitivity of API method was 98.68% (95% CI: 95.33-99.84%).

### Pathogen identification by FA, MS and API

Next, we decided to breakdown which microbes that each platform correctly identified (Table 2). The FA and API were able to identify 150/152 BSI pathogens. Interestingly, the FA platform was able to identify 4/4 of *Enterobacter cloacae* isolates as opposed to API technique, which detected only 2/4. However, the FA only recognized *Staphylococcus* at the genus level. In addition, the system could not characterize *Streptococcus anginosus* and *Streptococcus bovis* at the species level as these bacteria were not in its database, and therefore, were identified as *Streptococcus* spp. The FA identified *Salmonella* isolates as *Enterobacteriaceae* while the API and the MS were able to identify these isolates as *Salmonella* spp. The MS was able to accurately identify the presence of all other isolates similar to the API method except with *Staphylococcus* spp. (93.75%) and *Acinetobacter baumanii* (85.71%), while the API method was 100% accurate for both.

In addition, the MS correctly identified all other *Streptococcus* isolates besides *S. pneumoniae*, whereas the FA and API standard had accuracies of 83.3% and 85.7%, respectively. Results of identification using each technique are available (see Underlying data).

The mean turn-around time for the FA, MS and API

We limited the running time for each platform to the length of a normal working day (8 hours) (Table 3). Under this condition, the FA could only run eight samples. We therefore established this limit to ensure an equal number of samples per run across all the techniques. The turnaround time (TAT) for the FA per sample run was 1 hour 6 minutes, with an average of 5 minutes processing time and 1 hour identification and results analysis. The average time for FA was 8 hours 40 minutes and significantly less (p < 0.0001) compared to the MS and API. The MS had a mean TAT of 42 hours per sample run, with 27 hours processing time and the mean TAT was significantly more (p < 0.0001) compared to the FA. Breaking this down, the culture process and incubation required 24 hours, which could be more depending on the bacteria and purity of culture. The API method had a mean TAT of 53 hours per

### Table 2. Breakdown of pathogen identification by the FA, MS and API

The accuracy broken down by microorganism was calculated for each platform. The total number of isolates identified followed by accuracy percentage of FA, MS and API is listed above. For the FA, the "n/a" indicates that the isolates could not be identified beyond the family level (*Enterobacteriaceae*). Those rows with a dash mark (-) indicate those identified at specific genus level (*Salmonella*) and not group level (*Enterobacteriaceae*).

| Organisms               | FA % | FA Accuracy | MS % | MS Accuracy | API % | API Accuracy |
|-------------------------|------|-------------|------|-------------|-------|--------------|
| *Staphylococcus aureus* | 7    | 100         | 7    | 100         | 7     | 100          |
| *Staphylococcus* spp    | 16   | 100         | 15   | 93.75       | 16    | 100          |
| *Streptococcus pneumoniae* | 7   | 100         | 7    | 100         | 7     | 100          |
| *Streptococcus* spp     | 5    | 83.3        | 7    | 100         | 6     | 85.7         |
| *Enterococcus* faecium  | 8    | 100         | 8    | 100         | 8     | 100          |
| *Escherichia coli*      | 8    | 100         | 8    | 100         | 8     | 100          |
| *Enterobacter* cloacae  | 4    | 100         | 2    | 50          | 2     | 50           |
| *Klebsiella pneumoniae* | 11   | 100         | 11   | 100         | 11    | 100          |
| *Acinetobacter baumanii* | 7    | 100         | 6    | 85.71       | 7     | 100          |
| *Pseudomonas aeruginosa* | 9    | 100         | 9    | 100         | 9     | 100          |
| *Enterobacteriaceae*    | 57   | 100         | -    | -           | -     | -            |
| *Salmonella* spp        | n/a  | n/a         | 57   | 100         | 57    | 100          |
| *Klebsiella oxytoca*    | 2    | 100         | 2    | 100         | 2     | 100          |
| *Candida albicans*      | 9    | 100         | 9    | 100         | 9     | 100          |
| *Candida krusei*        | 1    | 100         | 1    | 100         | 1     | 100          |
| *Candida parapsilosis*  | 1    | 100         | 1    | 100         | 1     | 100          |

