

Efflux Pump Mediated Resistance to Fluconazole in *Candida glabrata* in Vulvovaginal Candidiasis Patients

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Abstract:

Vulvovaginal candidiasis is a common fungal infection that affects the female genital system. Resistance to antifungals is an emergent problem worldwide.

We aimed to detect the prevalence of different Candida species associated with vulvovaginal candidiasis, determine their antifungal susceptibility pattern, and evaluate the molecular mechanisms associated with Fluconazole resistance.

Methodology: This study included 300 patients. Candida species have been identified phenotypically. Antifungal susceptibility was tested using a disc diffusion method. The molecular mechanisms of Fluconazole-resistance were determined by analyzing the expression levels of Fluconazole target, efflux pump and efflux pump-regulator genes by RT-PCR.

Results: Candida spp were detected in 75/300 (25%) of cases. The most frequently isolated species was C. albicans (61.8%), whereas the predominant species of non-albicans was C. glabrata (29%). Nystatin was the most effective agent. Fluconazole-resistance was observed markedly in C. glabrata (54.5%), and efflux-pump was the predominant mechanism of resistance, which was associated with overexpressed CgPDR1, CgCDR1 and CgSNQ2 genes. Upregulation of the efflux-pump genes and their regulator were associated with cross-resistance to different azoles.

Conclusion: C. glabrata is a common cause of non-albicans vulvovaginal candidiasis. The majority of clinical resistance in C. glabrata is attributed to the upregulation of efflux-pump genes.

Keywords: Vulvovaginal candidiasis; *C. glabrata*; Fluconazole resistance; efflux pump.

1. INTRODUCTION:

One of the most common fungal infections affecting women of childbearing age is vulvovaginal candidiasis (VVC). *Candida albicans* (*C. albicans*) is the most frequent cause of

VVC. There is, nevertheless, a marked change in the aetiology of VVC to the non-albicans *Candida* (NAC) species. The majority of NAC vulvovaginitis is caused by *C. glabrata* (1). Vulvovaginal candidiasis encountered at least one time by the majority of the women of reproductive age all through their lifetime and some of them experience recurrence (2). While an acute, single, simple episode of vaginitis can be diagnosed and treated easily, women infected with resistant species may visit many health care workers with several tried therapeutic agents. These patients frequently act as a therapeutic confront for health care providers. Besides, pain, discomfort, anxiety, and disturbance in sexual function, vaginal candidiasis may increase a women's risk of getting other sexually transmitted diseases (3).

Azole drugs are frequently prescribed for *Candida* infections. The azole antifungals inhibit *Candida* by targeting lanosterol 14- α -demethylase, a crucial step in biosynthesis of ergosterol. Fluconazole is the most common azole antifungal agent, while it is used as first-line for the treatment candidiasis, its efficacy has been decreased by the development of resistance, especially in *C. glabrata* (4).

Resistance to antifungal drugs is an emergent problem worldwide, resulting in increased difficulty of the choice of effective antifungal therapy (5).

Knowledge of the basis of resistance to azole antifungal is important to conserve this class of antifungal and get rid of this clinical problem (4). In the azole-resistant *C. glabrata* isolates, regular constitutive upregulation of multidrug transporters of the ATP-binding cassette transporter was detected. These transporters are encoded by several genes including *CgCDR1*, *CgCDR2*, and *CgSNQ2* and regulated by the zinc finger transcription factor *CgPdr1*(6). Increasing reports of azole resistance in *C. glabrata* isolates from Egypt have been published over the past decade (7, 8, 9), however, literature addressing their molecular mechanisms is scarce.

2. MATERIALS AND METHOD

2.1. Study Design

Between August 2018 and June 2019, a hospital-based cross-sectional study of 300 patients presented with a clinical picture of VVC presented at the outpatient clinics of Obstetrics and Gynecology at Al-Azhar Assiut University Hospital was performed. Patients who had uterine bleeding or used vaginal douching within the last few hours were excluded from the study. The ethical approval of the research was received from the ethics committee of the Faculty of Medicine, Assiut University, and carried out in compliance with the terms of the Helsinki Declaration (approval number 17-200-164). Informed consent from all the included patients was obtained before the collection of specimens. Patients' clinical data and associated risk factors were assessed.

2.2. Sample processing

Vaginal swabs were collected from the posterior fornix of the vagina by sterile swabs through Cusco's speculum. All swabs were inoculated on SDA (Himedia, Mumbai, India) and incubated for 24- 48 hours at 37°C. By colony morphology and Gram stain, *Candida* isolates on SDA have been defined.

2.3. Phenotypic identification of different *Candida* species

The isolated yeasts have been identified phenotypically by Germ tube formation (10), growth at 45°C for differentiation between *C. albicans* isolates from the *C.dubliniensis* isolates (12), Cornmeal agar (Himedia, Mumbai, India) (13). Hicrome *Candida* Differential agar (Himedia,

Mumbai, India), and KB006 HiCandida Identification Kit (Himedia, Mumbai, India) which were performed according to manufacturers' instructions.

2.4. Antifungal susceptibility

Six antifungal agents, Fluconazole (25 µg), Itraconazole (10 µg), Voriconazole (1 µg), Nystatin (100 U), Miconazole (50 µg) and Amphotericin-B (100 U), were used to perform an antifungal susceptibility test on *Candida* isolates by disc diffusion method (Himedia, India). In brief, an inoculum with a turbidity of 0.5 McFarland level for each isolate in sterile 0.85 % saline was streaked on Mueller-Hinton agar complemented with 0.5 µg/ml methylene blue dye and 2% glucose (11), plates were incubated at 35°C for 24h. Inhibition zones were interpreted according to CLSI interpretive breakpoints (12).

2.5. Fluconazole resistance genes expression quantification by Real time PCR

2.5.1. RNA extraction

Total RNA has been derived from *C. glabrata* isolates using Direct-zolTM RNA miniprep reagent (Cat.No. R2051) (Zymo research, California, USA) according to the manufacturer's instructions. Briefly, the isolates have been grown for 24 hours at 37 °C in yeast peptone dextrose (YPD) broth (Himedia, India). Then 1ml of each specimen was centrifuged for two minutes at 2000 xg, the pellet was homogenized in 600 µl of TRIzolTM reagent with vortex, the homogenate was centrifuged at 12000 xg for 2 min, and then the supernatant moved to the RNase-free Eppendorf tube, adding an equivalent volume of ethanol (95-100%) to the lysed sample in TRIzolTM reagent and was well mixed, then the mixture was moved into a Zymo-Spin Column after three washes and DNase I treatment. The RNA was eluted in an RNase-free Eppendorf tube, the RNA concentration and purity were measured using a NanoDrop spectrophotometer (NanoDrop 2000C, ThermoFisher, USA).

2.5.2. Reverse transcription

Reverse transcription has been performed on 500 ng of total RNA using COSMO cDNA synthesis Kit (Willowfort, UK) according to manufacturers' instructions. The reaction occurred in a thermal cycler (T3 Thermocycler, Germany) with a single amplification cycle and incubation time of 5 minutes at 25°C, 15 minutes at 45°C and 5 minutes at 85°C. Under the same reverse transcription reaction conditions, all the samples tested were transcribed.

