

## A Genetic Identification of Candida Species Causing Intravenous Catheter-Associated Candidemia in Heart Failure Patients

**Authors :** Seyed Reza Aghili, Tahereh Shokohi, Shirin Sadat Hashemi Fesharaki, Mohammad Ali Boroumand, Bahar Salmanian

**Abstract :** Introduction: Intravenous catheter-associated fungal infection as nosocomial infection continue to be a deep problem among hospitalized patients, decreasing quality of life and adding healthcare costs. The capacity of catheters in the spread of candidemia in heart failure patients is obvious. The aim of this study was to evaluate the prevalence and genetic identification of Candida species in heart disorder patients. Material and Methods: This study was conducted in Tehran Hospital of Cardiology Center (Tehran, Iran, 2014) during 1.5 years on the patients hospitalized for at least 7 days and who had central or peripheral vein catheter. Culture of catheters, blood and skin of the location of catheter insertion were applied for detecting Candida colonies in 223 patients. Identification of Candida species was made on the basis of a combination of various phenotypic methods and confirmed by sequencing the ITS1-5.8S-ITS2 region amplified from the genomic DNA using PCR and the NCBI BLAST. Results: Of the 223 patients samples tested, we identified totally 15 Candida isolates obtained from 9 (4.04%) catheter cultures, 3 (1.35%) blood cultures and 2 (0.90%) skin cultures of the catheter insertion areas. On the base of ITS region sequencing, out of nine Candida isolates from catheter, 5(55.6%) *C. albicans*, 2(22.2%) *C. glabrata*, 1(11.1%) *C. membranifaciens* and 1 (11.1%) *C. tropicalis* were identified. Among three Candida isolates from blood culture, *C. tropicalis*, *C. carpophila* and *C. membranifaciens* were identified. Non-candida yeast isolated from one blood culture was *Cryptococcus albidus*. One case of *C. glabrata* and one case of *Candida albicans* were isolated from skin culture of the catheter insertion areas in patients with positive catheter culture. In these patients, ITS region of rDNA sequence showed a similarity between *Candida* isolated from the skin and catheter. However, the blood samples of these patients were negative for fungal growth. We report two cases of catheter-related candidemia caused by *C. membranifaciens* and *C. tropicalis* on the base of genetic similarity of species isolated from blood and catheter which were treated successfully with intravenous fluconazole and catheter removal. In phenotypic identification methods, we could only identify *C. albicans* and *C. tropicalis* and other yeast isolates were diagnosed as *Candida* sp. Discussion: Although more than 200 species of *Candida* have been identified, only a few cause diseases in humans. There is some evidence that non-*albicans* infections are increasing. Many risk factors, including prior antibiotic therapy, use of a central venous catheter, surgery, and parenteral nutrition are considered to be associated with candidemia in hospitalized heart failure patients. Identifying the route of infection in candidemia is difficult. Non-*albicans* candida as the cause of candidemia is increasing dramatically. By using conventional method, many non-*albicans* isolates remain unidentified. So, using more sensitive and specific molecular genetic sequencing to clarify the aspects of epidemiology of the unknown candida species infections is essential. The positive blood and catheter cultures for candida isolates and high percentage of similarity of their ITS region of rDNA sequence in these two patients confirmed the diagnosis of intravenous catheter-associated candidemia.

**Keywords :** catheter-associated infections, heart failure patient, molecular genetic sequencing, ITS region of rDNA, Candidemia

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