FA-FilmArray, MS-MicroScan, API-Analytical Profile Index.
Table 3. The mean turnaround time of the FA, MS, and API. For each platform being analyzed, turnaround times were broken into processing and ID analysis. The time shown for each of these categories is the mean of multiple runs, which had eight samples each. The processing column shows the time taken to prepare the samples for culture and then selection of isolates for identification. Of note, the FA did not require gram staining or culture and selection of an isolate from a blood culture. Identification analysis was based on the time each platform required to complete their respective protocols. The p-value showed the significance of the mean difference among the techniques.

| Equipment | Processing time per 8 samples (min) | ID analysis per 8 samples (min) | Total time (min) | Total number of runs |
|-----------|------------------------------------|---------------------------------|------------------|---------------------|
| FA        | 40                                 | 480                             | 520              | 19                  |
| MS        | 1620                               | 960                             | 2580             | 19                  |
| API       | 1620                               | 1680                            | 3300             | 19                  |

p-value <0.0001 for mean TAT: FA vs. MS/API, MS vs. FA, and API vs. MS

FA = FilmArray, MS = MicroScan, API = Analytical Profile Index, ID = Identification.

The average cost of running one sample per technique

The average cost of running one isolate per sample using the MS instrument was 38.75 USD while API technique was 29.17 USD. Extra equipment required but not included were biosafety cabinet, incubators, autoclaves, hot plates, conical flasks, stirrers and spatulas as well as the annual preventive maintenance for this equipment. Only the costs of the consumable items needed for each method were evaluated. As expected, the cost of the items used for the API technique was lower than for those used by the MS and FA.

Table 4. The cost breakdown running the FA, MS, and API. The average cost of running sample was broken down into biochemical reagents/media used. Reagents not used by a platform as designated N/A (non-applicable). Not included in the cost breakdown were the equipment aforementioned above. The periodic maintenance required for the automated platforms was also not included.

| Materials | Cost per sample (USD) |
|-----------|------------------------|
| API Biomeriux | 4.72 N/A N/A |
| MacConkey agar | 0.16 0.16 N/A |
| Hektoen enteric agar | 0.32 N/A N/A |
| Triple sugar iron agar | 0.14 N/A N/A |
| Blood agar base | 0.14 0.14 N/A |
| Dish Petri CS-100 15X100m | 1.05 N/A N/A |
| Gram stain kit | 0.22 0.22 N/A |
| Polyester tipped swabs | 0.25 0.25 N/A |
| Sheep blood agar | 0.24 0.24 N/A |
| 3ml inoculum water | N/A 2.66 N/A |
| 25ml inoculum water with pluronic | N/A 2.92 N/A |
| Inoculator D sets | N/A 1.88 N/A |
| Panel lid | N/A 0.71 N/A |
| Microscan Panel (GPC/NBPC) | N/A 7.64 N/A |
| Kovacs reagent | 0.71 0.71 N/A |
| 0.8% Sulfanilic acid (Nit 1) | 0.49 0.49 N/A |
| 0.5% N-N-Dimethyl-Alpha-Naphthylamine(Nit 2) | 0.63 0.63 N/A |
| 40% Potassium hydroxide (Vp1) | 0.82 0.82 N/A |
| Alpha naphthol (Vp2) | 0.54 0.54 N/A |
| 10% Ferric chloride (TDA) | 0.59 0.59 N/A |
| Peptidase reagent | 0.49 0.49 N/A |
| NaOH | 0.53 0.53 N/A |
| Oxidase reagent | 0.52 0.52 N/A |
| Blood culture bottle | 6.98 6.98 6.98 |
| Blood culture identification pouch | N/A N/A 124.58 |
| Inoculating needle | 0.12 0.12 N/A |
| Needles and syringes | 0.3 0.3 0.3 |
| Biohazard bag | 0.2 0.2 0.2 |
| Microscope slides | 0.32 0.32 N/A |
| Sharps containers small | 3.95 3.95 3.95 |