2.5.3. Real time-qPCR analysis

The expression levels of Fluconazole resistance genes (*CgERG11*, *CgCDR1*, *CgSNQ2*, and *CgPDR1*), as well as the housekeeping gene (*β actin* used as a normalizing gene), were carried out by using quantitative real-time PCR. Primers used were tested by primer BLAST program (<https://www.ncbi.nlm.nih.gov/tools/primer-blast>) and were mentioned in the table (1). The expression levels of genes were performed using the Step One PlusTM Real-Time PCR Systems (Applied Biosystems, USA) in 20 µl PCR reaction mixture containing, 10 µl HERA Plus SYBR Green Master mix (Willowfort, UK), 1 µl of each primer solution (10 µM), 5 µl cDNA sample and water was added to complete the volume to 20 µl. The conditions for thermal cycling were 95°C for 4 minutes, followed by 40 cycles of 15 s at 95°C and 30 s at 60°C, followed by melting curve analysis. The relative expression was determined using the 2^{-ΔΔC_t} Method (13). Fluconazole susceptible *C. glabrata* clinical isolates were used as a calibrator isolate for gene expression analysis.

2.6. Statistical analyses:

GraphPad Prism 8.4 (GraphPad, La Jolla, CA, USA) has been used for statistical analyses. Data were expressed as mean ± standard deviation or standard error. Using the χ^2 or Fisher's

exact test, categorical variables were compared, and the Mann-Whitney U test was used for continuous variables. At $P < 0.05$, the difference was statistically significant.

Table 1. Primers for RT-qPCR analysis of target gene expression(13).

Gene	Primer and probe sequence (5'→3')	Gene number
<i>CgACT1</i>	F: TTGGACTCTGGTGACGGTGTTA R: AAATAGCGTGTGGCAAAGAGAA	CAGL0K12694g
<i>CgERG11</i>	F: TGTCTTGATGGGTGGTCAACA R: CTGGTCTTTCAGCCAAATGCA	CAGL0E04334g
<i>CgCDR1</i>	F: AGATGTGTTGGTTCTGTCTCAAAGAC R: CCGGAATACATTGACAAACCA	CAGL0M01760g
<i>CgSNQ2</i>	F: GCGGAAGATCGCACGAAG R: GGCGCGAGCGGGATA	CAGL0I04862g
<i>CgPDR1</i>	F: AACGATTATTCAATTGCAACAACG R: CCTCACAATAAGGAAAGTCTGCG	CAGL0A00451g

3. RESULTS

3.1. Prevalence of vulvovaginal candidiasis patients

Three hundred vulvovaginal swabs were obtained from 300 patients presented with a clinical picture indicative of VVC and cultured on SDA, Candida isolates were detected in 75 patients. Seventy-six Candida isolates were recovered from 75 patients as one patient had a mixed infection by two different isolates.

3.2. Risk factors associated with vulvovaginal candidiasis:

In this study the association between VVC and many risk factors (age, hormonal use, antibiotics, steroid, IUD, DM, history of vaginitis and frequent intravaginal douches) were assessed; these risk factors are listed in table (2). The age of the studied patients ranged between 18 to 55 years with mean 34.5 ± 8.9 years. Out of the 75 vulvovaginal candidiasis patients 69 (92%) aged ≤ 40 years, the remaining 6 patients (8%) aged above 40 years with mean age 32.6 ± 7.1 . In this study, the statistical analysis showed that women ≤ 40 years of age had a threefold higher risk of developing VVC than older women (OR=3.1, $P=0.009$), also this study showed that patients with frequent intravaginal douching were at a higher risk for acquiring VVC. ($P = 0.00$). Moreover, ladies who had a prior history of vaginitis were more probable to have VVC than those who did not (RR: 1.9, OR: 2.3, $P= 0.002$). While no statistically significant difference was found among patients with VVC and vulvovaginitis non-candidiasis patients regarding the consumption of current hormonal contraception, the recent usage of antibiotics, taking steroid therapy, presenting with IUD in situ ($P > 0.05$).

3.3. Identification of Candida species:

Based on the results of the different phenotypic tests used for the identification of the different Candida species, the predominant isolated species was *C. albicans* (47 isolates, 61.8%) followed by *C. glabrata* (22 isolates, 29%), *C. krusei* (5 isolates, 6.6%), and lastly *C. parapsilosis* (2 isolates, 2.6%). 74 vulvovaginal swabs (98.3%) showed the growth of only one species of Candida while one sample (1.3%) showed the growth of more than one species of Candida (*C. albicans* and *C. glabrata*).

3.4. Antifungal susceptibility:

The sensitivity of 76 Candida isolates to antifungals were tested for 2 polyenes (Nystatin and Amphotericin B) and 4 azoles (Fluconazole, Voriconazole, Itraconazole, and Miconazole) by

the disc diffusion method, Nystatin exhibited an excellent efficacy against all *Candida* spp except one *C. glabrata* isolate was resistant (1.3%). A good activity of Amphotericin B was detected against *C. parapsilosis*, *C. albicans* and *C. glabrata* (100%, 89.8 and 81.8%) respectively, but less effect was observed against *C. krusei* (60%). In this study susceptibility to different azoles drugs was various among different *Candida* spp. Fluconazole and Voriconazole showed outstanding efficacy against 47 *C. albicans* isolate with a sensitivity of 100%, less susceptibility of *C. albicans* was detected to Itraconazole (80.9%) and notably little effect of Miconazole against *C. albicans* (23.4%) was recorded. Regarding *C. glabrata* Miconazole was the most effective azole drug with (95.5%) sensitivity. Voriconazole showed (68.1%) sensitivity, it has been observed that Fluconazole and Itraconazole had the least effect on *C. glabrata* with (45.5 % and 36.4%) sensitivity. Regarding the 12 Fluconazole-resistant *C. glabrata* isolates a detailed analysis of cross-resistance among the four tested azoles revealed that one isolate was resistant to all azoles, three isolates were resistant to three azoles (Fluconazole, Itraconazole, and Voriconazole), and 8 isolates were resistant to itraconazole and Fluconazole. *C. krusei* was the most resistant species to azole drugs among different *Candida* species in this study; all isolates were resistant to Fluconazole and Itraconazole. Miconazole and Voriconazole, resistance rates were 60% and 40%, respectively. *C. parapsilosis* two isolates showed complete susceptibility to all tested azoles as shown in table 3.

Table 2. Risk factors of vulvovaginal candidiasis:

Risk factor	Total No. of patients (300)	No. of VVC	% of infection	Relative risk	OR* (95% CI)	P-value
Age					3.1	
≤ 40	272	69	28	2.5	(1.27-7.61)	
> 40	28	6	11.1			0.009*
Hormonal use					1.63	
Yes	45	15	33.3	1.42	(0.82-3.22)	0.161
No	255	60	26.6			
Antibiotics					0.732	
Yes	25	5	20	0.79	(0.265-2.024)	0.55
No	275	70	25.5			
Steroid					2.47	
Yes	9	4	44.4	1.82	(0.648-9.48)	0.17
No	291	71	24.4			
IUD use					0.32	
Yes	20	2	10	0.38	(0.071-1.39)	0.18
No	280	73	26.1			
DM					0.493	
Yes	7	1	14.3	0.566	(0.058-4.1)	0.44
No	293	74	25.3			
History of vaginitis					2.3	
Yes	146	48	32.9	1.9	(1.34-3.95)	0.002*
No	154	27	9.2			
Frequency of intravaginal douching					0.32	
Occasionally or never	156	54	34.6	0.42	(0.183-0.569)	0.00*
Frequently	144	21	14.5			

*OR: odds ratio *p-value <0.05: statistically significant

Table 3. Analysis of antifungal sensitivity pattern in different *Candida* spp. by disc diffusion method:

