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Sequencing of CA-INT-L gene of Candida Spp. In infected urinary tract among Iraqi women

Lina Mohammed Kassid

College of Education for Pure Science Ibn-Al-Haitham, University of Baghdad, Baghdad, Iraq

Atyaf Saied Hamied

College of Education for Pure Science Ibn-Al-Haitham, University of Baghdad, Baghdad, Iraq

Email: atyaf.s.h@ihcoedu.uobaghdad.edu.iq

Abstract--The most common nosocomial fungal infection in hospitals is urinary tract candidiasis. *Candida albicans* is the most prevalent cause of nosocomial fungal urinary tract infections, however *Candida* species distribution is changing rapidly. At the same time, the rise in urinary tract candidiasis has resulted in the emergence of antifungal-resistant *Candida* species. This study aimed to diagnose *Candida* Spp. In women with UTI and reveal the nucleotides sequences of CA-INT-L Gene to look for mutation within the gene. This study included 100 women patients suffering from urinary tract infections and vaginal swabs samples from those individuals were taken to identify the presence of *Candida*. They were between the ages of 22 and 67. *Candida* identification has been accomplished using a variety of chemical and microscopically techniques. 100 samples have been clinically diagnosed with *Candida* Spp. But only 62 of the samples were positive by Vitik. This number has also reduced to only 25 after using the PCR. The sequence of the CA-INT-L showed different variations within the gene of the isolates.

Keywords---Sequencing, urinary, among Iraqi

Introduction

Candida is a kind of microbe found in the gastrointestinal tract. (Crook, 1984; Truss, 1981). *Candida* spp. infections are commonly referred to as candidiasis (Schuster and Fisher 2022 ; Hamied , 2021)

Bloating, gas, diarrhea, and stomach cramps are some of the symptoms of candidiasis. Other symptoms include headaches, sinusitis, palpitations, and food and environmental sensitivities (Kogan, Castillo, and Barber 2016). When

Candida is present as a fungus in the intestines, the rhizomes pierce the gut walls, and endotoxins from the Candida overgrowth begin to permeate the rest of the body, this is known as polysystemic candidiasis (Basmaciyan et al. 2019). Candidiasis is the most common fungal infection, especially in people who have a weakened immune system. The use of long-acting antibiotics, immunosuppressive medications, and patients with HIV infection all contribute to a high prevalence of candidiasis (Arya N. R and Naureen B. Rafiq, 2022).

According to Abi-Said et al. (1997), the genus Candida contains approximately 154 species. Six species are the most often isolated from human illnesses. Candida albicans is the most common of these species. Candida tropicalis, Candida glabrata, Candida parapsilosis, Candida krusei, and Candida lusitanae have all been identified as Candida infection causal agents. (Mohsin and Ali, 2021)

Candida albicans is the most prevalent pathogen isolated from urine, accounting for 50-70 percent of all pathogens identified. The next most prevalent species, Candida glabrata and Candida tropicalis, respectively account for 10-35 percent of cases. Candidaemia caused by C. glabrata is becoming more common in specific types of individuals, such as those with hematological malignancies and transplant recipients. Approximately 50% of all identified species in the biggest prospective study of kidney transplant recipients were C. glabrata, and 30% were C. albicans (Kim et al. 2019 ; Othman et al , 2018).

Method

This study comprised 100 women patients with urinary tract infections who visited the urology department at Al-yarmook teaching hospital, and vaginal swabs samples from those individuals were taken to identify the presence of Candida. They were between the ages of 22 and 67. Candida identification has been accomplished using a variety of chemical and microscopically techniques.

DNA extraction

The vaginal swabs samples have been briefly centrifuged. Then the DNA have been extracted from the swabs samples by using the commercial kit Fungal/Bacterial/ Yeast DNA MiniPrep™, (Catalog No. D6005). After the completion of the DNA extraction the eluted DNA have subjected to electrophoresis in order to ensure the accuracy of DNA extraction technique.

Polymerase chain reaction of INT gene

In order to amplify the target region within the CA-INT-L gene, a mixture prepared in a new sterile tube for each sample. The mixture reaction contains the following components; 5µl of Taq PCR PreMix, 10 picomols/µl (1 µl) of each sense primer and its anti-sense, 1.5µl of extracted DNA, then the final volume completed to 25µl by adding 16.5 µl of nuclease free water. The primers sequences that have been used to target the specific region are listed in the table (1). After the addition of each components, the tubes have sealed and placed in the thermal cycler machine and programmed as stated in table (2).

