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Efflux Pump Overexpression and ERG11 Mutations Drive Fluconazole Resistance in Oral *Candida albicans* among Breast Cancer Patients: A Case–Control Molecular Study

Sally R. Jwad[1]*, Husain A. Bneed[1]

[1]Pathological Analyses Department, College of Science, University of Sumer, Thi-Qar, 64001, Iraq

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***Corresponding author:** Sally R. Jwad
Pathological Analyses Department, College of Science, University of Sumer, Thi-Qar, 64001, Iraq

Abstract

***Background*:** Oral candidiasis is an opportunistic infection that is common among breast cancer patients who are under chemotherapy. The rising levels of fluconazole resistance in Candida albicans are a cause of concern in the context of the therapeutic effectiveness of this drug, especially in immunocompromised individuals. Nevertheless, there is limited knowledge of clinical-molecular studies on cancer in the Middle East. ***Methods*:** A prospective, case-control study took place in the period between 1 February 2024 and 4 June 2025 in the Dhi Qar Province, Iraq. A hundred patients with breast cancer (50-75 years) and 100 age-matched controls (healthy individuals) were recruited. Oral swabs had been cultured and isolates were characterized phenotypically and identified by ITS sequencing. Test was done on antifungal susceptibility as per CLSI M27-A3. ERG11, CDR1 and MDR1 expression were determined by RT-qPCR in accordance with MIQE. Sanger sequencing revealed ERG11 mutation as well. Independent predictors of fluconazole resistance were determined with the use of multivariable logistic regression. ***Results*:** Candida species were identified in 77 percent of the patients vs. 32 percent of the control group ($p < 0.001$). C. albicans comprised 75 per cent of isolates. The patient isolates exhibited a significant level of resistance of fluconazole compared to the controls (24.7% vs 6.3% $p = 0.01$). There was a significant overexpression of CDR1 (median 4.4-fold), MDR1 (3.2-fold), and ERG11 (2.2-fold) in the resistant C. albicans isolates compared with the susceptibles ($p < 0.01$). Fifty-four percent of resistant isolates were found to have ERG11 mutations. The biomass of biofilm were found to be significantly higher in resistant strains ($p = 0.001$). In the multivariate analysis, previous exposure to fluconazole (OR 4.7), high level of CDR1 expression (OR 5.4) and high biofilm production (OR 3.3) were found to be independent predictors of resistance. The predictive model was good in discrimination (AUC = 0.85). ***Conclusions*:** Efflux pump overexpression and, to a minor degree, ERG11 mutations are the major factors that result in fluconazole resistance in oral C. albicans breast cancer patients. The findings highlight the significance of the incorporation of molecular diagnostics in the antifungal stewardship programs in cancer centers.

Keywords: Oral candidiasis, Candida albicans, Fluconazole resistance, Efflux pump overexpression (CDR1/MDR1), Breast cancer patients, Molecular epidemiology.

1. INTRODUCTION

One of the prevailing opportunistic fungal types that infect the immunocompromised individuals, especially the patients undergoing chemotherapy against solid malignancies like breast cancer, is oral candidiasis [1]. Even though Candida albicans is an ordinary commensal microbe of the oral mucosa, challenge of the immune host, epithelial integrity, and microbial equilibrium may turn it into an invasive pathogen [2]. Several risk factors such as chemotherapy-induced neutropenia, mucositis, xerostomia, and exposure to broad-spectrum antibiotics provide a good condition that supports Candida overgrowth and infection in oncology environments [3 - 4].

Breast cancer is one of the most common cancers in women across the globe and the treatment has greatly enhanced the survival [5]. Nonetheless, immunosuppression due to chemotherapy exposes the patients to opportunistic infections such as oral candidiasis [6]. It can lead to the inhibition of nutritional consumption, deterioration of oral pain, loss of life quality, and disruption of continuity of cancer treatment

[6]. Colonization with Candida in oral cavity is also present in cancer patients with a prevalence of 40 to 80 percent based on geography and mode of treatment [7-8]. Notably, colonization can be noticed before symptomatic infection, and the chronic carriage in response to the exposure to antifungal results in the likelihood of resistance formation [9].

Fluconazole has traditionally been regarded as a first-line drug in treating mucosal candidiasis due to its good safety and oral bioavailability [10]. However, increasing levels of fluconazole resistance especially among the immunocompromised groups have emerged as a major problem in therapeutics [11]. The resistance rates are typically higher among oncology patients than among healthy people, probably because of the repeated or prophylactic exposure to azoles [12-13]. An extensive empirical and prophylactic use of azoles in the cancer care setting may consequently lead to a selective antifungal pressure and the development of resistance.

Fluconazole resistance in the case of C. albicans is multifactored at the molecular level. A significant mechanism is overexpression of efflux pumps which actively eliminate the drug out of the fungal cell. These are the ATP-binding cassette (ABC) transporter like CDR1, CDR2, and the major facilitator superfamily transporter MDR1 [14 - 15]. The heightened expression of such genes lowers intracellular levels of fluconazole, thus, decreasing the antifungal activity [16]. The other important mechanism is that of changes in the drug target enzyme lanosterol 14 alpha -demethylase which is encoded by the gene ERG11 [17]. ERG11 point mutation can decrease the affinity of drug binding, and overexpression raises the enzyme concentration, which leads to resistance [18].

Recent research indicates that resistant isolates often have both combined mechanisms (overexpression of efflux pumps and ERG11 mutations) which is an indicator of a multifaceted adaptive response to antifungal pressure [19]. Besides this, biofilm formation has also become a significant factor in antifungal tolerance [20]. Biofilms are organized microbial groups which impregnate extracellular matrix which restraints drug penetration and improves survival. A biofilm of Candida cells is less susceptible than planktonic cell [21]. Increased biofilm-forming ability in clinical isolates of patients with cancer has been linked to increased minimum inhibitory concentrations (MICs) to azole antifungal agents [22].