Species (No.)	Antifungal	Susceptible		Susceptible dose dependent		Resistant	
		N0.	%	N0.	%	N0.	%
<i>C. albicans</i> (47)	Fluconazole	47	100	0	0	0	0
	Voriconazole	47	100	0	0	0	0
	Nystatin	47	100	0	0	0	0
	Amphotricin	42	89.8	3	6.3	2	4.3
	Itraconazole	38	80.9	5	10.6	4	8.5
	Miconazole	11	23.4	17	36.2	19	40.4
<i>C. glabrata</i> (22)	Fluconazole	10	45.5	0	0	12	54.5
	Voriconazole	15	68.1	3	13.6	4	18.3
	Nystatin	21	95.5	0	0	1	4.5
	Amphotericin	17	77.3		0	5	22.7
	Itraconazole	8	36.4	2	9.1	12	54.5
	Miconazole	21	95.5	0	0	1	4.5
<i>C. kurzi</i> (5)	Fluconazole	0	0	0	0	5	100
	Voriconazole	3	60	0	0	2	40
	Nystatin	5	100	0	0	0	0
	Amphotricin	3	60	1	20	1	20
	Itraconazole	0	0	0	0	5	100
	Miconazole	2	40	0	0	3	60
<i>C. parapsilosis</i> (2)	Fluconazole	2	100	0	0	0	0
	Voriconazole	2	100	0	0	0	0
	Nystatin	2	100	0	0	0	0
	Amphotricin	2	100	0	0	0	0
	Itraconazole	2	100	0	0	0	0
	Miconazole	2	100	0	0	0	0

3.5 Expression of Fluconazole resistance genes by quantitative real-time PCR:

The expression levels of Fluconazole resistance genes (*ERG11*, *CDR1*, *SNQ2*, and *PDR1*) in 22 *C. glabrata* isolates were quantified and normalized relative to the housekeeping gene, B-actin.

C. glabrata isolates were the most frequent Fluconazole-resistant candida species in this study; hence they were selected for the evaluation of the molecular mechanisms of resistance to Fluconazole.

Quantitative RT-PCR experiments revealed that the mean relative gene expression levels of *ERG11* was 1.43 ± 0.53 (mean \pm standard error). No statistically significant difference was found in the levels of *ERG11* expression in resistant isolates compared to susceptible isolates (P-value 0.159) (Fig 1a).

The mean relative gene expression level of *CDR1* was 3.45 ± 0.69 , a statistically significant difference in the *CDR1* expression level was detected between resistant isolates and susceptible isolates (P < 0.0001) (Fig 1 b). The mean relative gene expression levels of *SNQ2* gene was 3.71 ± 1.32 , with a statistically significant difference in the *SNQ2* expression levels between resistant and susceptible isolates (P = 0.038) (Fig 1c).

As regards, *PDR1* gene the mean relative gene expression levels was 1.56 ± 0.17 , the *PDR1* expression levels showed a statistically significant difference among resistant and susceptible isolates ($P = 0.0002$) (Fig 1d).

It was observed that the most frequent overexpressed gene in Fluconazole resistant *C. glabrata* isolates was *PDR1* (91.7%), followed by *CDR1* (83.3%) and *SNQ2* (75%), while *EGR11* was overexpressed only in (33.3%).

Simultaneous upregulation of more than one transporter genes of efflux pump mechanism (*CgCDR1* and *CgSNQ2*) and their regulator gene *CgPDR1* was noticed among the studied Fluconazole-resistant *C. glabrata* isolates. It was found that *CgCDR1*, *CgSNQ2*, and *CgPDR1* were simultaneously expressed in six isolates, while *CgCDR1* and *CgPDR1* were concurrently overexpressed in three isolates, two isolates upregulated *CgPDR1* and *CgSNQ2*, and only one isolate upregulated *CgCDR1* and *CgSNQ2* Concurrently.

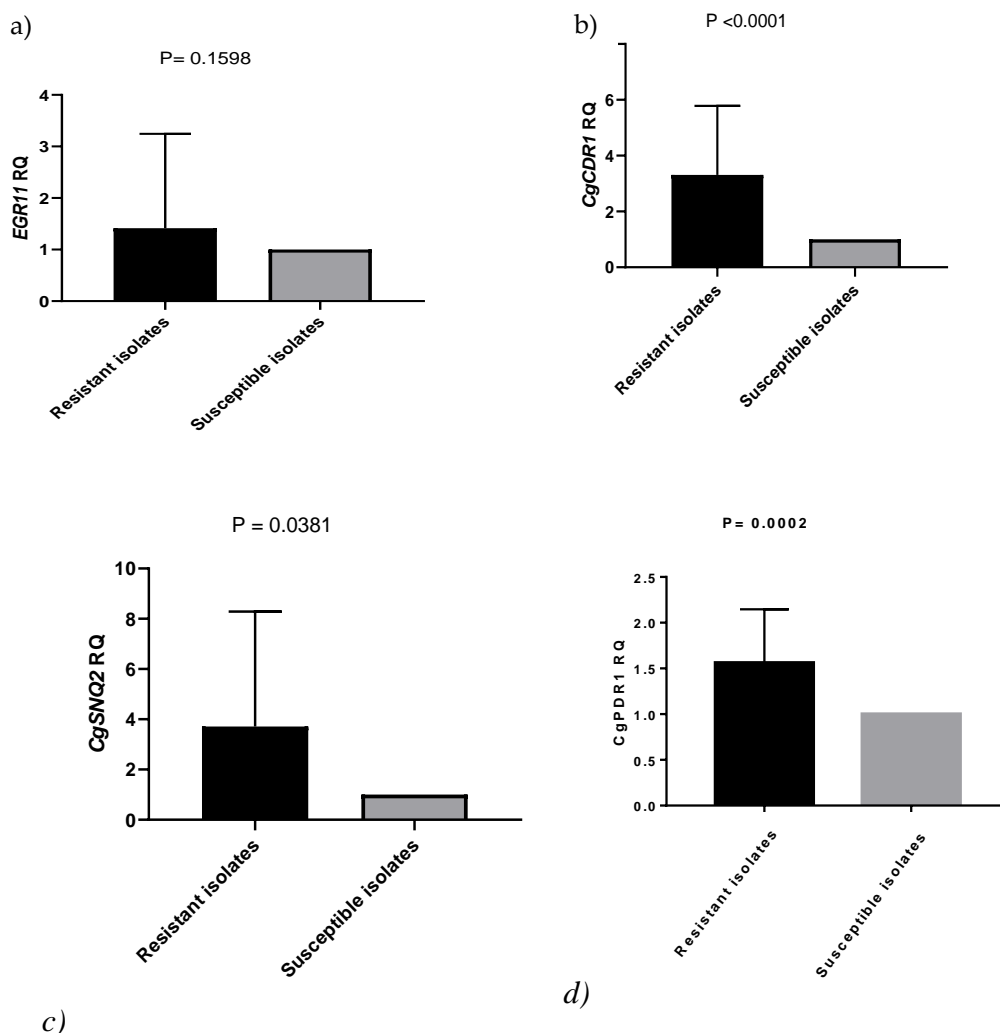


Figure 1. The mean fold change in the expression levels of the different tested genes. a) *CgERG 11* b) *CgCDR1* c) *CgSNQ2* d) *CgPDR1*.

4. DISCUSSION

Vaginal candidiasis is a widespread fungal infection of the female genital system induced mainly by *C. albicans* that may influence large numbers of reproductive-age women (14).