Table 1
Primer pair sequence targets the CA-INT-L gene

Primer	Sequence	Tm (°C)	GC (%)	Product size
Forward	5'ATAAGGGAAGTCGGCAAATAGATCCGTA3'	59.3	40 %	532 base pair
Reverse	5'CCTTGGCTGTGGTTTCGCTAGATAGTAGAT3'	60.9	46 %	

Table 2
The cycle steps and holdings conditions of the PCR programs for the CA-INT-L gene amplification

No.	Phase	Tm (°C)	Time	No. of cycle
1-	Initial Denaturation	95°C	3 min.	1 cycle
2-	Denaturation -2	95°C	45sec	35 cycle
3-	Annealing	72°C	45sec	
4-	Extension-1	72°C	1 min	
5-	Extension -2	72°C	7 min.	1 cycle

Results

The samples that have been collected were reached 100 samples that have already diagnosed with Candidiasis, but after using the Vitik system it has shown that only 62 of the samples were positive. This number has also reduced to only 25 after using the PCR. This distribution of the samples are shown in the figure (1).

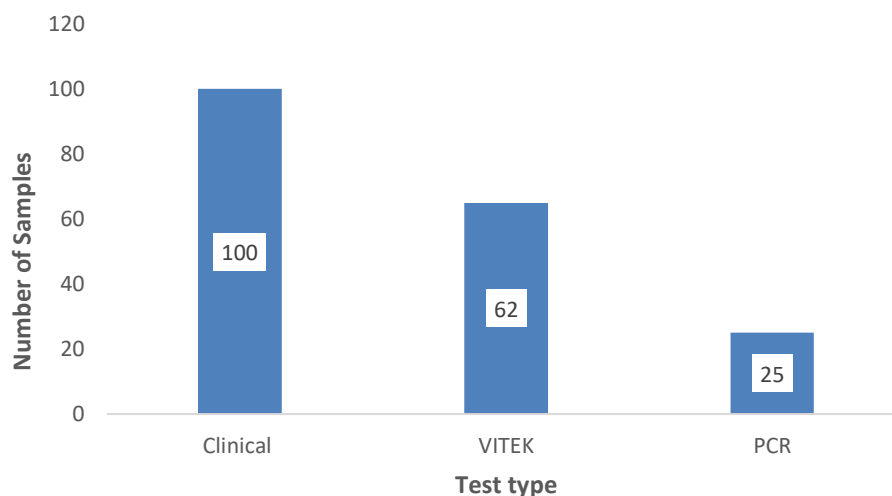


Figure (1); distribution of the positive samples according to the test that have been used

The amplified products have went through gel electrophoresis and the results of gel documentation are shown in figure (2). The results showed sharp single band with 532 base pair long.

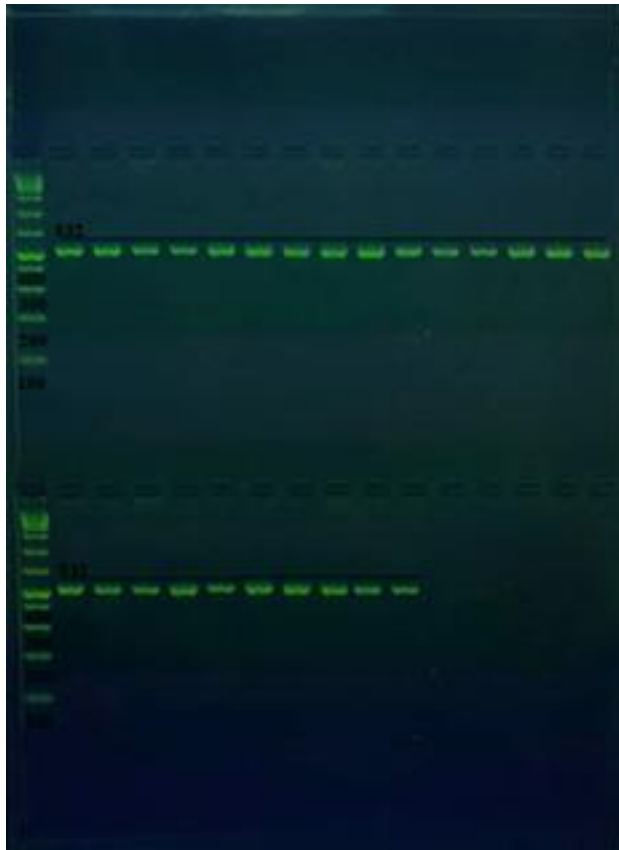


Figure (2) PCR product the band size 532 bp. The product was electrophoresis on 2% agarose at 5 volt/cm². 1x TBE buffer for 1:30 hours. N: DNA ladder (1000Plus).