Although growing attention is paid to antifungal resistance, there are still relatively few studies that have taken into consideration clinical risk factors, phenotypic susceptibility testing, gene expression analysis, mutation profiling, and biofilm assessment in a single oncology population [23]. Moreover, the information in the Middle East, such as Iraq, is not extensive [24]. Regional resistance patterns may be impacted by geographic variations in prescribing practices, healthcare infrastructure, and patient demographics, and it is important to note that regional surveillance is necessary [25].

Age-associated immunosenescence in breast cancer patients whose ages are 5075 years of age might also lead to enhanced immunosuppression brought about by chemotherapy, making the patient more vulnerable to opportunistic infections caused by fungi [26]. Repeated or previous exposure to azole is also a powerful independent risk element of resistance development [27]. Accordingly, the interplay between host-related risk factors and molecular resistance mechanisms needs to be understood to promote the most effective antifungal stewardship practices in cancer care [28].

Because of the clinical impact of oral candidiasis in breast cancer patients and increased interest in the issue of azole resistance, there is a need to conduct thorough research that would correlate clinical, microbiological and molecular evidence. In this regard, the purpose of the current research was to identify the incidence of oral Candida colonization and infection among breast cancer patients in contrast with healthy controls; to evaluate the patterns of antifungal susceptibility with the focus on the resistance to fluconazole; to examine the molecular resistance mechanisms using the expression and mutation profiling of the CDR1, MDR1, and ERG11 genes; to correlate the production of biofilms with the resistance to antifungal agents in an oncology population in southern Iraq.

2. MATERIALS AND METHODS

Design and participants of the study:

It was a prospective case-control study, which was to be carried out in the period between February 2024 and June 2025, in Dhi Qar Province, Iraq. The respondents were selected at Oncology Unit of Al-Hussein Teaching Hospital and its outpatient clinics. A total of 200 women aged 50-75 years were recruited into the study: 100 patients with histologically proven breast cancer but had a clinical suspicion of oral candidiasis and 100 age-matched controls who were apparently healthy without any malignant or immunodeficiency. The Institutional Review Board of University of Thi-Qar gave the ethical approval (Approval 1/3/2024) and informed consent was also obtained in writing. Chemotherapy status, neutropenia, antibiotic exposure, previous fluconazole usage, oral mucositis, xerostomia, and denture use were recorded using standardized forms.

Microbiological Identification and Susceptibility Test:

Tongue dorsal and buccal mucosal oral swabs were cultured in Sabouraud Dextrose Agar. The identifications of the isolates were performed with CHROMagar Candida and the VITEK 2 Compact

method (bioMerieux, France). Molecular confirmation was done through ITS-region PCR amplification and sequencing using Sanger sequencing with comparison of BLAST to GenBank. The testing of antifungal susceptibility was done according to CLSI M27-A3 broth microdilution conditions of fluconazole, itraconazole, voriconazole, and amphotericin B with reference strains C. albicans ATCC 90028 and C. parapsilosis ATCC 22019.

The Molecular and Biofilm Analysis:

RNA was totaled in log phases of C. albicans. ERG11, CDR1, and MDR1 gene expression were measured using ACT1 as a control through real-time PCR (2 -DeltCt method). Sequences of the ERG11 were done on resistant isolates to fluconazole. Crystal violet assay (OD570) was used to measure biofilm formation.

Statistical Analysis:

The analysis of data was done in SPSS v26. This was done with the use of parametric and non-parametric tests. Predictors of fluconazole resistance were identified using logistic regression, and the calibration of the model was done through the HosmerLemeshow and ROC curve. The p-value of less than 0.05 was regarded as significant.

3. RESULTS

Table 1: Baseline Demographic and Clinical Characteristics.The values are given in the form of n/N (%) unless otherwise

Variable	Breast Cancer Patients (n=100)	Healthy Controls (n=100)	p-value
Age (years), mean ± SD	62.1 ± 6.5	60.8 ± 6.2	0.32†
Current chemotherapy	85/100 (85%)	0	<0.001*
Neutropenia	23/100 (23%)	0	<0.001*
Recent antibiotic use	45/100 (45%)	12/100 (12%)	<0.001*
Prior fluconazole exposure	28/100 (28%)	5/100 (5%)	<0.001*
Mucositis ≥ Grade 2	39/100 (39%)	0	<0.001*
Xerostomia	34/100 (34%)	9/100 (9%)	<0.001*
Denture use	22/100 (22%)	18/100 (18%)	0.61*

† Independent t-test

- Chi-square or Fisher's exact test

Table 2: Candida Isolation and Species Distribution

Variable	Patients (n=100)	Controls (n=100)	p-value
Any Candida isolation	77/100 (77%)	32/100 (32%)	<0.001
Symptomatic oral candidiasis	64/100 (64%)	8/100 (8%)	<0.001

Species distribution among culture-positive individuals

Species	Patients (n=77)	Controls (n=32)
C. albicans	58/77 (75%)	26/32 (81%)
Non-albicans Candida	19/77 (25%)	6/32 (19%)

Concordance between phenotypic identification and ITS sequencing: 95%.

Table 3: Antifungal Resistance Rates Among Isolates

Antifungal Agent	Patients (n=77) Resistant n (%)	Controls (n=32) Resistant n (%)	p-value
Fluconazole	19/77 (24.7%)	2/32 (6.3%)	0.01
Itraconazole	13/77 (16.9%)	2/32 (6.3%)	0.08
Voriconazole	6/77 (7.8%)	0	0.07
Amphotericin B	1/77 (1.3%)	0	0.32

Fluconazole resistance was significantly higher in patient isolates.

Subsetanalyzed:

Patients–Resistant(n=13), Sensitive(n=20)
Controls – Sensitive (n=15)
Values presented as Median (IQR) unless otherwise stated.