Though vulvovaginal candidiasis is extensively distributed all over the world, some socioeconomic factors can impact its incidence. So, service planning managers should use updated epidemiological data from each area (15). In the current research, the incidence of vulvovaginal candidiasis was 25% of all enrolled vulvovaginitis patients. A nearly similar prevalence rate (26%) was detected in Iran (16) and in Egypt 27.8% (8).

Also, this result is well compared to many other researches showing incidence rates of VVC among 20 % and 30 % (17, 18, 19, 20, 21). Other research, however, recorded a much higher VVC occurrence which accounted for prevalence rates of VVC between 41% and 84.5% (22, 23, 24, 25). In contrast, a much lower frequency of VVC was recorded in Brazil (5.44%) (26). The difference in the numbers of patients for each area, socioeconomic background of specimen patients, patient awareness of personal hygiene, and self-treatment could be attributed to this variation (15).

As the occurrence of VVC between women of reproductive age from different ethnicities and areas is different, it is essential to examine the risk factors for VVC between women of childbearing period in order to provide a reference for the treatment and prevention of VVC (2).

In this study, the association between VVC and many risk factors including age, hormonal use, antibiotics, steroid, IUD, DM, history of vaginitis, and frequent intravaginal douches were assessed.

Out of the 75 Vulvovaginal candidiasis patients 69 (92%) aged ≤ 40 years, the remaining 6 patients (8%) aged above 40 years with mean age 32.6 ± 7.1 .

In this study, the statistical analysis found that women ≤ 40 years of age had a threefold higher risk of developing VVC compared to older women (OR=3.1, P=0.009). This outcome was agreed with Zeng et al, who found that women under the age of 40 had a twofold higher risk of CVV (OR= 2,431, P= 0,032) than older women (2), also other studies reported that the peak of vaginal candidiasis occurs among 20 and 40 years of age (27, 28). This might be attributed to higher sexual activity, use of various contraceptives hormonal and physiological changes in this age group. From the other hand, age progression decreases the influence of the estrogen hormone in ladies that may result in decreased rates of infection in older ladies. The majority of ladies older than 46 years have entered menopause and did not use contraceptives to prevent pregnancy (29).

Also, this study showed higher rates of VVC in patients with frequent intravaginal douching (P =0.00), this result of previous studies agreed with this finding (30, 31). The explanation may be that intravaginal douches may trigger vaginal tissue damage and disrupt the vaginal microecosystem, leading to a decrease in vaginal homeostasis, encouraging yeast growth and thus triggering VVC. In contrast to this, one study detected that the association between intravaginal practices and VVC was not statistically significant (32).

Moreover, in the current work, women who had a previous history of vaginitis were more likely to suffer VVC than those who did not (RR: 1.9, OR: 2.3, P= 0.002). This finding was concordant with some previous epidemiological studies which believed that there was an association between symptomatic episodes of VVC and a history of lower genital tract infection (30, 33).

There was no statistically significant difference between VVC patients and other vulvovaginitis patients regarding the consumption of current hormonal contraception, the recent usage of antibiotics, taking steroid therapy, or presenting with IUD in situ ($P > 0.05$).

Comparable results were detected by Ozcan et al. as they found no statistical association between these risk factors and VVC (34). Na et al also found no relation between oral contraceptive pills and VVC (31). In contrast to these results, Jacob et al. detected a significant association between VVC and the use of gynecological/systemic antibiotics and oral/vaginal contraceptives also Na et al stated that there was a correlation among the use of IUD and VVC (31, 35).

As a result of increased prevalence of non-albicans species and their different antifungal susceptibility profiles, precise detection of *Candida* at the level of the species is essential (36).

Among VVC samples, 74 (98.3%) showed the growth of only one species of *Candida* while one sample (1.3%) showed the growth of two different species of *Candida* (*C. albicans* and *C. glabrata*), this result was in accordance with Amouri et al who mentioned that typically in VVC, One species is defined, however in some ladies two or more species have been isolated (1-10 %) (30), Mahmoudi et al, who have indicated that most vulvovaginal mixed infections are triggered by interactions among *C. albicans* and *C. glabrata*, also agree with this result (37).

In the present study, the predominant isolated species was *C. albicans* (47 isolates, 61.8%) accompanied by *C. glabrata* (22 isolates, 29%), *C. krusei* (5 isolates 6.6%), and lastly *C. parapsilosis* (2 isolates 2.6%).

The most prevalent isolated species became *C. albicans* (61.8 %), while the total prevalence of non-albican species became (38.2 %). Similar result was obtained from Egypt by ElFeky et al. as they reported 60.3% of VVC caused by *C. albicans* while the overall frequency of non-albicans species was 39.7% (38).

A higher rate of *C. albicans* in VVC (86.6%) was reported from a former study in Egypt by El-Sayed and Hamouda, (39), also from Kuwait by Alfouzan et al who reported (73.9%) rate (40).

In contrast to these results regarding the predominance of *C. albicans*, Deorukhkar et al and Jimoh et al detected a higher rate of NAC in VVC (60% and 51.5%), respectively (41, 42).

Recently, there has been a significant change in the etiology of candidiasis among NAC species. In some studies, NAC species now represent 10 % to 45 % of VVC cases. The most frequent reason of NAC-VVC is *C. glabrata*. (43).

C. glabrata is often isolated as a one of the natural flora of healthy individuals. For a long time, it was not considered a significant etiological agent of infections in humans. However, during the last few decades, the occurrence of mucosal and systemic infections induced by *C. glabrata* has risen markedly. This is a consequence of the extensive and widespread usage of broad-spectrum antibiotic therapy and immunosuppressive agents along with (44).

C. glabrata became the second most frequent isolate in the present research (29%) in VVC; similar findings were detected in studies in Saudi Arabia (31%), in Turkey (34.5%), and in Australia (20%) (45, 46, 47).

In contrast to the preceding reports, in the Bitew and Abebaw study, *C. krusei* became the dominant non-albicans of *Candida* species, representing 17.2% of the total isolates (48). In the present study *C. krusei* represented 6.6% of the isolated *Candida*, many studies have reported *C. krusei* rates ranging from 3% to 15.7% (38), (24, 45, 46, 49).

In agreement with the prevalence of *C. parapsilosis* in this study (2.6%), Bitew and Abebaw reported a similar rate (2.3%) of isolation of *C. parapsilosis* in VVC (48).

Due to the widespread usage of over-the-counter antifungal agents and the recovery of clinical isolates which show inherent or acquired resistance to antifungal medicines in vitro susceptibility testing of antifungal agents has become highly significant (50).

The 76 *Candida* isolates were tested for their sensitivity to 2 antifungal belonged to the polyenes group (Nystatin and Amphotericin B) and 4 antifungal belonged to the azoles group (Fluconazole, Voriconazole, Itraconazole, and Miconazole) by the disc diffusion method; Nystatin exhibited an excellent efficacy against all *Candida* spp otherwise, only one *C. glabrata* isolate was resistant, this result agreed with other results reported by Fan et al and Choukri et al (51), (52) who reported the sensitivity rates of different *Candida* species to Nystatin were 100%. This can be explained by Wang et al mentioned that the excellent antifungal efficacy of Nystatin was correlated with comparatively low frequency of use in the clinical environment, in addition to the peculiar mechanism of altering cell membrane permeability (53).

Both Nystatin and Amphotericin B are belonging to the same drug class (polyenes) and have a similar mechanism of action, but Amphotericin B has the advantage that can be taken systemically, in the present study a good activity of Amphotericin B was detected against *C. parapsilosis*, *C. albicans* and *C. glabrata* (100%, 89.8%, 81.8%), respectively. But less effect was observed against *C. krusei* (60%). Similar findings were reported by many studies who revealed that resistance to Amphotericin B is less frequent in the isolates of different *Candida* spp. (38, 49, 54, 55).

