Detection of pathogenic bacterium causing bloodstream infection by 16S rDNA gene PCR with a GeXP analyzer

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Objective: Because bloodstream infections have a high mortality rate, rapid microbiological diagnosis is required to clinical efficient therapy. To develop a method of fast bacteria identification for pathogens causing bloodstream infection by GeXP analysis system based on the bacterial highly conserved region of 16S rDNA gene.

Methods: We performed culture and real-time 16S rDNA gene PCR followed by direct sequencing. Clinical amples were cultured on Columbia blood agar plates were incubated aerobically for 48 hours at 37 °C and Brucella blood agar plates were incubated under anaerobic conditions for 72 hours at 37 °C. The 16S rDNA gene were amplified using the common methodology and sequenced with primer 5ʿ-GAGCGGATAACAATTTCACACAGG-3ʿ.

Results: Ten clinical frequent bacterial strains were detected correctly at the species level. Candida albicans, herpes simplex virus I, II, HBV DNA and the blank control were all negative. The identification concordance was 100% by GeXP analysis system and conventional culture method at the genus level and it was 87.8% at the species level(36/38. Gram-positive and Gram-negative bacilli bacteria accounted for 48.9% and 43.8% respectively and fungi for 7.3% in 252 strains isolated from blood specimens. The most frequent Gram-negative bacilli isolated were Escherichia coli of 66 strains accounting for 26.2%, Salmonella of 46 strains accounting for 18.3%, Klebsiella pneumoniae of 34 strains accounting for 13.5%. The most frequent gram-positive pathogenic bacteria isolated were Staphylococcus aureus of 31 strains accounting for 12.3% and coagulase negative Staphylococcus coagulase of 25 strains accounting for 9.9%.

Conclusion: 16S rDNA Gene PCR with a GeXP genetic analysis system could detect blood culture positive sample directly and it was a fast, accurate method of bacteria identification for pathogens causing bloodstream infection.

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