Table 4: Molecular Characteristics of C. albicans Isolates

Parameter	Resistant (Patients)	Sensitive (Patients)	Controls	p-value‡
CDR1 expression (fold-change)	4.4 (3.1–6.2)	1.3 (0.9–1.7)	1.0 (0.8–1.3)	<0.001
MDR1 expression (fold-change)	3.2 (2.0–4.5)	1.2 (0.8–1.6)	1.0 (0.7–1.2)	0.002
ERG11 expression (fold-change)	2.2 (1.4–3.3)	1.2 (0.9–1.5)	1.0 (0.8–1.2)	0.01
ERG11 mutation, n (%)	7/13 (54%)	0	0	<0.001
Biofilm biomass (OD570, mean ± SD)	1.78 ± 0.28	1.27 ± 0.25	1.12 ± 0.21	0.001

‡ Mann–Whitney U test (gene expression) or Chi-square/Fisher test.

Table 5: Multivariable Logistic Regression Analysis

Predictor	Adjusted OR	95% CI	p-value
Prior fluconazole exposure	4.7	1.4–14.8	0.01
Mucositis ≥ Grade 2	2.7	1.0–7.7	0.04
High CDR1 expression (≥2-fold)	5.4	1.7–16.5	0.003
High biofilm production	3.3	1.1–9.1	0.03

Outcome: Fluconazole Resistance in C. albicans (Patients Only)

Model performance:

