Evaluation of Data Correction Methods for Positive Blood Culture Results

Ojan Assadian, M.D., DTMH[1], Petra Apfalter, M.D., DTMH[2], Florian Daxböck, M.D.[1], Klaus-Peter Adlassnig, PhD[3], Walter Koller, M.D.[1]

[1]Division of Hospital Hygiene, Institute of Hygiene, University of Vienna, [2]Division of Clinical Microbiology, Institute of Hygiene, University of Vienna, [3]Section of Medical Expert and Knowledge-Based Systems, Department of Medical Computer Sciences, University of Vienna

Background

The outcome of patients with bacteremia is influenced by the initial selection of adequate antimicrobial therapy[1]. However, at the early stage of a bloodstream infection, microbiological identification and susceptibility of the causative organism are not available. Therefore, a calculated (empirical) antimicrobial therapy has to be started, based on the knowledge of the most likely microorganism and its susceptibility pattern. In hospitals, analysis of blood culture results is widely used. However, because of the difficulty of distinguishing true episodes of infection from specimen contamination and the generation of repeated results from one patient in the course of treatment, crude data has to be corrected for common skin contaminants and duplicate results before further analysis is performed. In this context, the objective of our study was to evaluate the influence of different data correction methods on ranking of pathogens and the cumulative antibiotic susceptibility pattern of blood culture isolates from surgical intensive care units (ICUs) to obtain a data correction preprocessing method for implementation in a knowledge-based surveillance system for bloodstream infections.

Methods

For acquisition of electronically stored microbiology results, the database query tool FlexScan of MONI (Monitoring of Nosocomial Infections) was used[2]. A retrospective analysis of positive blood cultures obtained from nine surgical ICUs of the Vienna General Hospital, Austria, was performed from January 1998 through December 1999, yielding a total of 572 positive blood culture results.

Raw data method (RDM): Data acquired by MONI without further correction, including all positive blood culture results obtained from patients of nine surgical ICUs.

Duplicate-free method (DFM): Correction of raw data by elimination of patient's duplicate results - any consecutive result with the same microorganism from a blood culture with the same antibiogram within a two-week period.

Microbiology data method (MDM): Regarding possible contamination of blood cultures, common skin contaminants were defined as organisms, which are part of the normal skin flora, including coagulase-negative staphylococci, *Corynebacterium sp.*, alpha-hemolytic streptococci, *Bacillus sp.*, *Propionibacterium acnes*, and *Neisseria sp.* other than *N. gonorrhoeae* or *N. meningitidis*.

All other bacteria and fungi were regarded as obligate pathogens and therefore always considered as true cause of bacteremia. Bacteremia caused by common skin contaminant organism was assumed as true, if an organism of the same species was isolated from two or more sets of blood cultures obtained within 5 days from the same patient. In this case, this was counted as a single episode of bacteremia.

Statistical analysis: Differences of proportions between RDM, DFM and MDM were calculated by applying the t-test; a p-value of = 0.05 was considered significant.

Results

S. epidermidis, *S. aureus*, and *C. albicans* were the most common organisms, regardless of the applied data-correction method. However, regarding the proportion of *S. epidermidis* expressed as percentage of all episodes, proportions differed statistically significant when correcting data using DFM vs. MDM (40.7% vs. 28.2%, p=0.001) and RDM vs. MDM (40.2% vs. 28.2%, p=0.001). No statistical significant difference was observed using RDM vs. DFM (40.2% vs. 40.7%, p=0.888).

Regarding differences in resistance pattern of *S. epidermidis*, none of the data-correction methods would have yield a different recommendation compared to no data correction, considering a cut off level of 30% as limit for appropriateness of an antibiotic for empirical therapy. However, for *S. aureus*, correction methods influenced recommendations for Gentamicin.

Conclusion

The MDM gives better estimation of the proportion of organisms isolated from blood cultures. Regarding susceptibility pattern and implications on empiric antibiotic therapy, the MDM has no advantage over the DFM or RDM. Because of the complex "if/then" rules for data correction of large datasets, the MDM strongly depends on the availability of computer systems, since this method is highly time and concentration consuming and consecutive human errors are inevitable.

References

1. Byl B, Clevenbergh P, Jacobs F, Struelens MJ, Zech F, Kentos A, Thys JP. Impact of infection diseases specialists and microbiological data on the appropriateness of antimicrobial therapy for bacteremia. Clin Infect Dis 1999; 29:60-6
2. Assadian O, Adlassnig KP, Rappelsberger A, Koller W. MONI – An intelligent infection surveillance software package. In: Adlassnig KP (ed.) Intelligent systems in patient care. 2001. Austrian Computer Association, Vienna, 49-56.