

News Release

Title

Comprehensive detection of pathogens in immunocompromised children with bloodstream infections by next-generation sequencing

Key Points

- Sequencing reads of bacteria isolated in blood culture were identified by next-generation sequencing (NGS) in all plasma/serum samples of patients with blood stream infection (BSI). In two patients, causative bacteria were detected by NGS one week before onset of the infection.
- The causative organisms were identified by NGS in three of 23 children with suspected BSI.
- An NGS-based approach has great potential for identifying pathogens of infectious diseases in the clinical settings.

Summary

Associate Prof. Yoshinori Ito, Dr. Jun-ichi Kawada, Dr. Kazuhiro Horiba in Department of Pediatrics, Nagoya University Graduate School of Medicine (Dean: Kenji Kadomatsu, M.D., Ph.D.), and Dr. Yusuke Okuno in Center for Advanced Medicine and Clinical Research, Nagoya University Hospital, and their colleagues evaluated the utility of next-generation sequencing (NGS) for detecting causative microorganisms in blood samples of bloodstream infection (BSI) patients.

BSI is a severe complication in immunocompromised patients. Next-generation sequencing allows us to analyze comprehensively and quantitatively all microorganisms present in a clinical sample in comparison with blood culture. However, there are currently no established methods to identify causative pathogens by NGS.

In this study, plasma/serum samples from 35 patients were used for sequencing and the results were compared with those from blood culture. Sequencing reads of bacteria isolated in blood culture were identified by NGS in all plasma/serum samples at the onset of BSI. Additionally, bacteria isolated in blood culture were identical to the “dominant” bacteria by NGS in 8 of 12 patients. In two patients with catheter-related BSI, causative bacteria were detected in plasma/serum samples at 7 days before disease onset. Finally, causative pathogens (*Tatlockia micdadei*, *Escherichia coli*, and human adenovirus 2) were identified in three patients in the suspected BSI group. NGS has several advantages over other diagnostic methods and is becoming a new method to identify causative microorganisms in severe infectious diseases.

Research Background

Next-generation sequencing (NGS) is a culture-free method that can analyze

comprehensively and quantitatively the entire microbial community within a clinical sample. Therefore, several studies have attempted to identify pathogens in many infectious diseases, including febrile illness, respiratory and gastric/digestive infection, acute encephalitis/encephalopathy, and bloodstream infection (BSI). These reports demonstrated a wide distribution of microbial genes, however, the interpretation of these sequence data for diagnostic application remains unclear. Thus, there are currently no established methods to identify pathogenic microorganisms of infectious diseases in clinical settings.

Research Results

BSI is a severe complication in immunocompromised patients. In this study, plasma/serum samples from 35 patients were used for sequencing and the results were compared with those from blood culture. Sequencing reads of bacteria isolated in blood culture were identified by NGS in all plasma/serum samples at the onset of BSI. Additionally, bacteria isolated in blood culture were identical to the “dominant” bacteria by NGS in 8 of 12 patients. In two patients with catheter-related BSI, causative bacteria were detected in plasma/serum samples at 7 days before disease onset. Finally, causative pathogens (*Tatlockia micdadei*, *Escherichia coli*, and human adenovirus 2) were identified in three patients in the suspected BSI group. NGS has several advantages over other diagnostic methods and is becoming a new method to identify causative microorganisms in severe infectious diseases.

Research Summary and Future Perspective

Our study demonstrates that the NGS-based approach for detection of microorganism-derived sequences may be a useful and reliable method for identifying the causative pathogens in cases of bloodstream infection. NGS can detect causative bacteria and fungi that are difficult to grow in culture and viruses. Additionally, NGS may help to diagnose a disease before disease onset. An NGS-based approach has great potential for identifying pathogens of infectious diseases in the clinical settings.

Publication

Kazuhiro Horiba, Jun-ichi Kawada, Yusuke Okuno, Nobuyuki Tetsuka, Takako Suzuki, Shotaro Ando, Yasuko Kamiya, Yuka Torii, Tetsuya Yagi, Yoshiyuki Takahashi, Yoshinori Ito. Comprehensive detection of pathogens in immunocompromised children with bloodstream infections by next-generation sequencing. *Scientific Reports*, 2018; 28: February.

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