

Candida tropicalis distribution and drug resistance is correlated with ERG11 and UPC2 expression

Dan Wang

hospital

Na An

hospital

Yuwei Yang

hospital

Xiangui Yang

Abertawe Bro Morgannwg University Health Board

Yingzi Fan

hospital

Jiafu Feng (✉ jiafufengacad@foxmail.com)

hospital <https://orcid.org/0000-0003-4240-0101>

Research

Keywords: *Candida tropicalis*, drug resistance, ERG11, UPC2

Posted Date: July 16th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-21992/v2>

License:   This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Version of Record: A version of this preprint was published at Antimicrobial Resistance and Infection Control on March 15th, 2021. See the published version at <https://doi.org/10.1186/s13756-021-00890-2>.

Abstract

Objective This study analyzed the distribution and drug resistance of *Candida tropicalis* (*C. tropicalis*) and the relationship between ERG11 and UPC2 expression and resistance to azole antifungal agents. **Methods** *C. tropicalis* was cultured and identified by Sabouraud Agar Medium, CHROM Agar Candida and ATB tests (Bio-Mérieux, France). Total RNA was extracted from the collected strains, and the ERG11 and UPC2 mRNA expression levels were analyzed by quantitative real-time PCR. **Results** In total, 2872 clinical isolates of *Candida*, including 319 strains of *C. tropicalis*, were analyzed herein; they were mainly obtained from the Departments of Respiratory Medicine and ICU. The strains were predominantly isolated from airway secretion samples, and the detection trend in four years was mainly related to the type of department and specimens. The resistance rates of *C. tropicalis* to fluconazole, itraconazole and voriconazole had been increasing year by year. The mRNA expression levels of ERG11 and UPC2 in the fluconazole-resistant group were significantly higher than they were in the sensitive group. In addition, there was a significant positive linear correlation between these two genes in the fluconazole-resistant group. **Conclusions** Overexpression of the ERG11 and UPC2 genes in *C. tropicalis* could increase resistance to azole antifungal drugs. The routine testing for ERG11 and UPC2 in high-risk patients in key departments would provide a theoretical basis for the rational application of azole antifungal drugs.

Introduction

Candida tropicalis (*C. tropicalis*) is widely distributed in nature and is the main bacterium that colonizes human skin, the oral cavity, and the digestive tract. Moreover, *C. tropicalis* is also an important conditional pathogenic *Candida* species that can cause nosocomial infection, the detection rate of which is second only to *Candida albicans* (*C. albicans*)[1]. Patients infected with *C. tropicalis* might suffer from infections in the lung, bloodstream, and urogenital tract, as well as systemic infection[2]. Importantly, the increasing drug-resistance of *C. tropicalis* has been reported in recent years. The global SENTRY antifungal surveillance report in 2013 showed that the resistance rate of *C. tropicalis* to fluconazole was 11.6% (in 31 countries total)[3]. Moreover, data from the China Invasive Fungal Resistance Monitoring Network (CHIF-NET) had shown that the resistance rate of *C. tropicalis* to fluconazole increased from 11.2% in 2009 to 42.7% in 2014[4]. Therefore, the infectious factors involved in *C. tropicalis* infection, the genotyping of drug-resistant strains, and the mechanism of drug resistance have caused widespread concern in recent years[5].

The resistance of *C. tropicalis* to azole antifungal drugs is mainly due to mutations and/or the overexpression of ergosterol synthase (i.e., the 14 α -demethylase, 14-DM)-encoding gene ERG11, the overexpression of the MDR1 gene (from the major facilitator super (MFS)-family)[6-7], and the overexpression of the ATP-binding cassette (ABC) transporter encoding CDR genes[8]. Among these disrupted genes, the mutation and overexpression of the 14-DM-encoding gene ERG11 have been extensively studied in relation to the drug resistance of *C. tropicalis*. The UPC2 gene encodes the zinc family transcription factor Upc2p, which exerts regulatory effects on the transcriptional level in *C.*

albicans[9]. However, it is still unclear whether the UPC2 gene could regulate the expression of ERG11 in *C. tropicalis*.