In this study susceptibility to different azoles drugs was various among different *Candida* spp. Fluconazole and Voriconazole showed outstanding efficacy against all *C. albicans* isolates, lower susceptibility of *C. albicans* isolates was detected to itraconazole (80.9%) while the notably little effect of Miconazole against *C. albicans* (23.4%) was observed.

No resistance to Fluconazole or very low resistance (0.6%) between vaginal *C. albicans* isolates has been documented in Australian studies in accordance with these results (56) and Kuwait (40). In contrast to these results, lower susceptibility rates of *C. albicans* to Fluconazole were recorded in Brazil studies (68%), India (84%), and from Egypt (89.5%) (57, 49, 38) respectively.

Many studies detected the resistance of *C. glabrata* to many azole antifungals, especially Fluconazole (58, 59, 60, 61, 62, 63).

In this study, *C. glabrata* is less susceptible to azole, which is the most popular agent used to treat VVC, high resistance rate was detected to Fluconazole (54.5%). In line with these

findings, studies from Egypt have documented a similar rate of Fluconazole resistance (50%) (38). On the other hand, Wang et al. detected a marked higher resistance rate of *C. glabrata* to Fluconazole 90.8% (53).

It was observed in this research that Miconazole was the most effective azoles drug (91.1%), followed by Voriconazole (68.1%). This are in agreement with Salehei et al, who demonstrated the highest sensitivity of *C. glabrata* to Miconazole and Voriconazole 100%, 60%, respectively (64). In contrast to these findings, ElFeky et al detected lesser susceptibility rates against Miconazole and Voriconazole 38.5% and 50%, respectively (38).

C. krusei, recorded to be intrinsically resistant to Fluconazole (65), was 100% resistant to Fluconazole and Itraconazole in the current research. In accordance with these findings, several studies reported 100% resistance of *C. krusei* to Fluconazole (48, 64, 66).

Therefore, these *in vitro* susceptibility results warrant clinicians dealing with cases of *C. krusei* vaginitis, that has intrinsic resistance to Fluconazole may use other alternative antifungals for treatment (48).

C. krusei isolates were 60% susceptible to Voriconazole, the sensitivity of Voriconazole to *C. krusei* vaginal isolates in the present research was compatible with Bitew and Abebaw results who found that Voriconazole was the most effective azole against *C. krusei* 60%, Rex and Stevens reported that there is no obvious reason for the disparity in susceptibility among Fluconazole and voriconazole to *C. krusei*, because all azole medications have a similar mechanism of action, i.e. ergosterol synthesis inhibition (67).

In the present study the 2 *C. parapsilosis* isolates were susceptible to all tested azoles in accordance with this finding Xiao et al mentioned that because of its high sensitivity to nearly all antifungal agents, *C. parapsilosis* vaginitis is easy to cure (68).

Mainly because of the wide use of Fluconazole in the prophylaxis and treatment of fungal infections, *Candida* spp. has developed several mechanisms for resistance to azole antifungals (69). The occurrence of antifungal resistance is generally moderate in normally sensitive fungi, particularly as relative to antibiotic resistance in bacteria. Nevertheless, due to the limited number of antifungal agents available, antifungal resistance is a fundamental issue. So that, understanding the different mechanisms of antifungal resistance is essential. This can aid in the design and developing alternative treatments. In addition, understanding the mechanisms of molecular resistance can define the resistance genes that can be used for diagnosis of resistance by molecular diagnostic tools (70).

Common overexpression of ATP-binding cassette transporters has been shown in studies of azole-resistant *C. glabrata* isolates, these transporters are encoded by different genes including *CgCDR1*, *CgCDR2*, and *CgSNQ2* (71), the zinc finger transcription factor *CgPdr1* regulates these transporters (72). However, it is well documented that the most significant factor involved in *C. glabrata* resistance to azole antifungal agents is the overexpression of the *CDR1* gene (73).

This has been also confirmed in this study as ten out of twelve Fluconazole-resistant *C. glabrata* (83.3%) expressed *CDR1* gene at higher levels than the susceptible control isolates with the differences between the two groups being statistically significant (p-value < 0.0001). In agreement with this result, many studies detected a statistically significant difference

in *CDR1* expression level between Fluconazole resistant and susceptible groups (71, 74, 75, 76).

It was found that 9 of 12 Fluconazole-resistant *C. glabrata* isolates (75%) upregulated *SNQ2* another ATP-binding cassette transporter at a significant level than susceptible control ($P=0.0381$). In accordance with these results, Tumbarello et al detected a significant difference in mRNA expression of *CgSNQ2* between resistant and susceptible isolates (77), in contrast Yao et al found that the expression of *CgSNQ2* did not differ in resistant isolates from susceptible one (6).

Also, azole resistance may be attributed to upregulation of genes coding for enzymes responsible for biosynthesis of ergosterol mainly α demethylase, encoded by *ERG11* (44).

Although overexpression of the *ERG11* gene was found for some of the Fluconazole resistant isolates (33.3%), statistical analysis revealed that the mean levels of upregulation in the group of resistant strains were not statistically different than in the susceptible control group. p value = 0.159.

Similarly, Szweda et al (2015) noticed the overexpression of the *ERG11* gene in some of the Fluconazole resistant isolates, despite being the statistical analysis of the mean level of upregulation between the group of resistant strains and the susceptible ones was not significant (69).

In agreement with these results Sanguinetti et al did not detect any statistically significant differences in transcription level among the population of Fluconazole resistant and susceptible clinical isolates (73). Upregulation of the *ERG11* gene was also studied previously by Marichal et al who detected an eight-fold rise in *ERG11* mRNA levels in clinical *C. glabrata* isolate, azole-resistant, which resulted from the chromosomal duplication (73, 78).

In addition, Whaley et al revealed that *ERG11* does not seem to have an effective role in the resistance of clinical azole in *C. glabrata*. Overexpression of *ERG11* has been detected in only two isolates of their clinical isolates of *C. glabrata*. Upregulation was subsequently observed in one isolate due to duplication of the whole *ERG11*-containing chromosome, and the phenotype was skipped with subsequent passage into azole-free media (4). In contrast Samaranyake et al mentioned that the overexpression of *CgERG11* has a role in *C. glabrata* resistance to Fluconazole (79). Another azole resistance mechanism in *C. glabrata* seems to be the overexpression of *PDR1* gene that encodes the transcriptional activator protein, involved in controlling the level of expression of genes encoding drug efflux transporters including *CDR1* and *SNQ2* (80).

This mechanism was first revealed by Tsai et al, who demonstrated the attribution of *CgPDR1* gene upregulation in clinical azole-resistant isolates and mutants to azole resistance by *CgCDR1* upregulation (81).

In accordance with these findings, 91.7% of Fluconazole-resistant isolates overexpressed *PDR1* at a statistically significant level than the susceptible isolates ($P=0.0002$). Similar to this result many studies ensured the role of *PDR1* in Fluconazole resistance (81, 75, 82, 83).

But on the contrary, Yao et al found that the expression levels of *CgPDR1* among the azole-resistant and azole-susceptible isolates did not differ significantly (71).

Simultaneous upregulation of more than one efflux pump genes (*CgCDR1*, *CgPDR1* and *CgSNQ2*) was noticed among the studied Fluconazole resistant *C. glabrata* isolates. *CgCDR1*, *CgSNQ2*, and *CgPDR1* were expressed in six isolates simultaneously, while *CgCDR1* and *CgPDR1* were concurrently overexpressed in three isolates, two isolates upregulated *CgPDR1* and *CgSNQ2*, and only one isolate upregulated *CgCDR1* and *CgSNQ2*.

