Rapid detection and identification of pathogens in patients with continuous ambulatory peritoneal dialysis (CAPD) associated peritonitis by 16s rRNA gene sequencing

ABSTRACT

Peritonitis still remains a serious complication with high rate of morbidity and mortality in patients on CAPD. Rapid and accurate identification of pathogens causing peritonitis in a CAPD patient is essential for early and optimal treatment. The aim of this study was to use 16S rRNA and ITS gene sequencing to identify common bacterial and fungal pathogens directly from the peritoneal fluid without culturing. Ninety one peritoneal fluids obtained from 91 different patients on CAPD suspected for peritonitis were investigated for etiological agents by 16S rRNA and ITS gene sequencing. Data obtained by molecular method was compared with the results obtained by culture method. Among the 45 patients confirmed for peritonitis based on international society of peritoneal dialysis (ISPD) guidelines, the etiological agents were identified in 37(82.2%) samples by culture method, while molecular method identified the etiological agents in 40(88.9%) samples. Despite the high potential application of the 16S rRNA and ITS gene sequencing in comparison to culture method to detect the vast majority of etiological agents directly from peritoneal fluids; it could not be used as a standalone test as it lacks sensitivity to identify some bacterial species due to high genetic similarity in some cases and inadequate database in Gene Bank. However, it could be used as a supplementary test to the culture method especially in the diagnosis of culture negative peritonitis.