INTRODUCTION

Nontuberculous mycobacteria (NTMs) were initially recognized as pathogens in the mid-1950's [1]. More and more species were discovered with recognize ofby medical workers and improvement of inspection detection techniques. Some NTM species of them may cause diseases in humans [1]. NTM has been reported in mMore than 170 species of NTMs have been reported worldwide, including two types: rapidly growing mycobacteria (RGMs) and slow growing mycobacteria (SGM) [2]. *Mycobacterium mucogenicum* *(M. mucogenicum)* belongs to the RGM group of RGM, which and is considered to be an environmental microorganism with a worldwide distribution. It is associated with a wide spectrum of clinical diseases, including osteomyelitis, respiratory tract, bloodstream, and disseminated infections in both immunocompetent and immunosuppressed individuals [3]. However, time-consuming techniques and low detection rates for identifying this pathogen usually leads to delayed or missed diagnosis. So, we need a rapid and boardbroad-spectrum method to identify some rare pathogens. Next-generation sequencing (NGS) is an unbiased approach whose RefSeq contains 4,152 whole whole-genome sequences of viral taxa, 3,446 bacteralbacterial genomes or scaffolds, 206 human pathogenic fungi related to human infection, and 140 human parasites associated with human diseases. It NGS identifies the nucleotides in the targeted samples and compares the detected nucleotides against the catalogue library of pathogens, thereby listing the possible causative agents in the clinical samples [4-7]. However, there are little few reports in of formalin-fixed, paraffin-embedded (FFPE) specimens., And and whether the clinical significance of detection results using FFPE specimens is useful or not is unclear.

Here, we report a case with of disseminated infection with the pathogen identified ascaused by *M. mucogenicum* diagnosed by NGS using FFPE specimens.

DISCUSSION

M. mucogenicum, a ubiquitous RGM, has been recognized as a species since 1995. The organism was first called *M.ycobacterium chelonae*-like organism (MCLO) as causing diseases in humans in 1982, during two outbreaks of peritonitis associated with peritoneal dialysis in the United StatesUSA in 1976 and 1978[10]. *M. mucogenicum* is more closely related to the *M. fortuitum* group by 16S rDNA sequencing than other *M.Mycobacterium* groups [8]. This mucoid surface provides the ability to form a protective biofilm, which contributes to infection of central venous catheters (CVC) and skin and soft- tissue, usually post-traumatically, clinically the more common sites for *M. mucogenicum* infections[11]. Moreover, it can cause respiratory infections, bloodstream infections, oateomyelitisosteomyelitis, and disseminated infections, which is common happened in immunocompromised hosts[3,12]. Some equipments exposed to contaminated water contaminated by *M. mucogenicum* can lead to nosocomial infection, including central central-venous venous-catheter-related and hemodialysis-related infections [1,13].

There was no evidence of immunodeficiency in this our patient. UndoubtedllyUndoubtedly, it's it is very necessary to determine the source of infection. ButHowever, regretfully, we did n't not have the evidence of NTM pneumonia with NTM-infected. We can't could not perform fiber bronchoscope bronchoscopy on her because that she underwent had cardiac insufficiency at the initial examination, and her pneumonia was improved rapidly after anti-NTM treatment. Apparently, itIt is unlikely that the infection was nosocomial. Due to the pulmonary lesions and multiple skin lesions and the good therapeutic effectresponse, it is reasonable to presume that the source route of infection with this microorganism iswas via from the upper to the lower respiratory tract, then go through the bloodstream infection, finally to skin and soft-tissue, that cause the whole infectious process.

As toFor identification of this microorganism, there are several major

methods ~~as follows:~~. The first is conventional culture ~~methodology~~. ~~It~~ Culture is still difficult and delay~~ed to culture~~can lead ~~leading~~ to missed diagnosis ~~by conventional culture methodology~~[14]. The second is DNA sequencing, with 16S rRNA gene, *rpoB*, and *hsp65* being recognized as useful targets[15-17]. ~~But~~ However, due to its targeting, limitations ~~is unavoidable~~ in identification ~~for~~ of uncertain pathogens are unavoidable. The third is ~~Matrix~~matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF). Several investigators have demonstrated that MALDI-TOF mass spectrometry ~~could~~ can accurately identify mycobacteria[18-19]. ~~But~~ However, these methods are not available in many laboratories.

Moreover, ~~the result of~~ biopsy ~~on~~ of the right psoas was not ~~satisfied~~satisfactory. So, we ~~took a try~~tried to perform NGS using FFPE specimens. NGS works well with short nucleic acid sequences, thus, it can in theory be used ~~easily~~ to analyze fragmented DNA and RNA extracted from standard FFPE clinical specimens ~~in theory~~. In ~~the~~ previous research~~es~~, it ~~can be~~has been used for ~~whole~~ whole-genome sequencing, mainly in cancer patients [20-21]. Using FFPE tissues for pathogen identification ~~was~~ has also been reported in recent years, such as 16S ~~PCR~~ polymerase chain reaction from brain tissue [22], RNA sequencing of 1918 influenza samples [23] and diagnosis of corneal infection~~s diagnosis~~ [24].

To our knowledge, this is the first report ~~on~~ of *M. mucogenicum* confirmed by ~~the~~ NGS using FFPE specimens. ~~In this study, it is~~It was feasible to use metagenomic NGS of DNA extracted from FFPE clinical specimens to identify the causative microorganism. This method holds ~~great~~ promise for the ~~relatively~~ rapid detection of microorganisms, including rare pathogens ~~and~~ in cases in which conditional cultures ~~were~~ have not been attempted or have failed to yield positive results.

After ~~a~~ combination therapy ~~of~~ with clarithromycin, doxycycline and TMP-~~-~~SMX, the patient was treated for ~~over~~ > 12 mo~~nths~~, and ~~the~~ improvement was observed. ~~But~~ However, the optimal duration of

antimicrobial therapy for disseminated infection with *M. mucogenicum* ~~related~~ is unknown. It is certain that prolonged therapy for ~~one to two~~1–2 years ~~even more~~ contributes to ~~eradicate~~ eradication of infection and reduced ~~the~~ chance of ~~the~~ recurrence [1].