Of 6 Fluconazole resistant *C. glabrata* isolates that upregulated *CgCDR1*, *CgSNQ2*, and *CgPDR1* simultaneously, 3 isolates showed cross resistance to three azole antifungals (Fluconazole, Itraconazole and Voriconazole)

Interestingly, the one *C. glabrata* isolate that was resistant to four tested azole antifungals did not upregulate *CgCDR1* but upregulate the other tested genes. Similarly, Sanguinetti et al found the two isolates that were resistant to the four azoles (Fluconazole, Itraconazole, Ketoconazole, and Voriconazole, did not upregulate *CgCDR1* but showed over expression only of *CgSNQ2* (73).

CONCLUSIONS:

C. albicans was the predominant isolated species in VVC, whereas *C. glabrata* was the most prevalent non-albican species, and the main risk factors for VVC were the age of women ≤ 40 years old, besides using frequent intravaginal douching or a previous history of vaginitis.

Antifungal susceptibility pattern was variable among the different vulvovaginal *Candida* species; Nystatin, however, was the optimal option for treating VVC caused by different *Candida* species. Fluconazole-resistance was observed markedly in *C. glabrata*, most of the clinical resistance in *C. glabrata* was due to the upregulation of ABC transporters.

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Conceptualization, E.A. and A.T.; Methodology, M.E, E.A and R.F. Formal analysis, A.S, R.F and A.T. Investigation, E.A, A.T and M.E.; Writing—original draft, A.S, A.M and R.F.; Writing—review and editing, A.G,E.A, M.E, R. F, A.S and A.M; Supervision, A.G, R.F and A.M. All authors have read and agreed to the published version of the manuscript.

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Conflicts of Interest:

The authors declare no conflict of interest.

REFERENCES

1. Gonçalves B, Ferreira C, Alves CT, Henriques M, Azeredo J, Silva S. Vulvovaginal candidiasis: Epidemiology, microbiology and risk factors. *Critical Reviews in Microbiology*. 2016.
2. Zeng X, Zhang Y, Zhang T, Xue Y, Xu H, An R. Risk Factors of Vulvovaginal Candidiasis among Women of Reproductive Age in Xi'an: A Cross-Sectional Study. *Biomed Res Int*. 2018;2018:1–8.
3. Sasikala G, Udayasri B. Speciation and antifungal susceptibility profiles of *Candida* isolates from vaginitis patients attending STD Clinic at a Tertiary Care Hospital. 2018;2018–21.
4. Whaley SG, Berkow EL, Rybak JM, Nishimoto AT, Barker KS, Rogers PD. Azole antifungal resistance in *Candida albicans* and emerging non-*albicans* *Candida* Species. *Front Microbiol*. 2017;7:1–12.
5. Christopher D, Pfeiffer, Gregory P, Samsa et al. Quantitation of *Candida* CFU in Initial Positive Blood Cultures. *J Clin Microbiol*. 2011;49(8):2879–83.
6. Yao D, Chen J. Mechanisms of azole resistance in clinical isolates of *Candida glabrata* from two hospitals in China. *Infect Drug Resist*. 2019;12:771–81.
7. Mashaly G, Shrief R. *Candida Glabrata* complex from patients with healthcare-associated infections in Mansoura university hospitals, Egypt: Distribution, antifungal susceptibility and effect of Fluconazole and Polymyxin b combination. *Germes*. 2019;9(3):125–32.
8. Halim M, El-Feky E, Sayed A, Kadry D, Sayed A, Abdella R. Prevalence of *Candida Non albicans* Species Associated with Vulvovaginal Candidiasis in Egyptian Women. *Int J Health Sci (Qassim)*. 2015 Jan 3;Vol 2:304–13.
9. Saad D, Mahmoud N, El-seidi EA, Mahmoud M, Hassan S. Alexandria University Faculty of Medicine Species identification and antifungal susceptibility pattern of *Candida* isolates in cases of vulvovaginal candidiasis. *Alexandria J Med [Internet]*. 2016;52(3):269–77. Available from: <http://dx.doi.org/10.1016/j.ajme.2015.10.001>
10. Bhavan PS, Rajkumar R, Radhakrishnan S, Seenivasan C, Kannan S. Culture and Identification of *Candida Albicans* from Vaginal Ulcer and Separation of Enolase on SDS-PAGE. *Int J Biol*. 2010;2(1):84–93.
11. Clinical and Laboratory Standards Institute (CLSI). Method for antifungal disk diffusion susceptibility testing of yeasts: approved standard, M44-A. Wayne (PA): CLSI; 2004.
12. CLSI. M44-A2: Method for Antifungal Disk Diffusion Susceptibility Testing of Yeasts; Approved Guideline—Second Edition. *CLSI Doc*. 2009;M44-A2(August):29(17).
13. Li QQ, Skinner J, Bennett JE. Evaluation of reference genes for real-time quantitative PCR studies in *Candida glabrata* following azole treatment. *BMC Mol Biol*. 2012;13
14. Abdullahi Nasir I, Uchenna E, Onyia J, Ifunanya AL. Prevalence of vulvovaginal candidiasis among nonpregnant women attending a tertiary health care facility in Abuja, Nigeria. *Res Rep Trop Med*. 2015;37–42.
15. Kiasat N, Rezaei-Matehkolaei A, Mahmoudabadi AZ, Mohamadpour KH, Molavi S, Khoshayand N. Prevalence of vulvovaginal candidiasis in Ahvaz, Southwest Iran: A Semi-Large scale study. *Jundishapur J Microbiol*. 2019;12(3):4–9.
16. Mohamadi J, Havasian MR, Panahi J, Pakzad I. Antifungal drug resistance pattern of *Candida* spp isolated from vaginitis in Ilam-Iran during 2013-2014. *Bioinformation*. 2015;11(4):203–6.
17. Figueroa JR, Rangel VM, Ibarra FJO, Román GC, Zúñiga MB. Effectiveness of a clinimetric scale for diagnosing vulvovaginal candidiasis. *Ginecol Obstet Mex*. 2004;72:219–26.