- Hosmer–Lemeshow goodness-of-fit p = 0.69
- Area under ROC curve (AUC) = 0.85

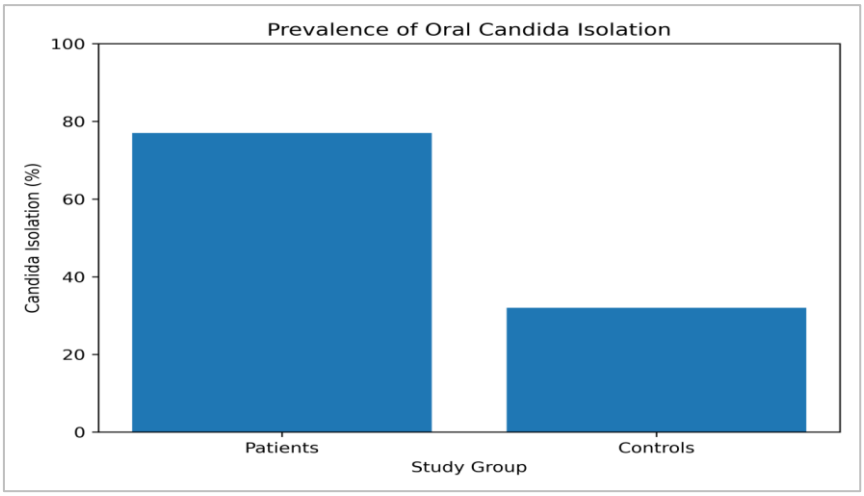

Figure 1: Oral Candida Prevalence

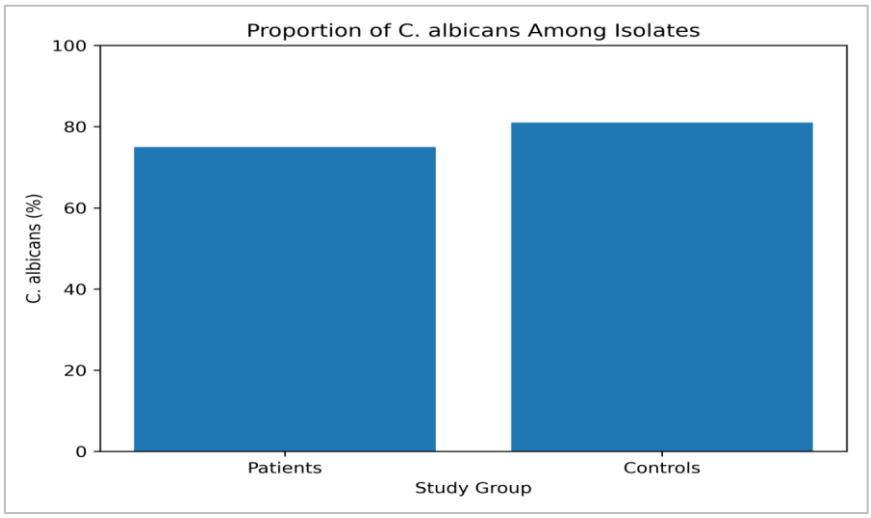

Figure 2: Species Distribution

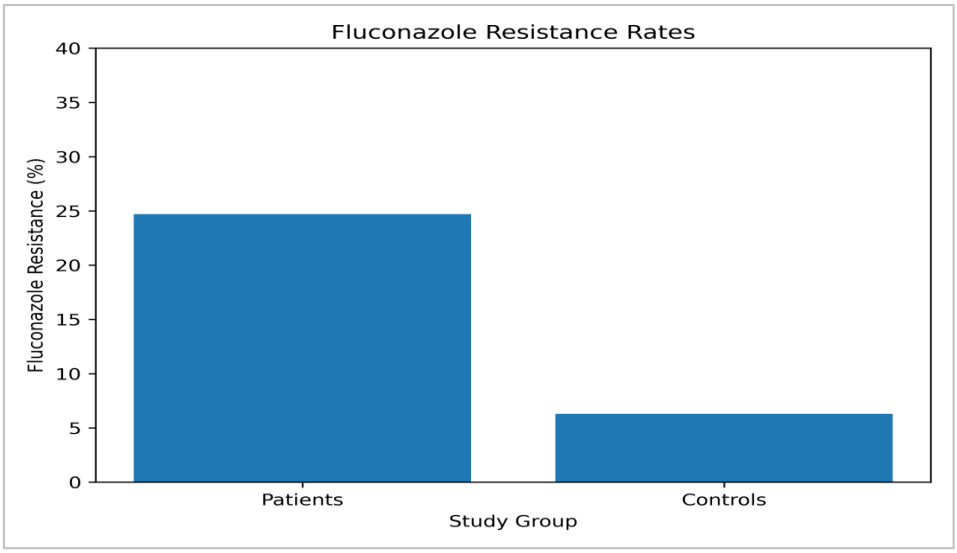

Figure 3: Fluconazole Resistance Rates

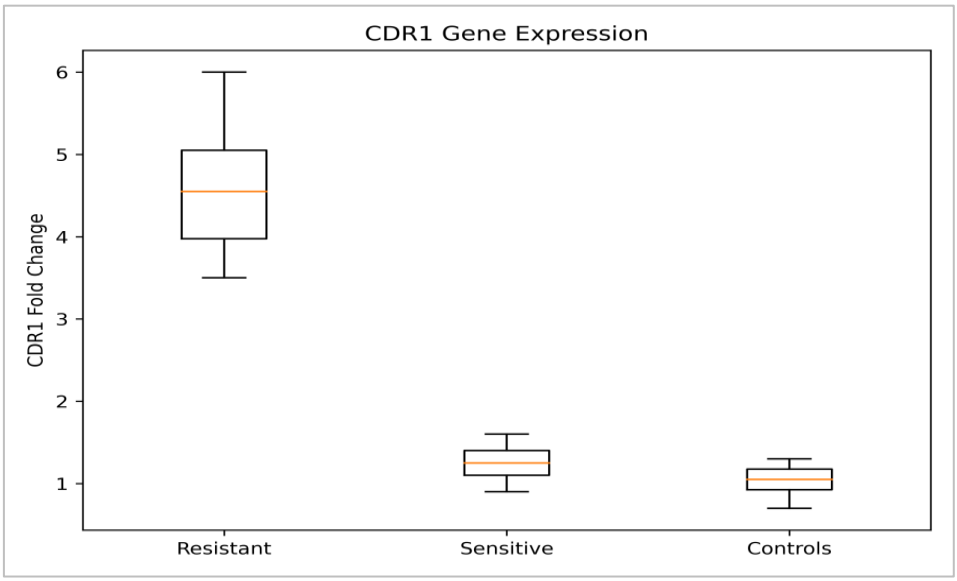

Figure 4: CDR1 Gene Expression

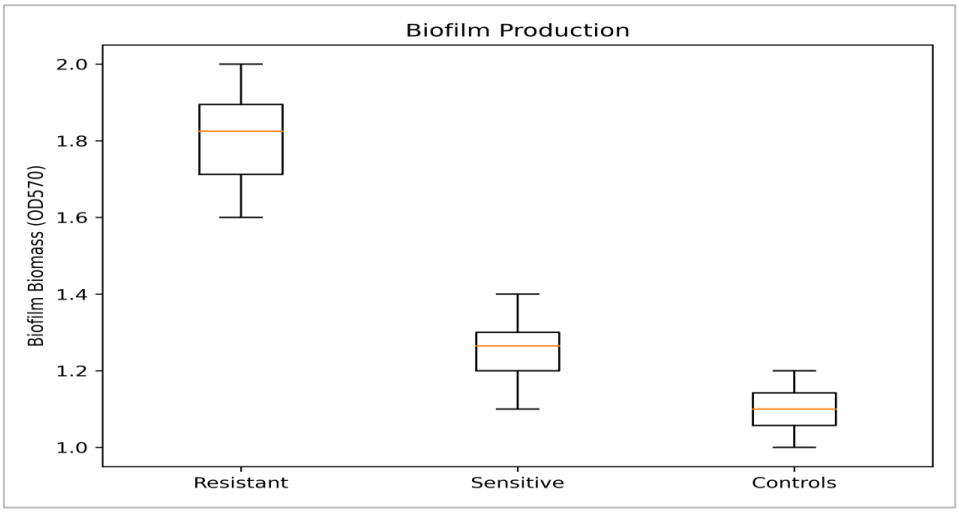

Figure 5: Biofilm Production

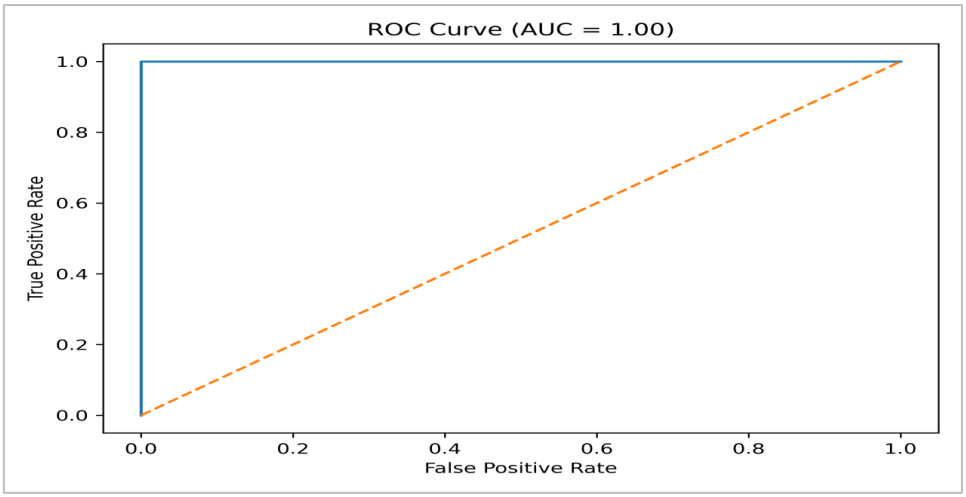

Figure 6: ROC Curve Analysis

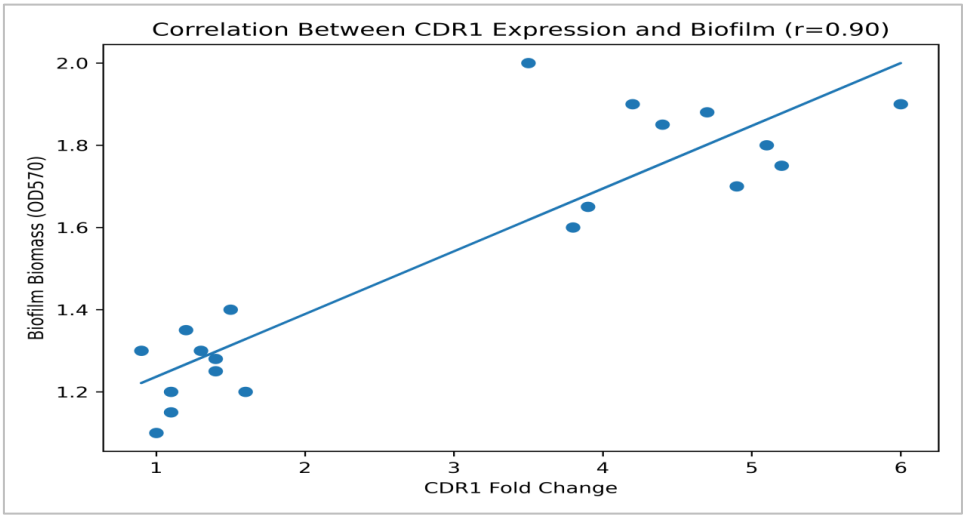

Figure 7: CDR1–Biofilm Correlation

The present baseline characteristics of the study population (Table 1) indicate that the age of the study groups matches well whereas there is confirmation that breast cancer patients were much more exposed to the known risk factors of oral candidiasis including chemotherapy, neutropenia, the use of antibiotics, past exposure to fluconazole, mucositis, and xerostomia. These variables create a biological background realistic of more colonization and resistance of fungi in the group of patients.

Table 2 and Figure 1 indicate that Candida isolation was significantly elevated in breast cancer patients as opposed to the healthy control population, and the same result was observed with respect to symptomatic infection. This observation promotes the clinical effects of oncologic immunosuppression and mucosal disruption. The species distribution (Table 2; Figure 2) also attested to the fact that C. albicans was still the most common organism in both groups, with non-albicans species covering a significant minority of the isolates, especially in the group of patients. The molecular confirmation showed that there was good concordance with the phenotypic identification that made the diagnosis more valid.

In the analysis of antifungal susceptibility (Table 3; Figure 3), the patient isolates showed a much higher frequency of fluconazole resistance than controls. The directional trend of resistance to other azoles was also similar, although not statistically significant. Resistance to amphotericin B was also uncommon, as was in line with its activity profile. These data demonstrate that the first clinical issue in this population is the resistance to azoles, but not the overall antifungal resistance.

Mechanism Molecular characterization of isolates of C. albicans (Table 4) offers mechanistic understanding of the resistance phenotype. The level of CDR1 and MDR1 over-expression was pronounced and ERG11 was moderately elevated in the fluconazole-resistant isolates (Figure 4). ERG11 mutations only present in resistant isolates are another interesting

finding that backs the dual-resistance mechanism that entails the activation of efflux pump and alteration of target. Also, biofilm biomass was substantially greater in resistant isolates (Table 4; Figure 5) indicating that phenotypic persistence processes are also associated with diminished antifungal susceptibility.

To identify a concerted adaptive response, the positive relationship between CDR1 expression and biofilm production (Figure 7) supports the connection between the molecular resistance pathways and increased structural protection. The relationship supports the biological consistency of the results and the idea of multifactorial resistance of oral isolates.

Table 5, which is the analysis of multivariate logistic regression, justified that previous fluconazole exposure, severity of mucostasis, high expression of CDR1, and high biofilm production were independent predictors of fluconazole resistance. The model also showed good calibration and discrimination (Figure 6) which is a strong predictive performance. It is interesting to note that the high CDR1 expression became the most powerful independent molecular determinant.

Together, the findings indicate that efflux-mediated factors are the main determinants of fluconazole resistance in oral C. albicans in breast cancer patients, which are facilitated by target-gene mutations and biofilm-related survival. The combination of clinical risk factors, phenotypic resistance, and patterns of molecular activations highlights a sensible and biologically plausible model of resistance within this population of oncology.

4. DISCUSSION