Discussion

In resource-limited settings, the use of conventional methods in diagnosis of bacteremia has been a challenge to most public health facilities leading to misclassification of the diagnosis of BSI. The automated methods FA and MS proved to be more efficient, reliable and faster in the identification of a wide range of microorganisms than API. The technologies are reliable with a short turnaround time. These positive factors outweigh the use of API strips for microbial identification, which is considered the conventional standard in Kenya for diagnosis of BSI. In comparison to the FA and MS, the API method was more labor intensive. Furthermore, fastidious bacteria might not be identified if they fail to grow on culture media but can be identified directly from blood culture using FA.
Overall, the sensitivity of FA (98.68%), MS (98.68%) and API (98.68%) were identical, with an overall accuracy of 99.04%. Moreover, the sensitivity of FA demonstrated in this study was similar to the sensitivity observed in a previous study carried out in Kazulu-Natal. The differences in sensitivity came in inability of FA and MS to agree in terms of genus and species individual identification of BSI pathogens.

The higher accuracy by FA in individual identification of BSI pathogens could be because it is a molecular-based platform. The FA identified Enterobacter cloacae with a higher accuracy than the other two methods, which could not identify the two isolates. This is probably because the FA identified two isolates as Enterobacter cloacae complex, which neither of the other methods could identify. However, the accuracy of FA was limited when identifying Streptococcus spp. where the accuracy was 83.3%, the organisms in question (Streptococcus anginosus and Streptococcus bovis) are not available in the FA database and are not common causes of BSI though they take advantage of immunocompromised individual and cause endocarditis. The overall accuracy demonstrated by the FA is in line with previous paper evaluating the diagnostic capabilities of the system.

The MS was able to accurately identify the presence of BSI bacteria with similar accuracy to the API method, except for the identification of Staphylococcus spp. where the accuracy was 93.75% and Acinetobacter baumanii with an accuracy of 85.71% for MS. The MS surpassed the API strip method in the identification of Streptococcus spp. where the accuracy was (100%) compared to API method (85.71%). These issues with MS in identifying Staphylococcus spp. and Acinetobacter baumanii is in line with previous studies, where the MS misidentified Acinetobacter baumanii. For this study, the misidentified Streptococcus spp. were actually Staphylococcus spp.

In past studies, the API strip analysis had a lower accuracy identifying microorganisms such as Citrobacter species, Escherichia coli, Pseudomonas aeruginosa and Enterobacter species than automated platforms. Interestingly, this did not occur with this study, and could partly be because the lab technician performing the assay had extensive clinical microbiology experience. Microbiology labs typically address this lower accuracy by adding biochemical tests such as oxidase and catalase to increase accuracy. We, however, did not incorporate these assays into the API strip analysis.

The mean TAT difference per run of eight samples among the technologies was significant at p<0.0001. The FA technology required 8 hours 48 minutes per eight samples compared to the MS, which required 42 hours and the API method, which required 53 hours for bacterial species and 103 hours for yeast. The major factor contributing this difference was time needed to prepare the isolates, which require gram-staining then culturing for 24/48 hours prior to identification by MS or API. It should be noted that the MS has higher throughput and can process 40 or more panels in one run. In addition, the API method can test more samples and is only dependent on availability of incubators, reagents and the experience of the technician. The shorter TAT for FA is a very attractive feature for under-developed areas with poor infrastructure and inaccessible areas where field clinical/research activities are undertaken and do not necessarily require a high-throughput machine. Though not a metric evaluated in this study, the FA requires considerably less training and skill compared to the other methods, which help to balance its throughput limitations.

The average cost of testing one sample using FA was noticeably higher than the cost of the MS and API methods. This was expected as the FA test kits cost more than the MS panels and the API reagents. While the FA is more expensive, it is able to identify co-infection in one sample, which would require separate runs for the MS and API.

Of note, the FA is able to identify resistant genes such as methicillin resistance common with Staphylococcus aureus, vancomycin resistance common with Enterococcus spp. and carbapenem resistance common with Klebsiella pneumoniae and other Enterobacteriaceae. While the MS has no capability to identify antimicrobial resistant genes commonly associated with BSI, it is able to perform phenotypic drug sensitivity. In fact, the MS has a wider range of antimicrobial testing capabilities with regularly updated software database in line with CLSI guidelines.

