

## Molecular diagnosis of *Candidemia* of intensive care unit patients based on sequencing analysis of ITS regions

Zaidan Khlaif Imran<sup>1\*</sup> and Zahra Wanas Alshammry<sup>2</sup>

1,2 All women Science college ,Babylon University, Hilla. Iraq

**Abstract :** Invasive candidiasis (IC) bears high risk of morbidity and mortality in the intensive care units (ICU). The *Candida* spp was the main cause of hospitalized bloodstream infections and it is associated with mortality highly rate. ICU receive huge number of patients exposed to multi-accidents types such as terrorist attacks; Cerebrovascular accidents (CVA), etc., most of these cases lead to penetration of *Candida* spp to blood stream. The aim of the study was prospective, accurate and rapid identification molecular methods for detection of *Candida* from blood stream and oral infections in intensive care units in Iraq. 400 samples clinically diagnosed candidemia were collected over a period from November / 2015 to April / 2016 from ICU of Margan Teaching Hospital and Hilla Teaching Hospital in the province of Babylon, Iraq, the Middle East. Out of 264 blood samples (53) were culture positive (32n=male, 21n=female), while 71 out of 136 oral swabs were culture positive. Out of which 63.8% isolates were *C. parapsilosis* 20.34% were *C. albicans* 12.7%, *C. membranifaciens* 2.97% and 0.25% for *C. sake*. Our conclusion : This study gave more attention of the risk factor of candidemia, and showed many *Candida* spp were penetrate blood stream and showed unique genetic polymorphism patterns of *Candida* in Iraq. The new recorded for the *C. parapsilosis*, *C. sake* and *C. membranifaciens* from blood samples for the first time in Iraq based on sequencing analysis of the whole ITS region and the ITS2 of the rDNA emphasizes the low precise of conventional identification methods.

**Keywords :** Invasive candidiasis, ITS and ITS2 sequencing analysis, multiple alignment sequence.