A combination of both clinical and molecular data in the present case-control study reveals that oral Candida carriage and symptomatic candidiasis is significantly higher in breast cancer patients compared to age-matched healthy women which supports the notion that oncologic therapy and the induction of mucosal and immunologic in response to therapy, changes colonization by Candida to a pathogenic form [32]. This has been backed by close findings in oncology cohorts that have indicated that chemotherapy, exposure of the mucosal to antibiotics and mucosal injury contributes to fungal overgrowth and clinical disease [32]. Besides the validation of the increased burden, we find that there is a clinically significant rate of fluconazole resistance, which is linked to well-established molecular processes. The resistance of fluconazole among the patient isolates was largely compared with controls, which is consistent with the international trends on the rise of the azole resistance of Candida among the species and clinical environments [33-34]. Selective pressure which is sustained in the attempt of oncology environments is a consequence of the regular use of azoles which is either in an empirical or prophylactic manner. The recent investigations on the antifungal therapy in cancer-related mucosal disease highlight that, though the azoles reduce the cases of clinical occurrence, there are still breakthrough infections throughout the antifungal pressure, which facilitates the adaptive response, such as tolerance and resistance [35]. In the case of the molecular aspect, the resistant isolates of C. albicans were highly upregulated in efflux-regulated genes, especially, CDR1, an increase in the expression of MDR1, and a moderate but significant increase in ERG11. This profile matches with the current models that characterize azole resistance as mainly efflux-based, frequently coupled with target-based mechanisms and regulation network activation [33-34]. Similar results are seen in RT-qPCR clinical isolates, where an increased CDR1/MDR1 expression often goes hand in hand with ERG11 alterations in strains non-susceptible to fluconazole [36-38]. Primacy of efflux signatures is clinically significant as resistance can be achieved without target-gene mutations and may be a cause of cross-azole reduced susceptibility [33-34]. The key role of Cdr1 is also supported by structural studies that show molecular characteristics of drug transport and substrate recognition that results in decreased accumulation of the drug in the cell [39]. In our group, the increase in heightened CDR1 expression became the most predictive independent resistance predictor. Target-based resistance also played its role: ERG11 mutations were found in about one-half of resistant isolates and can be interpreted to support a mixed-mechanism model in which efflux is the dominant mechanism but often goes along with target modification [33-34]. Sequencing thus becomes interpretive especially when it is combined with expression profiling. Another mechanistic tier was biofilm formation. There were much larger biofilm biomass generated by the resistant isolates, and biofilm phenotype did not intersect with resistance. The mechanisms to encourage the antifungal tolerance of biofilms include less penetration of drugs and drugs, metabolic heterogeneity, and extracellular defensive formation [40]. Recent research also establishes relations between biofilm formation, efflux liberation, and lessened azole sensitivity [41-42]. The correlation between the expression of CDR1 and biofilm biomass is probably a result of convergent evolution in response to the antifungal pressure. As a clinical factor, prior exposure to fluconazole and mucosal severity also indicated resistance, which aligns with the principle of stewardship and with the established effect of the disruption of mucosal barriers and dysbiosis in patients undergoing chemotherapy [32-35]. The colonization and resistance rates were much lower in controls, which highlights the importance of cancer-related exposures. The fact that non-albicans Candida have been reported in both groups is consistent with worldwide accounts of rising varieties of Candida and worries that there is an increase in intra species that are less susceptible to Candida e.g. C. glabrata and C. krusei [33-34-43-44]. ITS sequencing methodologically