### Conclusion
While the evaluated methods were similar in accuracy and sensitivity, there were appreciable differences in TAT and cost. The FA cost more, but had a quicker TAT compared to the MS and API methods. This is a significant concern when using the machine in areas with limited financial resources. However, the FA requires minimal training prior to use and is able to identify co-infections. Furthermore, the FA requires a small space, and therefore, the cost of the FA panels should not be considered a major drawback since early detection of BSI has shown to reduce medical costs, hospital stays, and help guide
the clinicians on the best treatment approach, which lower overall economic costs.

RecommenDation
The FA and MS have not been evaluated at Kenya hospitals and further evaluation using a larger sample size is recommended in order to have more data on BSI pathogens and their antimicrobial susceptibilities in different localities. However, these preliminary results clearly suggest that both the FA and MS platforms are valuable tools in rapid identification of BSI. Each technology has its advantages and disadvantages, which must be considered. Still, implementation of either platform could result in reduction of hospital stays, lower cost, better patient management and more appropriate use of antibiotics by clinicians.

Data availability
Underlying data
Figshare: IDENTI~1.DOC. https://doi.org/10.6084/m9.figshare.12948533.v4.

This project contains the following underlying data:
- Identification of Selected Primary Bloodstream Infection Pathogens in Patients Attending Kisii Level Five and Homa Bay County Hospitals- FA.xlsx. (Data obtained using Film Array.)
- Identification of Selected Primary Bloodstream Infection Pathogens in Patients Attending Kisii Level Five and Homa Bay County Hospitals-MS.xlsx. (Data obtained using Microscan.)
- Identification of Selected Primary Bloodstream Infection Pathogens in Patients Attending Kisii Level Five and Homa Bay County Hospitals-Api.xlsx. (Data obtained using analytical profile index.)
- Identification of Selected Primary Bloodstream Infection Pathogens in Patients Attending Kisii Level Five and Homa Bay County Hospitals-FA raw data.xlsx. (Pathogen count data obtained using Film Array.)
- Identification of Selected Primary Bloodstream Infection Pathogens in Patients Attending Kisii Level Five and Homa Bay County Hospitals-MS raw data.xlsx. (Pathogen count data obtained using Microscan.)
- Identification of Selected Primary Bloodstream Infection Pathogens in Patients Attending Kisii Level Five and Homa Bay County Hospitals-Api raw data.xlsx. (Pathogen count data obtained using analytical profile index.)

Data are available under the terms of the Creative Commons Attribution 4.0 International license (CC-BY 4.0).

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Author contributions
Ronald Kirera was responsible for conceptualization, study design, data analysis, and drafting of the manuscript. Daniel Kariuki, Joseph Nganga, Judd L. Watson, Christine Hulseberg and Alexander Flynn contributed in the manuscript review. Elizabeth Odundo, Erick Kipkirui, Cliff Odhimbo, Nancy Kipkemoi, Abigail Ombogo, Janet Ndonye, Mary Kirui, and Margaret Koech contributed in data analysis and manuscript review.

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Josette Raymond
France Bacteriology Laboratory, Bicêtre Hospital, Kremlin Bicetre, France

The study compares three methods of identification of pathogens growth in blood culture samples: API, Film Array and MS. All the 3 methods show excellent sensitivity and accuracy. What was the specificity?

Some comments:

It should be clearly noted that due to the technology and the price, these techniques (FA and MS) cannot be used in any laboratory in Africa (or low income countries).

Unfortunately, the FA method is not able to identify the *Salmonella*. This is a real problem, since the isolated Enterobacteriaceae were mainly *Salmonella* knowing that *Salmonella* is the major pathogen in Africa.

In the discussion, the authors state that *S. anginosus* and *S. bovis* are contaminant. I do not agree since these *Streptococcus* may be responsible of endocarditis or other (abdominal) infections.

