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Identification of the septic pathogen in the plasma by next generation sequencing

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Sepsis is a leading cause of death worldwide and the most common cause of death in patients who admitted to intensive care units. Sepsis is characterized by the life-threatening host immune response against invading microorganisms. However, the accurate diagnosis of the microorganism for sepsis remains difficult given that the yield rate of blood culture, which is currently the golden standard in sepsis, is merely 10-15%. Advances in genome sequencing technologies have led to a drastically decreased cost of Next-Generation Sequencing (NGS) and a wide range of applications, including identification of the circulating pathogenic nucleic acid in sepsis. Nowadays several methods have been developed to identify the pathogens through NGS approaches, but a number of biases exist in bioinformatic analyses. In the present study, we used the plasma of patients with sepsis at Taichung Veterans General Hospital (TCVGH) and aimed to identify circulating pathogenic nucleic acid through the NGS approach. We used pathogen sequences assignment directly from filtered NGS reads by k-mer and this approach is characterized by the fast-screening although high-memory is required. We found that pathogen-specific sequences may be identified in short time consume under the low survive reads after filtering host reads.

Biography

Yang-Zhan Huang is currently pursuing his Masters in Bioinformatics and Metagenomics at Institute of Genomics and Bioinformatics, National Chung Hsing University, Taiwan. He has worked for Applied Microbiology Laboratory and is interested in microorganism research.

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