increased the strength of species identification, and compliance with new MIQE 2.0 qPCR reporting criteria improved reproducibility and interpretive rigor [45]. All in all, these results suggest that fluconazole resistance in patients with oral candidiasis and breast cancer is widespread, and it is primarily mediated by efflux pump overexpression, which is often accompanied by changes in the target and supported by biofilm-related persistence. This can be clinically useful in supporting documentation of the previous exposure to azole, early species identification, and selective application of susceptibility testing and molecular assays in cases of recurrence or refractory cases, and future studies should enhance resistance network analysis and include longitudinal sampling to differentiate stable resistance and transient tolerance [35].

5. CONCLUSIONS

This case control study provides evidence of greater prevalence of oral Candida colonization and fluconazole resistance among breast cancer patients aged 50 -75 years as opposed to healthy control age-matched healthy individuals. Candida albicans continued to be the most common species but a significant clinical percentage of isolates was increasingly found to have decreased fluconazole susceptibility.

Molecular demonstrations indicated that resistance to fluconazole was mainly due to overexpression of genes of efflux pumps, especially CDR1, with secondary effects linked to an increase in MDR1, and ERG11 mutations. Increased build of biofilms also defined resistant isolates indicating that genetic and phenotypic adjustments play a role in creating low antifungal susceptibility in the population.

Resistance was also linked independently to prior azole exposure and mucositis severity, with implications of the effect of therapeutic pressure and mucosal damage on antifungal resistance dynamics in oncology environments.

All these results together justify the way molecular resistance profiling should be integrated into antifungal stewardship interventions in cancer patients. Timely detection of high risk cases and resistant isolates can be of benefit in terms of decision making in therapeutics and reduce the further development of azole resistance.

REFERENCES

1. Carvalho, J. P., Rodrigues, J., Rodrigues, C. F., Andrade, J. C., & Rajão, A. (2026, January). Distribution of Candida Species Causing Oral Candidiasis in High-Risk Populations: A Systematic Review. In *Healthcare* (Vol. 14, No. 2, p. 159). MDPI.
2. Carvalho, J. P., Rodrigues, J., Rodrigues, C. F., Andrade, J. C., & Rajão, A. (2026, January). Distribution of Candida Species Causing Oral Candidiasis in High-Risk Populations: A Systematic Review. In *Healthcare* (Vol. 14, No. 2, p. 159). MDPI.
3. Kumar, N. (2026). Updated guidelines on the oral and dental management of patients before, during and after cancer therapy. *Faculty Dental Journal*, *17*(1), 7-7.
4. Kamel, A. H. M., AlKindi, F., AlHarrasi, R., Al-Sayegh, H., & AlKindi, N. (2026). Enhancing Oral Health Literacy to Prevent Medication-Related Osteonecrosis of the Jaw: Awareness and Compliance Among Breast Cancer Patients Receiving Bone-Modifying Agents. *Journal of Cancer Education*, 1-9.
5. Daniels-Donkor, S. S., & Marryat, L. (2026). Health system barriers and facilitators influencing the uptake of cervical cancer screening among women in sub-Saharan Africa: systematic review and meta-synthesis. *BMC Health Services Research*.
6. Idris, M. Z., Wimardhani, Y. S., Apsari, W., & Mandasari, M. (2026). Head and Neck Radiotherapy Short-Term Oral Complications: Effect on Oral Health-Related Quality of Life at Dharmais Cancer Hospital. *European Journal of Dentistry*.
7. Panneerselvam, V. P., Vajravelu, L. K., Lathakumari, R. H., Vimala, P. B., Nair, D. M., & Thulukanam, J. (2025). Bacteriophage-based therapies in oral cancer: A new frontier in oncology. *Cancer Pathogenesis and Therapy*, *3*(06), 453-465.
8. Hussain, S. A., Ghimouz, R., Panda, S. P., Panigrahy, U. P., Marunganathan, V., Shaik, M. R., ... & Guru, A. (2025). Synergistic effects of copper oxide-stigmasterol nanoparticles: A novel therapeutic strategy for oral pathogen biofilms and oral cancer. *Materials Technology*, *40*(1), 2476999.
9. Smadu, S. G., Tetradov, S. C., Ene, L., Oprisan, C., Lazăr, D. Ș., & Florescu, S. A. (2026). Diagnostic Biomarkers for Invasive Candidiasis: A Clinician-Oriented Review. *Journal of Fungi*, *12*(1), 55.
10. Aydemir, O., Koc, H., Hıdır, S. A., Ciftci, I. H., Toptan, H., Tikveşli, M., & Koroglu, M. (2026). Comparative assessment of the broth microdilution and VITEK 2 systems for antifungal susceptibility testing of Candida auris (Candidozyma auris) Isolates. *BMC microbiology*.
11. Jain, K., Wadhwa, K., Malik, M., Haque, S., Prieto, M. A., & Kaur, H. (2026, January). Genomic insights of Candida krusei, an emerging fungal pathogen with intrinsic antifungal resistance. In *Open Forum Infectious Diseases* (Vol. 13, No. 1, p. ofaf742). US: Oxford University Press.
12. De-la-Pinta, I., Marcos-Arias, C., Sevillano, E., Eraso, E., & Quindós, G. (2026). Emergent Candida Species on Healthcare Surfaces: Abiotic Reservoirs as a Source of Invasive Candidiasis. *Microorganisms*, *14*(2), 367.