18. Oyelese A, Onipede A, Aboderin A, Adedosu A, Onayemi O. Sexually transmitted infections in Obafemi Awolowo University Teaching Hospital, Ile-Ife, Nigeria: A decade of clinic experience. *African J Clin Exp Microbiol.* 2004;6:1–5.
19. Jombo GTA, Opajobi SO, Egah DZ, Banwat EB, Denen Akaa P. Symptomatic Vulvovaginal Candidiasis and Genital Colonization by Candida Species in Nigeria. *J Public Heal Epidemiol.* 2010;2:147–51.
20. Moallaei H, Mirhendi H, Brandão J, Mirdashti R, L R. Comparison of Enzymatic Method Rapid Yeast Plus System with RFLP-PCR for Identification of Isolated Yeast from Vulvovaginal Candidiasis. *Iran J Med Sci.* 2011 Sep 1;14:443–50.
21. J. Mintz and M. Martens. "Prevalence of Non-Albicans Candida Infections in Women with Recurrent Vulvovaginal Symptomatology . *Adv Infect Dis.* 2013;3(2):238-242.
22. Roudbary M, Roudbarmohammadi S, Bakhshi B, Farhadi Z, Nikoosmanesh F. Identification of Candida species isolated from Iranian women with vaginal candidiasis by PCR-RFLP method. *Pelagia Res Libr.* 2013;3(6):365–9.
23. Pakshir K, Yazdani M, Kimiaghalam R. Etiology of vaginal candidiasis in Shiraz, Southern Iran. *Res J Microbiol.* 2007;9:696–700.
24. Bello MD, Gonzalez A, Barnabé C, Larrouy G. First characterization of Candida albicans by random amplified polymorphic DNA method in Nicaragua and comparison of the diagnosis methods for vaginal candidiasis in Nicaraguan women. *Mem Inst Oswaldo Cruz.* 2002;97:985–9.
25. Ugwa E. Vulvovaginal candidiasis in Aminu Kano teaching hospital, North West Nigeria: Hospital-based epidemiological study. *Ann Med Health Sci Res.* 2015;5(4)::274-278.
26. Lopes PHS, Pacini VL, Norberg AN. Genital Infection by Gardnerella vaginalis and Candida spp. among Women in Nova Iguaçu City, Rio de Janeiro Province, Brazil. *Sci research.* 2017;04(03):1–7.
27. E E. AkorthaVictor, Oluoha NwaugoVictor Oluoha Nwaugo NOC. Antifungal resistance among Candida species from patients with genitourinary tract infection isolated in Benin City, Edo state, Nigeria. *African J Microbiol Res.* 2009;3:694–9.
28. Holland J, Young ML, Lee O, Chen SCA. Vulvovaginal carriage of yeasts other than Candida albicans. *Sex Transm Infect.* 2003;79:249-50.
29. Nelson M, Wanjiru W, Margaret MW. Prevalence of Vaginal Candidiasis and Determination of the Occurrence of Candida Species in Pregnant Women Attending the Antenatal Clinic of Thika District Hospital, Kenya. *Open J Med Microbiol.* 2013;3:264–72.
30. Amouri I, Sellami H, Borji N, Abbes S, Sellami A, Cheikhrouhou F, et al. Epidemiological survey of vulvovaginal candidosis in Sfax, Tunisia. *Mycoses.* 2011;54(5):499–505.
31. Na D, Weiping L, Enfeng Z, Chan W, Zhaozhao X, Honghui Z. Risk factors for candida infection of the genital tract in the tropics. *Afr Health Sci.* 2014;14:835–9.
32. Brown JM, Hess KL, Brown S, Murphy C, Waldman AL, Hezareh M. Intravaginal practices and risk of bacterial vaginosis and candidiasis infection among a cohort of women in the United States. *Obstet Gynecol.* 2013 Apr;121(4):773–80.
33. P. Giraldo, A. Von Nowaskonski, F. Gomes, I. Linhares, N. A. Neves and SSw. "Vaginal colonization by Candida in asymptomatic women with and without a history of recurrent vulvovaginal candidiasis,." *Obstet Gynecol.* 2000;95(3):413–416.
34. Ozcan SK, Budak F, Yucesoy G, Susever S, Willke A. Prevalence, susceptibility profile and proteinase production of yeasts causing vulvovaginitis in Turkish women. *APMIS.* 2006;114:139–45.
35. Jacob L, John M, Kalder M, Kostev K. Prevalence of vulvovaginal candidiasis in

- gynecological practices in Germany: A retrospective study of 954,186 patients. *Curr Med Mycol*. 2018;4:6–11.
36. Fallahi AA, Korbacheh P, Zaini F, Mirhendi H, Zeraati H, Noorbakhsh F, et al. *Candida* species in cutaneous candidiasis patients in the Guilan province in Iran; identified by PCR-RFLP method. *Acta Med Iran*. 2013;51:799–804.
 37. Mahmoudi Rad M, Zafarghandi S, Abbasabadi B, Tavallae M. The epidemiology of *Candida* species associated with vulvovaginal candidiasis in an Iranian patient population. *Eur J Obstet Gynecol Reprod Biol*. 2011;155(2):199–203.
 38. ElFeky DS GN. Evaluation of Virulence Factors of *Candida* Species Isolated from Superficial Versus Systemic Candidiasis. *Egypt J Med Microbiol*. 2016;25(1):27–36.
 39. El-sayed HM, Hamouda AA. *Candida albicans* causing vulvovaginitis and their clinical response to antifungal therapy. *Egypt J Med Microbiol*. 2007;16(1):53–62.
 40. Alfouzan W, Dhar R, Ashkanani H, Gupta M, Rachel C, Khan ZU. Species spectrum and antifungal susceptibility profile of vaginal isolates of *Candida* in Kuwait. *J Mycol Med*. 2015;25:23-8.
 41. Deorukhkar SC, Saini S, Mathew S. Non- *albicans* *Candida* infection: An emerging threat. *Interdiscip Perspect Infect Dis*. 2014;2014.
 42. Jimoh O, Inabo HI, Yakubu SE, Ankuma SJ, Olayinka AT. Prevalence and Speciation of Non-*albicans* Vulvovaginal Candidiasis in Zaria. *J Nat Sci Res*. 2016;6:51–7.
 43. Makanjuola O, Bongomin F, Fayemiwo SA. An update on the roles of non-*albicans* *Candida* species in vulvovaginitis. *J Fungi*. 2018;4(121):1–17.
 44. Rodrigues CF, Silva S, Henriques M. *Candida glabrata*: A review of its features and resistance. *Eur J Clin Microbiol Infect Dis*. 2014;33:673–688.
 45. Al-Nedaithy SSA. Spectrum and proteinase production of yeasts causing vaginitis in Saudi Arabian women. *Med Sci Monit*. 2002;8:498-501.
 46. Gültekin B, Yazici V, Aydin N. Distribution of *Candida* species in vaginal specimens and evaluation of CHROMagar *Candida* medium. *Mikrobiyol Bul*. 2005 Jul;39(3):319–24.
 47. Pirota M V., Garland SM. Genital *Candida* species detected in samples from women in Melbourne, Australia, before and after treatment with antibiotics. *J Clin Microbiol*. 2006;44:3213–7.
 48. Bitew A, Abebaw Y. Vulvovaginal candidiasis: Species distribution of *Candida* and their antifungal susceptibility pattern. *BMC Womens Health*. 2018;18(94):1–10.
 49. Babin D, Kotigadde S, Rao P, Rao T. Clinico-mycological profile of vaginal candidiasis in a tertiary care hospital in Kerala. *Int J Res Biol Sci*. 2013 Mar 8;3:55–9.
 50. Maraki S, Mavromanolaki VE, Stafylaki D, Nioti E, Hamilos G, Kasimati A. Epidemiology and antifungal susceptibility patterns of *Candida* isolates from Greek women with vulvovaginal candidiasis. *Mycoses*. 2019;62(8):692–7.
 51. Fan S, Liu X, Wu C, Xu L, Li J. Vaginal nystatin versus oral Fluconazole for the treatment for recurrent vulvovaginal candidiasis. *Mycopathologia*. 2015 Feb;179:95–101.
 52. Choukri F, Benderdouche M, Sednaoui P. In vitro susceptibility profile of 200 recent clinical isolates of *Candida* spp. to topical antifungal treatments of vulvovaginal candidiasis, the imidazoles and nystatin agents. *J Mycol Med*. 2014;24: 303-7.
 53. Wang FJ, Zhang D, Liu ZH, Wu WX, Bai HH, Dong HY. Species distribution and in vitro antifungal susceptibility of vulvovaginal *Candida* isolates in China. *Chin Med J (Engl)*. 2016;129:1161-5.
 54. Dharwad S, M SDR. Species Identification of *Candida* Isolates in Various Clinical Specimens with Their Anti- fungal Susceptibility Patterns. *J Clin Diagnostic Res*. 2011;5(6):1177–81.