The amplified products have been sent to Macrogen company for sequencing, and once the results have received the nucleotides sequences have been analyzed by BLASTn tool from NCBI database and the results are shown in the figure (3). The results of sequences have been aligned to plus strand of *Candida albicans* isolate region internal transcribed spacer 1 under the ID; ON010023.1 and scored 187 bits the length of database sequence showed 95% similarities with the sequences of that obtained from this study.

Candida albicans						
No.	Type of substitution	Location	Nucleotide	Sequence with compare ID	Source	Identities
1	Transversion	56	G/C	ID: ON010023.1	Candida albicans isolate SAMAKA_N17_NF internal transcribed spacer 1	95%
	Transversion	61	A/C			
	Transition	65	G/A			
	Transition	67	G/A			
	Gap	79	T			
	Gap	84	A			
4	Transversion	188	A/C	ID: ON010023.1	Candida albicans isolate SAMAKA_N17_NF internal transcribed spacer 1	95%
	Transition	194	G/A			
	Transition	204	A/G			
	Gap	206	T			
	Gap	211	A			
	Transition	223	G/A			
	Transition	246	C/T			
	Transition	259	G/A			
6	Transition	134	T/C	ID: ON010023.1	Candida albicans isolate SAMAKA_N17_NF internal transcribed spacer 1	95%
	Transition	140	T/C			
	Transition	174	T/C			

	Transition	177	A/G			
	Transition	180	G/A			
7	Transition	140	A/G	ID: ON010023.1	Candida albicans isolate SAMAKA_N17_NF internal transcribed spacer 1	95%
	Transition	155	C/T			
	Transversion	156	G/C			
	Transition	188	A/C			
	Transversion	189	C/G			
	Transversion	194	G/A			
	Gap	206	T			
	Gap	211	A			
	Transversion	224	G/A			
8	Transition	155	C/T	ID: ON010023.1	Candida albicans isolate SAMAKA_N17_NF internal transcribed spacer 1	95%
	Transversion	156	G/C			
	Transversion	174	C/A			
	Transversion	175	C/G			
	Transition	188	A/C			
	Transition	194	G/A			

	n					
	Gap	206	T			
	Gap	211	A			
	Transition	224	G/A			
9	Transition	188	A/C	ID: ON010023.1	Candida albicans isolate SAMAKA_N17_NF internal transcribed spacer 1	95%
	Transition	189	C/G			
	Transition	192	G/A			
	Transition	194	G/A			
	Gap	245	T			
	Gap	249	C			
	Transition	223	G/A			
	Transition	246	C/T			
	Transition	259	G/A			

Discussion

Invasive candidiasis (IC) is a leading cause of death and morbidity in the United States. *Candida* spp. account for 8 to 9% of all nosocomial bloodstream hospital acquired infection, with the risk being greater in the intensive care unit (ICU) and among cancer patients. Premortem diagnosis is not made in about half of the instances (Edmond et al., 1999).

Blood culture is the current gold standard for diagnosing IC, and it takes 24 to 48 hours for it to turn positive. It's possible that identifying the exact *Candida* sp. will take much longer, delaying antifungal therapy (Horn et al., 2009). Studies consistently demonstrate that delaying proper antifungal medication for 12 to 48 hours is linked with considerably higher all-cause mortality that is independent of other risk factors; adjusted odds ratios vary from 2.17 to 4.75 (Bassetti et al., 2007).

Various non-culture laboratory approaches for quick IC diagnosis have been developed during the last few decades. The polymerase chain reaction (PCR) is a promising technique for identifying fungal diseases, with high throughput, sensitivity, and specificity. A meta-analysis of 54 trials found that the pooled sensitivity and specificity for the diagnosis of candidemia were 0.95 and 0.92, respectively (Avni et al., 2011). This study succeeded to detect the presence of *Candida* in vaginal swabs samples, in contrast to what have recommended by previous study using the whole blood as the optimal sample for the detection of *Candida* DNA (He et al., 2020).

The results of PCR failed to showed false negative samples, this results disagree with previous study that showed two false-negative results by PCR assay (sensitivity: 94.1%) (Jiang et al. 2016). Targeting the 18sRNA gene have been previously showed numerous benefits upon using other regions. Previous study has demonstrated the efficacy of the 18S rRNA gene to detect fungal pathogen in clinical samples (Embong et al. 2008).

The sequence alignment results of the isolated samples to the NCBI database showed high number of variations in the isolated samples of this study, as it has shown previously by earlier study that loss-of-heterozygosity events were commonly associated with acquired resistance (Ford et al., 2005).

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