In this study, the distribution and drug resistance of *C. tropicalis* infection were explored, to determine the epidemiological characteristics of *Candida* in hospital. Moreover, the relationship between ERG11 and UPC2 expression and resistance to fluconazole was investigated to provide a basis for disease diagnosis and treatment in the clinic.

Materials And Methods

Strain sources

The samples obtained from each clinical department of the First Affiliated Hospital of Chengdu Medical College from January 2016 to December 2019 were sent to the laboratory, and the fungi were isolated and identified based on conventional methods. For strains repeatedly obtained from the same patient at the same site, only one strain was counted.

Fungal culture and preliminary identification

The strains were inoculated onto and cultured with Sao Paulo medium (Antu Biotechnology Co., Ltd., Zhengzhou, Henan, China). The unknown fungi that were isolated were streaked on slides and subjected to Gram staining. When spores or mycelium were observed, the strain was transfected into Chromagar color development medium (Antu Biotechnology Co., Ltd.), and then it was cultured at 35°C for 48 h. The fungal species were initially identified according to the different colors of the colonies.

Fungal identification and drug susceptibility test

The identification and susceptibility testing of the isolated fungi were performed with the ATB tests (Bio-Mérieux Co., Ltd., Lyon, France), the yeast identification kit (colorimetric method) (Bio-Mérieux Co., Ltd.) and the yeast-like fungal susceptibility kit (microdilution method) (Bio-Mérieux Co., Ltd.), according to the Performance Standards for Antifungal Susceptibility Testing of Yeasts (CLSI M60) recommended by the Clinical and Laboratory Standards Institute (CLSI)[10]. For fluconazole, the sensitivity referred to the minimum inhibitory concentration (MIC) $\leq 2 \mu\text{g/ml}$ and the drug resistance $\geq 8 \mu\text{g/ml}$. The quality control strain for the identification and drug-sensitivity test was *Candida parapsilosis* (ATCC22019).

Quantitative real-time PCR

In total, 50 strains of *C. tropicalis* (20 fluconazole-susceptible and 30 fluconazole-resistant strains) were collected. Total RNA was extracted from exponential-phase YPD broth cultures with an RNA extraction kit (Sangon Biotechnology Co., Ltd., Shanghai, China), according to the manufacturer's instructions. Cells were collected by centrifugation at 10,000 rpm for 1 min and then washed in DEPC-treated ddH₂O. Then the cells were re-suspended in 600 µl Snailase Reaction Buffer and 50 µl Snailase, which was vigorously shaken. The suspension was incubated at 37°C for 5 min, followed by the centrifugation. The supernatant was collected, and 400 µl Bufler Rlysis-Y was added. The supernatant was incubated at 65°C for 5 min and then quickly frozen at -20°C for 5 min. Then 200 µl Buffer YCA was added, following by centrifugation. The supernatant was collected, and RNA was recovered by chloroform extraction, followed by ethanol precipitation, which was finally re-suspended in 50 µl DEPC-treated ddH₂O. The cDNA template was obtained from the total RNA with the HiScript II Q RT SuperMix reverse transcription kit (Vazyme Biotechnology Co., Ltd., Nanjing, Jiangsu, China). Totally 2 µl total RNA, 4 µl 4×gDNA wiper Mix and 10 µl RNase free ddH₂O were mixed and incubated at 37°C for 5min. Then 4 µl 5×HiScript II qRT SuperMix was added, which was mixed gently. Reverse transcription was performed at 50°C for 15min and then at 85°C for 5 s in a thermocycler. The obtained cDNAs were diluted by 10 folds with distilled water. Quantitative real-time PCR was performed with ChamQ Universal SYBR qPCR Master Mix (Vazyme Biotechnology Co., Ltd.) on a CFX96 real-time quantitative PCR instrument (BIO-RAD, California, USA). Primers were synthesized by Sangon Biotech with the following sequences: ERG11, forward 5'-TGCCTGGTTCTTGTTCATTT-3' and reverse 5'-AATCGTTCAAGTCACCACCCT-3'; UPC2, forward 5'-GAGTGGAAACAACAACAACA-3' and reverse 5'-TAAATCCCCTAACCTGAAAGA-3'; and ACT1, forward 5'-TTTACGCTGGTTTCTCCTTGCC-3' and reverse 5'-GCAGCTTCCAAACCTAAATCGG-3'. The reaction conditions were as follows: 95°C for 30 s; 95°C for 10 s, and 60°C for 30 s, for a total of 40 cycles. The real-time quantitative PCR quality control strain was *C. tropicalis* (ATCC750), and ACT1 was used as an internal reference[11].

