Bruker's IR Biotyper®: Paving the way to real-time outbreak control

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Abstract

Klebsiella pneumoniae, a gram-negative bacterium of considerable clinical significance, has emerged as a formidable global health threat over recent decades. It is associated with a wide array of infections, from pneumonia and urinary tract infections to septicemia and hospital-acquired infections, posing a substantial challenge to healthcare systems worldwide. Given its notable propensity to acquire antibiotic resistance and thrive in diverse environments, *K. pneumoniae* requires timely epidemiological surveillance to facilitate infection control. In this study, the performance of the IR Biotyper®, a Bruker Fourier transform infrared (FT-IR) spectroscopy system, was evaluated for *K. pneumoniae* isolates typing [1].

Introduction

Klebsiella pneumoniae plays a significant role in the occurrence of infections acquired both in community and hospital settings. The emergence of various multidrug-resistant (MDR) strains within high-risk *K. pneumoniae* clonal lineages, associated with distinct sequence types (ST), frequently leads to outbreaks, posing a substantial threat to public health.

Effectively tracking, comprehending, and mitigating *K. pneumoniae* outbreaks, along with the circulation of specific clones, presents a formidable challenge for infection control measures. Fourier transform infrared (FT-IR) spectroscopy has demonstrated its efficacy in bacterial typing across different intraspecies levels. This technique capitalizes on the distinctive infrared spectrum of each bacterial strain, serving as a unique fingerprint signature that facilitates precise identification.

Bacterial strain typing plays a pivotal role in investigating outbreaks by revealing clonality and possible transmission pathways as well as by establishing relatedness between clinical isolates and environmental sources. Selecting an appropriate typing method involves careful assessment of typeability, ease-of-use, interpretability, speed, reproducibility, cost-effectiveness and the availability of expertise. The IR Biotyper is a spectroscopic microorganism typing system based on FT-IR technology that achieves discriminatory power comparable to many molecular-based methods, delivering results within three hours, while being cost-efficient [2].

FT-IR spectroscopy, a well-established phenotypic method, has traditionally been employed to elucidate the molecular composition of a diverse array of samples. It can distinguish bacterial strains by measuring the absorption of IR light by the biomolecules present in the bacterial cell. The IR spectrum generated provides a unique fingerprint that reflects the overall cell composition, targeting key components such as nucleic acids, proteins, lipids, and carbohydrates. This allows e.g., for the identification of microorganisms at different subspecies levels [4].

Its ease of use, rapid results and cost-effectiveness may allow the IR Biotyper to become an indispensable tool for outbreak investigations.

Materials and methods

This study included 52 genotypically and phenotypically characterized MDR *K. pneumoniae* isolates, 41 belonging to ST307 and 11 to other STs. All except one isolate (PBIO2009, a ST307 reference isolate) were obtained in the context of an outbreak that occurred in North-East Germany in 2019.

The strains were cultivated on Columbia blood agar (Becton Dickinson) for 24±2 h at 37 °C. IR spectra were acquired from dried spots of bacterial suspensions in ethanol solution, using the IR Biotyper Kit and following the Instructions For Use.

After the isolates were analyzed by the IR Biotyper, exploratory data analysis was performed with the IR Biotyper software (4.0), applying hierarchical cluster analysis (HCA) with Euclidean metric and average linkage, and principal component analysis (PCA).

The accuracy of the IR Biotyper system to detect clonality was evaluated by comparison with sequence types as well as capsular (K locus) and polysaccharide (O locus) types. Concordance of results between IR Biotyper and whole-genome sequencing results was assessed by Adjusted Rand index (AR, 95% CI), calculated with the Comparing Partitions online tool [3].