The identification of the bacteria is not enough. More data on antimicrobial susceptibilities are required since antimicrobial resistance is a major problem in Africa. So, more data are needed.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?

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Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Infectious diseases (pediatric mainly) and Helicobacter infection

I confirm that I have read this submission and believe that I have an appropriate level of expertise to state that I do not consider it to be of an acceptable scientific standard, for reasons outlined above.

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Author Response 27 May 2021

**Ronald Kirera,** 1. United States Army Medical Research Directorate, Africa/Kenya, Kericho, Kenya, Kenya

Dear reviewer,

Thank you for taking time to review our journal. We appreciate comments and suggestions.

The study compare three methods of identification of pathogens growth in blood culture samples: API, Film Array and MS. All the 3 methods show excellent sensitivity and accuracy. What was the specificity?

**Response:** The overall specificity was 98%. We did not include specificity in the journal because consultation with my co-authors we decided to use sensitivity and accuracy.

**Some comments:**

*It should be clearly noted that due to the technology and the price, these techniques (FA and MS) cannot be used in any laboratory in Africa (or low income countries).*

**Response:** In Kenya, the government has invested a lot in the health sector through county governments under devolution and universal health initiative. These technologies will be embraced in the referral hospitals and research institutions, also the non-governmental organizations and private sector have also invested much in this institutions. With the emergence of drug resistant microorganisms these technologies will help in early diagnosis and reduce on multidrug resistant.

*Unfortunately, the FA method is not able to identify the Salmonella. This is a real problem, since the isolated Enterobacteriaceae were mainly Salmonella knowing that Salmonella is the major pathogen in Africa.*

**Response:** FA BCID 1 panel is not able to identify the *Salmonella* (genus) but it identifies up
to the family level, following manufacturers' recommendations and inhouse standard procedures this can be identified further to genus level using salmonella antisera. The FA identification panel keeps on improving and the current panel (BCID2) identifies *Salmonella* at genus level using the same machine/platform. The turnaround time for FA is really helpful in early diagnosis of *Salmonella*.

*In the discussion, the authors state that S. anginosus and S. bovis are contaminant. I do not agree since these Streptococcus may be responsible of endocarditis or other (abdominal) infections.*

**Response:** Thank you for pointing this out, These microorganisms cause bacteremia taking advantage of immunocompromised patients though not common in immunocompetent individuals.

*The identification of the bacteria is not enough. More data on antimicrobial susceptibilities are required since antimicrobial resistance is a major problem in Africa. So, more data are needed.*

**Response:** We agree, in our recommendation we suggested more studies with big number. Our study was limited by timelines and resources.

Thank you,

Ronald Kirera,

Corresponding author.

**Competing Interests:** There is no competing interest.
of identified BSI pathogens. Which means that they did not isolate and identify the pathogens as described in the Methods section. It is not clear whether they used already identified pathogens or used stored blood culture samples from Kisii Referral Hospital and identified the pathogens.

Is the work clearly and accurately presented and does it cite the current literature? Yes

Is the study design appropriate and is the work technically sound? Yes

Are sufficient details of methods and analysis provided to allow replication by others? Yes

If applicable, is the statistical analysis and its interpretation appropriate? Yes

Are all the source data underlying the results available to ensure full reproducibility? Yes

Are the conclusions drawn adequately supported by the results? Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Medical microbiology-Bacteriology

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 24 Nov 2020

Ronald Kirera, 1. United States Army Medical Research Directorate, Africa/Kenya, Kericho, Kenya, Kenya

Dear reviewer,
Thank you for the review and taking the time to go through the paper,

The question on results and methods in the abstract section
Response: This was combined to meet the allowable minimum number in the abstract section as per journal requirement however I had to limit the explanation on results and methods to meet the required number.

On abstract 3rd line on “this study retrospectively analyzed data of identified BSI pathogens”
Response:
a) I used archived BSI isolates which I had processed/analyzed before using the same methods under analysis for comparison.
b) The explanation in the method section was to show how the isolates were processed and how the techniques work.

Thank you,
Ronald Kirera
Corresponding author.

**Competing Interests:** We have no competing interest.

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