Statistical analysis

The distribution and drug sensitivity results of fungi were analyzed with WHONET 5.6 software. The distribution of *C. tropicalis* was analyzed by χ^2 test using SPSS 24.0 software. The distribution between four years was analyzed with χ^2 test, and the Cochran Q test was performed for the distribution of each year. The independent samples *t*-test was performed for the analysis of the ERG11 or UPC2 mRNA expression levels between the drug-sensitive and drug-resistant groups, and Spearman correlation analysis was also performed. $P < 0.05$ was considered statistically significant.

Results

Isolation of *Candida*

The distribution of various types of *Candida* strains detected in the hospital from 2016 to 2019 was analyzed. As shown in Fig. 1, a total of 2872 strains of *Candida* were detected. After the Cochran Q test, the composition ratio (i.e., the percentage of all detected *C. tropicalis* species) of various *Candida* species in each year showed statistical significance ($Q = 1101.094 - 1904.945$; all $P < 0.001$). For each year, *C. albicans* was the major strain, accounting for more than 60% of the total (up to 71.96% in 2017), which was followed by *Candida glabrata* (*C. glabrata*), accounting for approximately 15%. *C. tropicalis* ranked third, no significant change in the proportion between 2016, 2018 and 2019 (in which *C. tropicalis* represented approximately 13%, which fell to 7.04% in 2017). In addition, the comparison of the composition ratio of *Candida* over these four years also showed significant differences ($\chi^2 = 33.344$; $P = 0.004$). Additionally, the composition ratio of each kind of *Candida* was compared between these four years. Our results showed statistical significance only for *C. albicans* ($\chi^2 = 12.620$; $P = 0.006$) and *C. tropicalis* ($\chi^2 = 20.410$; $P < 0.001$), and the proportion of *C. albicans* exhibited a gradual decrease ($\chi^2 = 4.558$; $P = 0.033$) over these years. However, there were no differences in the detection over these years for *C. glabrata*, *C. tropicalis*, and *Candida krusei* (Additional file 1:Fig. S1).

Sources of *C. tropicalis* samples

The *C. tropicalis* samples collected from 2016-2019 were classified according to the sample sources, and the composition ratios were also analyzed. Our results showed that significant differences were observed in the proportion of samples from which *C. tropicalis* was detected in each year ($Q = 123.949 - 194.898$; $P < 0.001$) (Fig. 2). Moreover, for each year, the most common source of samples was airway secretion (more than 65%), which was followed by mid-stream urine (12%-25%). Although there was no significant difference in the composition ratio of the source for *C. tropicalis* samples for these four years ($\chi^2 = 14.858$; $P = 0.399$), the proportion of urine samples detected with *C. tropicalis* was significantly different between these years ($\chi^2 = 9.387$; $P = 0.025$). Furthermore, our results from the trend test showed that, except for the proportion in the stool samples ($\chi^2 = 3.550$; $P = 0.060$), the proportions in the airway secretions and urine samples increased over the years, but the proportions decreased for the other sample types year by year (all $P < 0.050$) (Additional file 2:Fig. S2).

Department distribution of *C. tropicalis*

The department sources of *C. tropicalis* from 2016-2019 were analyzed. Our results showed that, there were significant differences in the distribution of *C. tropicalis* in these departments from 2016 to 2019 ($Q = 40.746 - 92.691$; all $P < 0.001$). The departments with relatively high detection rates included the Departments of Respiratory Medicine, ICU, and Geriatrics (Fig. 3). Moreover, among the proportions of *C. tropicalis* detected in different departments, the detection rates of *C. tropicalis* in the Department of Respiratory Medicine were greater than 20% in 2016, 2017 and 2019, and they fell to 14.82% in 2018.

