



Pilot study of a novel whole-genome sequencing based rapid bacterial identification assay in patients with bacteremia

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Background

Bloodstream infections (BSI) are among the leading causes of morbidity and mortality. Yet, gold standard culture-based diagnostics have limited ability to guide therapeutic intervention due to multi-day turnaround time and low sensitivity. Day Zero Diagnostics has developed Blood2Bac™, a culture-free, species agnostic process to enrich bacteria directly from whole blood. Coupled with whole genome sequencing (WGS) and Day Zero Diagnostics' Keynome™ algorithmic tools for species identification (ID) and antimicrobial resistance (AMR) profiling, we conducted the first proof-of-concept feasibility study in an inpatient clinical setting.

Methods

Study participants were enrolled and specimens collected from Boston Medical Center. Eligibility criteria included hospitalized adults with suspected and/or documented BSI, irrespective of empiric antibiotic therapy duration. Whole blood samples were processed with Blood2Bac, sequenced on a nanopore platform, and bacterial ID determined with Keynome ID. Keynome ID results were compared with blood culture results to measure concordance.

Results

Specimens from 26 participants were processed with Blood2Bac and nanopore sequencing. Keynome ID calls were concordant with clinical blood culture for 96% (25/26) of samples, where 7 were concordant positive and 18 were concordant negative. In 3 concordant samples, Keynome ID called positive while concurrent blood cultures were negative. However, all IDs corresponded with positive blood culture results from the day prior, suggesting potentially higher sensitivity for the Blood2Bac compared to blood culture. The study to date has not resulted in any false positive calls. All positive Keynome ID calls are supported by prior microbiological clinical evidence. Two concordant positive IDs resulted in >95% of the genome recovered and Keynome concomitantly resulted in AMR predictions with 100% accuracy compared to pathogen phenotype. In 1 discordant specimen, the Keynome ID result was negative while blood cultures 8 hours before were positive. In this case, the patient was on empiric therapy for 8 days prior to samples collection and cultures were negative 19-hours post specimen collection.

Conclusion

These results highlight the sensitivity of a real-time blood WGS approach to identify BSI and its utility as a diagnostic to minimize unnecessary antibiotic exposure that is contributing to the antibiotic resistance crisis.