55. Noake T, Kuriyama T, White PL, Potts AJC, Lewis MAO, Williams DW, et al. Antifungal susceptibility of *Candida* species using the Clinical and Laboratory Standards Institute disk diffusion and broth microdilution methods. *J Chemother.* 2007 Jun;19(3):283–7.
56. Coignard C, Hurst SF, Benjamin LE, Brandt ME, Warnock DW, Morrison CJ. Resolution of Discrepant Results for *Candida* Species Identification by Using DNA Probes. *J Clin Microbiol.* 2004;42:858–861.
57. Kelen F. D. Dota, MSc, Alessandra R. Freitas, MSc, Marcia E. L. Consolaro TIES. A Challenge for Clinical Laboratories : Detection of Antifungal Resistance in *Candida* Species. *Lab Med.* 2011;42(2):87–93.
58. Guinea J. Global trends in the distribution of *Candida* species causing candidemia. *Clin Microbiol Infect.* 2014 Jun;20:5–10.
59. Sanguinetti M, Posteraro B, Lass-Flörl C. Antifungal drug resistance among *Candida* species: mechanisms and clinical impact. *Mycoses.* 2015 Jun;58:2–13.
60. Pfaller MA, Andes DR, Diekema DJ, Horn DL, Reboli AC, Rotstein C, et al. Epidemiology and outcomes of invasive candidiasis due to non-*albicans* species of *Candida* in 2,496 patients: data from the Prospective Antifungal Therapy (PATH) registry 2004–2008. *PLoS One.* 2014;9(7).
61. Andes DR, Safdar N, Baddley JW, Alexander B, Brumble L, Freifeld A, et al. The epidemiology and outcomes of invasive *Candida* infections among organ transplant recipients in the United States: results of the Transplant-Associated Infection Surveillance Network. *Transpl Infect Dis.* 2016 Dec;18(6):921–31.
62. Pfaller MA. Antifungal drug resistance: mechanisms, epidemiology, and consequences for treatment. *Am J Med.* 2012 Jan;125:3–13.
63. Kołaczowska A, Kołaczowski M. Drug resistance mechanisms and their regulation in non-*albicans* *Candida* species. *J Antimicrob Chemother.* 2016 Jun;71(6):1438–50.
64. Salehei Z, Seifi Z, Mahmoudabadi AZ. Sensitivity of vaginal isolates of *Candida* to eight antifungal drugs isolated from Ahvaz, Iran. *Jundishapur J Microbiol.* 2012;5:574–577.
65. Lyon GM, Karatela S, Sunay S, Adiri Y. Antifungal susceptibility testing of *Candida* isolates from The candida surveillance study. *J Clin Microbiol.* 2010;48:1270–5.
66. Sasikala G, Udayasri B. Speciation and antifungal susceptibility profiles of *Candida* isolates from vaginitis patients attending STD Clinic at a Tertiary Care Hospital. *J Dr NTR Univ Heal Sci.* 2018;7:94–7.
67. Rex JH, Stevens DA. Systemic antifungal agents. *Principles Pract Infect Dis.* 2010 Jan 1;8:549–63.
68. Xiao M, Fan X, Chen SC-A, Wang H, Sun Z-Y, Liao K, et al. Antifungal susceptibilities of *Candida glabrata* species complex, *Candida krusei*, *Candida parapsilosis* species complex and *Candida tropicalis* causing invasive candidiasis in China: 3 year national surveillance. *J Antimicrob Chemother.* 2015 Mar;70(3):802–10.
69. Szweda P, Gucwa K, Romanowska E, Dzierz Anowska-Fangrat K, Naumiuk Ł, Brillowska-Da Browska A, et al. Mechanisms of azole resistance among clinical isolates of *Candida glabrata* in Poland. *J Med Microbiol.* 2015 Jun;64(6):610–9.
70. Sanglard D, Coste A. Antifungal drug resistance mechanisms in fungal pathogens from the perspective of transcriptional gene regulation. *FEMS Yeast Res.* 2009;9:1029–1050.
71. Yao D, Chen J, Chen W, Li Z, Hu X. Mechanisms of azole resistance in clinical isolates of *Candida glabrata* from two hospitals in China. *Infect Drug Resist.* 2019;12, 771–78.
72. Vermitsky JP, Earhart KD, Smith WL, Homayouni R, Edlind TD, Rogers PD. *Pdr1* regulates multidrug resistance in *Candida glabrata*: Gene disruption and genome-wide expression studies. *Mol Microbiol.* 2006;61:704–22.

73. Sanguinetti M, Posteraro B, Fiori B, Ranno S, Torelli R, Fadda G. Mechanisms of azole resistance in clinical isolates of *Candida glabrata* collected during a hospital survey of antifungal resistance. *Antimicrob Agents Chemother.* 2005;49:668-79.
74. Shahrokhi S, Noorbakhsh F, Rezaie S. Quantification of CDR1 Gene Expression in Fluconazole Resistant *Candida Glabrata* Strains Using Real-time PCR. *Iran J Public Heal.* 2017;46(8):1118–22.
75. Sanguinetti M, Torelli R, Posteraro B, Sanglard D. Contribution of CgPDR1-Regulated Genes in Enhanced Virulence of Azole-Resistant *Candida glabrata*. *PLoS One.* 2011;6(3).
76. Whaley SG, Zhang Q, Caudle KE RP. “Relative Contribution of the ABC Transporters Cdr1, Pdh1, and Snq2 to Azole Resistance in *Candida glabrata*.” *Antimicrob Agents Chemother.* 2018;62(10):1–8.
77. Tumbarello M, Sanguinetti M, Treccarichi EM et al. Fungaemia caused by *Candida glabrata* with reduced susceptibility to Fluconazole due to altered gene expression: risk factors, antifungal treatment and outcome. *J Antimicrob Chemother.* 2008;62(6):1379–1385.
78. Marichal P, Bossche H Vanden, Odds FC, Nobels G, Fay S, Mose-larsen P. Molecular Biological Characterization of an Azole-Resistant *Candida glabrata* Isolate. *Antimicrob Agents Chemother.* 1997;41::2229-37.
79. Samaranayake YH, Cheung BPK, Wang Y, Yau JYY, Yeung KWS, Samaranayake LP. Fluconazole resistance in *Candida glabrata* is associated with increased bud formation and metallothionein production. *J Med Microbiol.* 2013;62:303–318.
80. Paul S, Schmidt JA, Moye-Rowley WS. Regulation of the CgPdr1 transcription factor from the pathogen *Candida glabrata*. *Eukaryot Cell.* 2011;10:187–97.
81. Tsai H, Krol AA, Sarti KE, Bennett JE. *Candida glabrata* PDR1 , a Transcriptional Regulator of a Pleiotropic Drug Resistance Network , Mediates Azole Resistance in Clinical Isolates and Petite Mutants. *Antimicrob Agents Chemother.* 2006;50(4):1384–92.
82. Cavalheiro M, Costa C, Silva-Dias A, Miranda I, Wang C, Pais P, et al. Unveiling the mechanisms of in vitro evolution towards Fluconazole resistance of a *Candida glabrata* clinical isolate: a transcriptomics approach. *Antimicrob Agents Chemother.* 2018;63:1–17.
83. Regulon P, Caudle KE, Barker KS, Wiederhold NP, Xu L, Homayouni R, et al. Genomewide Expression Profile Analysis of the *Candida glabrata*. *Eukaryot Cell.* 2011;10(3):373–83.