Furthermore, the amount of *C. tropicalis* detected in the ICU increased year by year, from 8.16% in 2016 to 37.03% in 2018, but it decreased to 12.35% in 2019. The proportions of *C. tropicalis* detected in the Department of Geriatrics were higher in 2016 (18.37%) and 2019 (23.46%) and lower in 2017 and 2018 (approximately 9%). The composition ratios of *C. tropicalis* detected in different departments between the four years suggested statistically significant differences ($\chi^2 = 58.045$; $P = 0.002$). However, in comparing the *C. tropicalis* amount detected in each department in each of the four years, statistically significant differences were observed in the amount of *C. tropicalis* in the Department of Geriatrics ($\chi^2 = 8.623$; $P = 0.035$) and the ICU ($\chi^2 = 27.148$; $P < 0.001$) (Additional file 3:Fig. S3).

Resistance of *C. tropicalis* to antifungal drugs

The resistance to azole antifungal agents such as fluconazole, itraconazole and voriconazole was analyzed in the samples of *C. tropicalis* collected from 2016 to 2019. Our results showed that *C. tropicalis* had high resistance rates to fluconazole, itraconazole, and voriconazole and even exhibited cross-resistance. In 2018, the resistance rate of *C. tropicalis* to fluconazole reached 39.2%, so there were most resistance fungus isolated in this year. There were no statistically significant differences in the resistance rates of *C. tropicalis* to azole antifungal drugs over these four years ($\chi^2 = 1.156$; $P = 0.979$).

Relative mRNA expression levels of ERG11 and UPC2 in *C. tropicalis*

To further study the resistance-related genes of *C. tropicalis*, the mRNA expression levels of ERG11 and UPC2 were detected with quantitative real-time PCR. Our results showed that the relative mRNA expression levels of ERG11 and UPC2 genes in *C. tropicalis* from the fluconazole-resistant group (27/30 strains fully resistant to fluconazole, itraconazole, and voriconazole) and fluconazole-sensitive group were normally distributed. Based on the **independent samples t-tests**, the relative mRNA expression level of ERG11 in the drug-resistant group was 1.579 ± 0.896 , while the relative mRNA expression of ERG11 in the sensitive group was 0.483 ± 0.259 , and the difference was statistically significant ($t = 4.511$; $P < 0.001$) (Fig. 4A). On the other hand, the relative mRNA expression level of UPC2 in the resistant group was 1.400 ± 0.919 , while the relative mRNA expression level of UPC2 in the sensitive group was 0.448 ± 0.272 , with a statistically significant difference ($t = 3.970$; $P < 0.001$) (Fig. 4B). These results suggest that the resistance of *C. tropicalis* to fluconazole is related to the expression levels of ERG11 and UPC2.

Correlation analysis of UPC2 and ERG11 mRNA expression in *C. tropicalis*

The mRNA expression levels of resistance-related genes (i.e., ERG11 and UPC2) in *C. tropicalis* were detected, and the correlation between the gene expression levels was further analyzed. Our results from Spearman correlation analysis showed that there was no linear correlation between the expression levels

of UPC2 and ERG11 in the sensitive group ($r = -0.074$; $P = 0.757$) (Fig. 5A). However, the UPC2 and ERG11 expression levels were positively correlated in the drug-resistance group ($r = 0.571$; $P = 0.001$) (Fig. 5B). These results suggest that the overexpression of fluconazole-resistant ERG11 in *C. tropicalis* may be related to the regulation of UPC2.