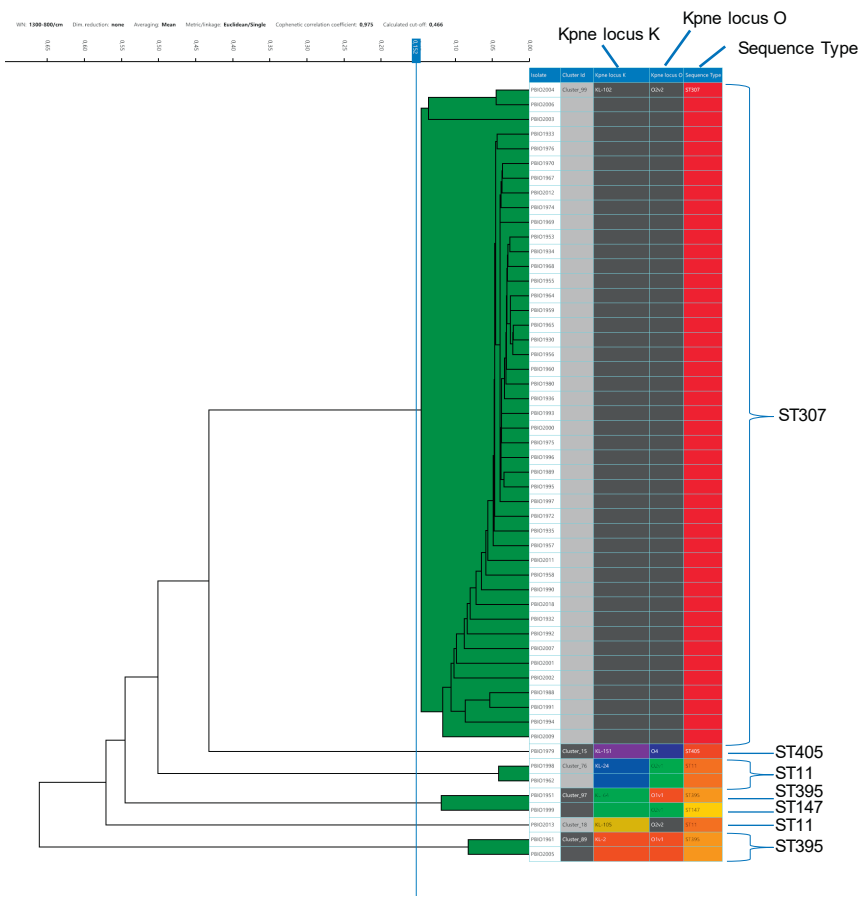
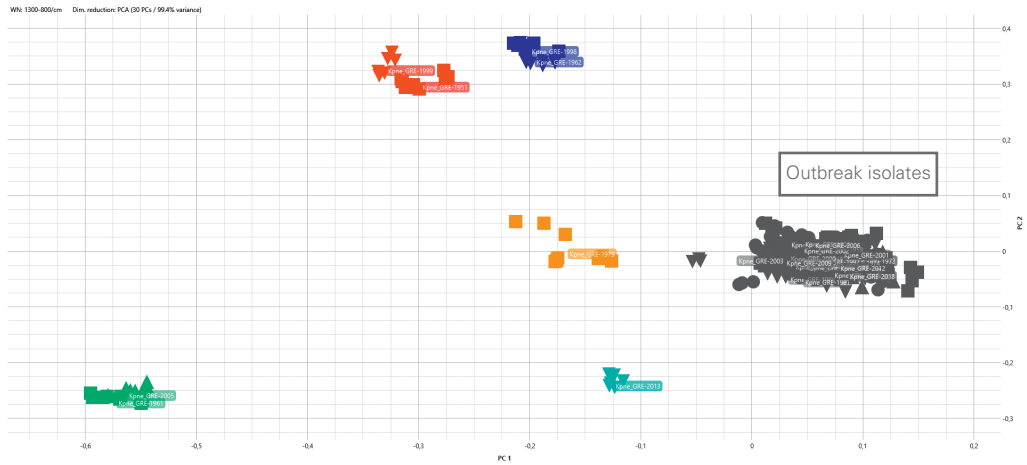


Figure 1
Correspondence between IR Biotyper clusters and ST, K and O loci [1]. The clustering cut-off value was automatically calculated by the IR Biotyper software.

Results

The study found that by applying HCA, the isolates were discriminated into six clusters, with the largest one comprising all ST307 isolates, and five smaller ones, corresponding to the non-ST307 isolates (Figure 1, [1]). IR Biotyper partitioning was in perfect concordance with the K locus (AR = 100%), in very good concordance with ST (AR = 99.1%), and lower concordance with the O locus (AR = 91%). PCA analysis showed a clear clustering of the outbreak isolates, as well as the clustering of the other isolates accordingly to the K locus (Figure 2, [1]).

Figure 2
2D PCA scatterplot [1]. Each geometric form corresponds to a spectrum, and the color corresponds to the locus K.



Conclusion

In summary, the data demonstrated that the IR Biotyper proved to be a novel and reliable method to reveal clonality among *K. pneumoniae* isolates and could represent a faster, easier and more cost-effective alternative to molecular methods, in the context of outbreak detection.

Despite IR Biotyper clustering showing a slightly weaker correlation with ST than with the K locus, for outbreak isolates this correlation seems strong enough to propose the IR Biotyper as a reliable real-time tool.

The combination of the IR Biotyper's typing results with its low cost and very short turnaround time suggests that it is a promising tool for strain typing that could make real-time outbreak investigation a reality.

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References

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