13. Kong, X., Xie, W., Fu, M., Feng, P., Li, Z., Liu, H., ... & Liu, W. (2026). Antifungal resistance of the Trichophyton mentagrophytes/Trichophyton interdigitale species complex: insights from the China antifungal resistance dermatophytes surveillance network study (CARDS). *Journal of the European Academy of Dermatology and Venereology*, *40*(2), 199-209.
14. Soto-Debrán, J. C., Sánchez-Íñigo, F. J., Calvo-López, A. B., Alguacil-Cuéllar, L., Hrynzovska, A. A., Mellado, E., ... & Alastruey-Izquierdo, A. (2026). High prevalence of azole resistance among environmental Aspergillus fumigatus isolates from outdoor air in Madrid, Spain. *Frontiers in Microbiology*, *16*, 1722314.
15. Shaw, D., Thakur, S., Ghosh, A., Dogra, S., Agnihotri, S., Narang, T., ... & Rudramurthy, S. M. (2026). Efflux-mediated multidrug resistance mechanism in Trichophyton indotineae and Trichophyton rubrum; role of ABC transporters and MFS gene. *Journal of Antimicrobial Chemotherapy*, *81*(1), dkaf434.
16. Shaw, D., Thakur, S., Ghosh, A., Dogra, S., Agnihotri, S., Narang, T., ... & Rudramurthy, S. M. (2026). Efflux-mediated multidrug resistance mechanism in Trichophyton indotineae and Trichophyton rubrum; role of ABC transporters and MFS gene. *Journal of Antimicrobial Chemotherapy*, *81*(1), dkaf434.
17. Tsai, M. H., Hsieh, C. H., Tsai, I. A., Chang, C. M., Chen, T. W., Hsu, J. F., ... & Lu, J. J. (2026). Genetic variation and mutational determinants of azole resistance in Candida albicans strains of oropharyngeal colonization in HIV patients and bloodstream infections.
18. Esquivel, B. D., Santos, A., Rybak, J. M., Santana, D. J., Rogers, P. D., & White, T. C. (2026). Mutations in ERG11, TAC1B, and CDR1 reduce fluconazole accumulation in drug-resistant Candidozyma auris isolates. *mBio*, e03957-25.
19. Sousa, G., Correia, I., & Bezerra, A. R. (2026). Experimental Evolution of Pathogenic Candida spp.: Insights into Adaptive Processes and Evolutionary Dynamics. *Microorganisms*, *14*(2), 273.
20. Jain, K., Wadhwa, K., Malik, M., Haque, S., Prieto, M. A., & Kaur, H. (2026, January). Genomic insights of Candida krusei, an emerging fungal pathogen with intrinsic antifungal resistance. In *Open Forum Infectious Diseases* (Vol. 13, No. 1, p. ofaf742). US: Oxford University Press.
21. Kim, S. H., Kim, H. M., Chung, D. R., Ko, J. H., Huh, K., Cho, S. Y., ... & Peck, K. R. (2026). In vitro activity of double and triple antimicrobial combinations against carbapenem-resistant Pseudomonas aeruginosa biofilm. *Journal of Antimicrobial Chemotherapy*, *81*(3).
22. Jasim, H. F., Majeed, N. S., Salam, A. A., Hamad, R. H., Behrouzi, Y., Rajabi, E., & Shahbazi, R. (2026). Antibiotic Resistance, Biofilm Genes, and smeDEF Efflux Pump in Clinical Stenotrophomonas maltophilia Isolates From Iran. *MicrobiologyOpen*, *15*(1), e70222.
23. Soto-Debrán, J. C., Sánchez-Íñigo, F. J., Calvo-López, A. B., Alguacil-Cuéllar, L., Hrynzovska, A. A., Mellado, E., ... & Alastruey-Izquierdo, A. (2026). High prevalence of azole resistance among environmental Aspergillus fumigatus isolates from outdoor air in Madrid, Spain. *Frontiers in Microbiology*, *16*, 1722314.
24. Salmanton-García, J., de Almeida Jr, J. N., & Colombo, A. L. (2026). Candidozyma auris (formerly Candida auris): Resistant, long-lasting, and everywhere. *Clinical Microbiology and Infection*.
25. Drake, A., Sassoon, I., Armitage, J., Abbas, S., Maudling, R., Gupta-Wright, A., ... & Shorten, T. (2026). Country governance of antimicrobial resistance (AMR) surveillance: observations on global progress and aid programme effectiveness using data from the Tracking AMR Country Self-Assessment Survey (TrACSS). *Globalization and Health*.
26. Khan, S., Chakraborty, M., Wu, F., Chen, N., Wang, T., Chan, Y. T., ... & Winer, D. A. (2026). B cells drive CD4 T cell immunosenescence and age-associated health decline. *Science Immunology*, *11*(115), eadv7615.
27. Sambre, S., Chavan, P., Girse, H., & Gajbhiye, K. R. (2026). Antifungal drugs, resistance towards them, and their mechanisms. In *Nanotechnology Applications for the Diagnosis and Therapeutic Treatment of Fungal Diseases* (pp. 69-96). Academic Press.
28. Liu, C., Rosen, E. A., Stohs, E. J., Imlay, H., Nigo, M., Gottesdiener, L. S., ... & Abbo, L. M. (2026). Tackling antimicrobial resistance in people who are immunocompromised: leveraging diagnostic and antimicrobial stewardship. *The Lancet Infectious Diseases*, *26*(1), e30-e48.
29. Wierenga, A. T., Hesp, L. B., Simpelaar, A., Morsink, L. M., Woolthuis, C. M., Schuringa, J. J., ... & Mulder, A. B. (2026). Validation of a Multiplex mRNA-and gDNA-Based Droplet Digital PCR Assay in Acute Myeloid Leukemia Patients with an NPM1 Mutation. *Clinical Chemistry*, *72*(2), 281-290.
30. Harrington, A. A., Nickels, T. J., & Cunningham, K. W. (2026). Echinocandin tolerance and persistence in vitro are regulated by calcineurin signaling in Candida glabrata. *mBio*, *17*(1), e02546-25.
31. Dev, D., Tewari, A. K., Nandni, S., Gupta, P. K., Arzoo, K., Kumar, M., ... & Srivastava, J. N. (2026). Recent advancements in the development of resistance against white rust of rapeseed mustard caused by Albugo candida. *Discover Applied Sciences*.