Discussion

C. tropicalis is a common conditional pathogenic fungus, and its rates of detection have been increasing over the past years. In this study, a total of 2872 strains of *Candida* were detected in samples collected from 2016 to 2019, of which *C. albicans* accounted for approximately 70%, while *C. tropicalis* ranked third, accounting for 12%. Moreover, the overall species composition of *Candida* showed statistically significant differences between the detection years. The analysis of the detection rate and drug sensitivity of *C. tropicalis* in our hospital showed that the resistance rate of *C. tropicalis* to azole antifungal drugs sharply increased. In this study, based on the increasing isolation rate and drug resistance rate of *C. tropicalis*, the distribution and drug resistance of *C. tropicalis* were analyzed, as well as the relationship between ERG11/UPC2 gene expression and resistance to azole antifungal drugs.

Our results showed that there was no significant difference in the overall species composition from *C. tropicalis* samples tested over these four years. Moreover, the main source of *C. tropicalis* was airway secretion, which might be related to the fungus being one of the upper respiratory tract-colonized fungi; further, *C. tropicalis* has been shown to form biofilms on invasive catheters (such as tracheal intubation) to resist disinfection[12]. *C. tropicalis* with reproductive growth is often detected in airway secretions. Therefore, it is necessary to rule out normal bacterial colonization or device contamination during diagnosis. Moreover, comprehensive prognosis should involve the patients' clinical manifestations and other test results. In addition, *C. tropicalis* was detected in the mid-stream urine samples, with a detection rate of 13%-25%, which had increased over the years. This phenomenon might be related to the increasing number of patients treated with invasive urinary tract operations and/or the increase in the number of mid-stream urine samples sent for examination. *C. tropicalis* has strong adhesion, penetration and destructive abilities in relation to mucous membranes, and its resistance to antifungal drugs is stronger than that of *C. albicans* [13]. When patients undergo invasive urinary tract operations, the urinary tract is exposed to the outside, and the body cannot effectively kill the fungi. These conditions would provide a convenient environment for the reproduction and growth of *C. tropicalis*, eventually leading to *Candida* infection.

The IDSA Invasive Candidiasis Clinical Practice Guidelines (2016) have pointed out that the high-risk factors for *Candida* infection include staying in the ICU, severe disease and/or broad-spectrum antibiotic used for more than 3 days[14]. This information suggests that the infection rate of *Candida* may be different in different clinical departments due to the disease severities. In this study, our results showed that from 2016 to 2019, the hospital departments with relatively high detection rates of *C. tropicalis* were the Departments of Respiratory Medicine and ICU, and detection mainly occurred in airway secretion samples. There were significant differences in the overall composition ratios of *C. tropicalis* between

these clinical departments and between the different years. The reason for the significant differences might be related to the high-risk factors for *Candida* infection and the types of diseases patients in these departments have. There were many patients with basic respiratory diseases in the Department of Respiratory Medicine; therefore, the detection rate of *C. tropicalis* was high, but it did decrease over these years. The results may be related to the correct collection of airway secretion samples and standardized submission for testing in the department. In addition, the detection rate of *C. tropicalis* in the ICU was high, and it increased year by year. These results might be because of the increasing number of critical and complicated patients and the subsequent repeated application of high-efficiency broad-spectrum antibacterial drugs[15]. Moreover, in the ICU, invasive procedures are often performed, such as tracheal intubation, tracheotomy and/or intubation[16], which might easily result in infection by conditional pathogenic fungi.

In this study, our results showed that there were no significant differences in the resistance rate of *C. tropicalis* to azole antifungals between these four years, but the resistance rate had been increasing year by year (with the rate of resistance to fluconazole being as high as 39.2%). The increased resistance rate of *C. tropicalis* to azole antifungal drugs might be related to the easy application of such drugs and the relatively mild adverse reactions[17]. In the clinic, a large number of patients with severe fungal infections and long-term application of these drugs were subjected to prophylactic treatments, which would lead to drug resistance [18]. Moreover, in this study, the ERG11 and UPC2 genes of 50 strains of *C. tropicalis* were assessed, and our results showed that the relative expression level of the ERG11 gene in the drug-resistant group was higher than it was in the sensitive group, which is in line with the findings from Cen *et al.*[19] regarding the high expression of ERG11 in fluconazole-resistant *C. tropicalis*. ERG11 overexpression could increase the amount of 14-DM in cells, which ensures ergosterol synthesis and the normal growth and reproduction of *Candida*, therefore leading to azole drug resistance[20-21]. Moreover, Jiang *et al.*[19] cloned Y132F and S154F ERG11 mutants from *C. tropicalis* and introduced them into *Saccharomyces cerevisiae* (*S. cerevisiae*) and showed that the sensitivity of *S. cerevisiae* to azole antifungal drugs, especially fluconazole, was decreased. These results suggest that Y132F and S154F are involved in the resistance of *C. tropicalis* to fluconazole. Moreover, our results showed that the expression level of UPC2 in the resistant group was also higher than that of the sensitive group, indicating that the overexpression of UPC2 may cause *C. tropicalis* to become resistant to azole antifungal drugs, which was consistent with the findings from Jiang *et al.*[22]. In this study, the correlation analysis of the ERG11 and UPC2 mRNA expression levels in *C. tropicalis* showed that there was a linear positive correlation between the genes in the drug-resistant group. These results indicated that when UPC2 was over-expressed in the fluconazole-resistant *C. tropicalis*, ERG11 would also be over-expressed. Therefore, the expression level of ERG11 might increase with the over-expression of UPC2. It has been known that UPC2 has transcriptional regulation in *C. albicans*. The over-expression of UPC2 in the fluconazole-resistant *C. albicans* can induce the over-expression of ERG11, a gene encoding 14-DM in the cell membrane, which can cause the strains to be resistant to fluconazole[23-24]. Therefore, our results suggest that the over-expression of UPC2 in the fluconazole-resistant *C. tropicalis* may effectively promote the over-expression of ERG11, and then increase the ergosterol synthase in cell membrane and

cause the resistance to azole antifungal drugs in *C. tropicalis*, especially fluconazole. However, Choi *et al.* [25] sequenced the UPC2 gene in *C. tropicalis*, and their results showed that the amino acid substitutions caused by mutations in the gene appeared not only in the resistance group overexpressing ERG11, but also in the sensitive group with no ERG11 overexpression. So far, no effective missense mutation has been detected in the UPC2 of fluconazole-resistant *C. tropicalis*, and therefore the reason for the overexpression of UPC2 needs further study. In this study, our results showed that the overexpression of ERG11 and UPC2 in *C. tropicalis* was related to fluconazole resistance, and they exhibited a linear relationship. If the expression of any gene of ERG11 and UPC2 can be routinely detected in clinic, the resistance of *C. tropicalis* to azole antifungal drugs would be evaluated according to the gene expression levels, which would bring more valuable guidance to the treatment of *C. tropicalis* infection. But drug resistance might be related to multiple factors, and in a few drug-resistant *C. tropicalis* without ERG11 and UPC2 overexpression, the mechanisms underlying drug resistance might be related to efflux pumps[26] and biofilm formation[27]. To fully understand the drug resistance mechanisms of *C. tropicalis*, it is necessary to comprehensively study the impacts of the mechanism on drug sensitivity. Based on these findings, further in-depth studies are still needed to investigate the transcriptional regulatory function of Upc2p in drug-resistant *C. tropicalis* and to explore how UPC2 overexpression regulates ERG11, thus leading to drug resistance to azole antifungal drugs.

Conclusions

In conclusion, *C. tropicalis* has become the most common pathogen responsible for non-*C. albicans* infection, and the drug resistance rate has gradually increased. It can often cause infections in patients with low immunity, basic diseases, invasive procedures, and/or long-term and large-dosage application of broad-spectrum antibiotics. Our results showed that the fluconazole resistance of *C. tropicalis* with ERG11 overexpression may be related to the regulation of the zinc family transcription factor Upc2p. Therefore, when selecting and administering azole antifungal drugs, in addition to drug sensitivity findings, clinicians should fully understand the species distribution, the formation of drug resistance, and the overexpression of ERG11 and UPC2 genes. Routine detection of ERG11 and UPC2 for high-risk patients in the clinic would contribute to early disease diagnosis and timely treatment to delay and prevent the development of resistance to *C. tropicalis*.