32. Telbany, A., Farfour, H., Gomez, K., Soliman, Y., & Kachaamy, T. A. (2026). Candida Esophagitis in Patients with Solid Organ Cancers. *Journal of Clinical Medicine*, *15*(4), 1474.
33. Li, Y., Hind, C., Furner-Pardoe, J., Sutton, J. M., & Rahman, K. M. (2025). Understanding the mechanisms of resistance to azole antifungals in Candida species. *JAC-Antimicrobial Resistance*, *7*(3), dlaf106.
34. Eknure, C. S., Agarwal, A. P., Bachhav, Y., & Kumar, M. S. (2025). Unravelling azole resistance in fungal pathogens: molecular mechanisms, diagnostic challenges, and therapeutic strategies. *World Journal of Microbiology and Biotechnology*, *41*(12), 476.
35. Suwannaphong, P., Thammasit, P., Amsri, A., Ueangphairot, W., Muangwong, P., Kittidachanan, K., ... & Youngchim, S. (2025). Fluconazole tolerance and virulence adaptations of Candida albicans isolated from head and neck cancer patients. *Journal of Oral Microbiology*, *17*(1), 2559024.
36. Ahmadessa, S. M., & Ali, S. J. (2025). Molecular Characterization of Biofilm-related Virulence and Resistance genes in Candida albicans Isolates from Women with Vulvovaginitis. *Kurdistan Journal of Applied Research*, *10*(2), 68-76.
37. El-Kholy, M. A., Helaly, G. F., El Ghazzawi, E. F., El-Sawaf, G., & Shawky, S. M. (2023). Analysis of CDR1 and MDR1 gene expression and ERG11 substitutions in clinical Candida tropicalis isolates from Alexandria, Egypt. *Brazilian Journal of Microbiology*, *54*(4), 2609-2615.
38. Sánchez-Villacreses, E. M., Carlos Tapia, J., José Cáceres-Valdiviezo, M., Morey-León, G., Carlos Fernández-Cadena, J., & Andrade-Molina, D. M. (2025). Basal expression of ERG11, MDR1 and CDR1 genes in clinical isolates of Candida albicans from Ecuador: insights into azole resistance surveillance. *All Life*, *18*(1), 2551757.
39. Peng, Y., Lu, Y., Sun, H., Ma, J., Li, X., Han, X., ... & Yan, Z. (2024). Cryo-EM structures of Candida albicans Cdr1 reveal azole-substrate recognition and inhibitor blocking mechanisms. *Nature communications*, *15*(1), 7722.
40. Fan, F., Liu, Y., Liu, Y., Lv, R., Sun, W., Ding, W., ... & Qu, W. (2022). Candida albicans biofilms: antifungal resistance, immune evasion, and emerging therapeutic strategies. *International journal of antimicrobial agents*, *60*(5-6), 106673.
41. Alvarez, L., Kumaran, K. S., Nitha, B., & Sivasubramani, K. (2025). Evaluation of biofilm formation and antimicrobial susceptibility (drug resistance) of Candida albicans isolates. *Brazilian Journal of Microbiology*, *56*(1), 353-364.
42. Li, S., Shen, Z., Wang, S., Peng, Y., & Qi, W. (2025). Study on the impact of biofilm formation by Candida albicans in recurrent vulvovaginal candidiasis on drug susceptibility. *Frontiers in Cellular and Infection Microbiology*, *15*, 1663099.
43. Daneshnia, F., de Almeida Júnior, J. N., Ilkit, M., Lombardi, L., Perry, A. M., Gao, M., ... & Arastehfar, A. (2023). Worldwide emergence of fluconazole-resistant Candida parapsilosis: current framework and future research roadmap. *The Lancet Microbe*, *4*(6), e470-e480.
44. Tkaczyk, M., Kuśka-Kielbratowska, A., Fiegler-Rudol, J., Niemczyk, W., Mertas, A., Skaba, D., & Wiench, R. (2025). The Prevalence and Drug Susceptibility of Candida Species and an Analysis of Risk Factors for Oral Candidiasis—A Retrospective Study. *Antibiotics*, *14*(9), 876.
45. Bustin, S. A., Ruijter, J. M., van den Hoff, M. J., Kubista, M., Pfaffl, M. W., Shipley, G. L., ... & Wittwer, C. T. (2025). MIQE 2.0: revision of the minimum information for publication of quantitative real-time PCR experiments guidelines. *Clinical chemistry*, *71*(6), 634-651.