Declarations

Acknowledgements

We thank Jun Luo and Lin Yin for providing *C. tropicalis* strains.

Author's contributions

DW and NA conducted experiments, participated in data analysis, and drafted the initial manuscript. YY, XY and YF collected information and performed statistical analysis. JF designed the study and critically revised the manuscript. All authors readed and approved the final manuscript.

Funding

Not applicable.

Availability of data and materials

The data analyzed in this study are included in the manuscript.

Ethics approval and consent to participate

This was a retrospective study in which did not contain experiments using animals and human studies. The anonymised patient data and strains were collected and used during routine clinical practice, with patient consent. The research was approved by the Ethics Committee of the First Affiliated Hospital of Chengdu Medical College, and it was performed in accordance with the approved guidelines. Written informed consent were obtained from all participants.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author details

¹Department of Laboratory Medicine, the First Affiliated Hospital of Chengdu Medical College, Chengdu 610500, Sichuan Province, China. ²Department of Laboratory Medicine, Mianyang Central Hospital, Mianyang 621000, Sichuan Province, China.

References

1. Zuza-Alves DL, Silva-Rocha WP, Chaves GM. An Update on *Candida tropicalis* Based on Basic and Clinical Approaches. *Front Microbiol.* 2017;13(8):1927.
2. Gow NAR, Netea MG. Medical mycology and fungal immunology: new research perspectives addressing a major world health challenge. *Philos T R Soc B.*2016; 371(1709):20150462.
3. Castanheira M, Messer SA, Rhomberg PR, Pfaller MA. Antifungal susceptibility patterns of a global collection of fungal isolates: results of the SENTRY Antifungal Surveillance Program (2013) . *Diagn Micr Infec Dis.* 2016;85(2):200-204.
4. Fan X, Xiao M, Liao K, Kudinha T, Wang H, Zhang L, et al. Notable increasing trend in azole non-susceptible *Candida tropicalis* causing invasive candidiasis in China(August 2009 to July 2014):molecular epidemiology and clinical azole consumption. *Front Microbiol.* 2017; 8:464.
5. Arastehfar A, Daneshnia F, Hafez A, Khodavaisy S, Najafzadeh MJ, Charsizadeh A, et al. Antifungal susceptibility, genotyping, resistance mechanism, and clinical profile of *Candida tropicalis* blood isolates. *Med Mycol.* 2019;0:1-8.
6. Fan X, Xiao M, Zhang D, Huang JJ, Wang H, Hou X, et al. Molecular mechanisms of azole resistance in *Candida tropicalis* isolates causing invasive candidiasis in China. *Clin Microbiol Infec.* 2019;25(7):885-891.
7. Ksiezopolska E, Gabaldon T. Evolutionary Emergence of Drug Resistance in *Candida* Opportunistic Pathogens. *Genes.* 2019; 9(9):461.
8. Rocha MF, Bandeira SP, Alencar LP, Melo LM, Sales JA, Paiva M, et al. Azole Resistance in *Candida albicans* from Animals:Highlights on Efflux Pump Activity and Gene Overexpression. *Mycoses.*2017;60(7):462-468.
9. Vasicek EM, Berkow EL, Flowers SA, Barker KS, Rogers PD. UPC2 is universally essential for azole antifungal resistance in *Candida albicans*. *Eukaryot Cell.* 2014; 13(7):933-46.
10. Clinical and Laboratory Standards Institute. Performance Standards for Antifungal Susceptibility Testing of Yeasts M60 . 1st ed. USA: CLSI;2017.
11. Saikat P, Shreya S, Arunaloke C, Ghosh AK. Selection and evaluation of appropriate reference genes for RTqPCR based expression analysis in *Candida tropicalis* following azole treatment. *Sci Rep-UK.*2020;10:1972.
12. Ladero M, Blanco M, Calderon M, Lucio L, Martin Y, Blanco M, et al. *Candida tropicalis* biofilm formation and expression levels of the CTRG ALS-like genes in sessile cells. *Yeast.* 2019; 36(2):107-115.
13. Maria J, Marco J, Laura C, Diana G, Nancy E, Eine E, et al. Differential recognition of *Candida tropicalis*, *Candida guilliermondii*, *Candida krusei*, and *Candida auris* by human innate immune cells. *Infect Drug Resist.* 2019; 12: 783- 794.

14. Pappas PG, Kauffman CA, Andes DR, Clancy CJ, Marr KA, Luis OZ, et al. Clinical Practice Guideline for the Management of Candidiasis: 2016 Update by the Infectious Diseases Society of America. *Clin Infect Dis*. 2016; 62 (4):e1-50.
15. Erika L, Helena H, Nasser A, Nahid K. Species Distribution and Antifungal Drug Susceptibilities of Yeasts Isolated from the Blood Samples of Patients with Candidemia. *Sci Rep-UK*. 2019;9:3838.
16. Chen G, Tang Z, Bai X, Song X, Liu K, Zheng G, et al. Distribution and drug resistance of pathogens from sputum culture on patients with severe multiple injuries after tracheotomy. *China Journal of Modern Medicine*. 2009; 19: 1246-1248.
17. Kux, Leslie. Draft Guidance for Industry on Drug interaction studies-study design, data analysis, implications for dosing, and labeling recommendations; availability. *Federal Register*. 2012;77(34):9946.
18. Jin L, Cao Z, Wang Q, Wang Y, Wang X, Chen H, et al. MDR1 overexpression combined with ERG11 mutations induce high-level fluconazole resistance in *Candida tropicalis* clinical isolates. *BMC Infect Dis*.2019;18:162.
19. Jiang C, Dong D, Yu B, Cai G, Wang X, Ji Y, et al. Mechanisms of azole resistance in 52 clinical isolates of *Candida tropicalis* in China. *J Antimicrob Chemoth*. 2013; 68(4):778-785.
20. Alizadeh F , Khodavandi A, Zalakian S. Quantitation of ergosterol content and gene expression profile of ERG11 gene in fluconazole-resistant *Candida albicans* . *Curr Med Mycol*. 2017;3(1):13-19.
21. Feng W, Yang J, Xi Z, Qiao Z, Lv Y, Wang Y, et al. Mutations and/or Overexpressions of ERG4 and ERG11 Genes in Clinical Azoles-Resistant Isolates of *Candida albicans*. *Microb Drug Resist*. 2017;23(5):563-570.
22. Jiang C, Ni Q, Dong D, Zhang L, Li Z, Tian Y, et al. The Role of UPC2 Gene in Azole-Resistant *Candida tropicalis*. *Mycopathologia*. 2016;181(11-12):1-6.
23. Lohberger A, Coste AT, Sanglard D. Distinct roles of *Candida albicans* drug resistance transcription factors TAC1, MRR1, and UPC2 in virulence. *Eukaryot Cell*. 2014; 13(1):127-42.
24. Sarah MP, Bassel A, Sandra W, Deken XD, Raymond M, Turcotte B. *Candida albicans* zinc cluster protein Upc2p confers resistance to antifungal drugs and is an activator of ergosterol biosynthetic genes. *Antimicrob Agents Ch*. 2005;49(5):1745.
25. Choi MJ, Won EJ, Shin JH, Kim SH, Lee WG, Kim MN, et al. Resistance Mechanisms and Clinical Features of Fluconazole-Nonsusceptible *Candida tropicalis* Isolates Compared with Fluconazole-Less-Susceptible Isolates. *Antimicrob Agents Ch*. 2016;60(6):3653-3661.
26. Shi G, Shao J, Wang T , Wu D, Wang C. Mechanism of berberine-mediated fluconazole-susceptibility enhancement in clinical fluconazole-resistant *Candida tropicalis* isolates. *Biomed Pharmacother*. 2017;93:709-712.
27. Barros PP, Rossoni RD, Ribeiro F, Junqueira JC, Jorge AO. Temporal profile of biofilm formation, gene expression and virulence analysis in *Candida albicans* strains. *Mycopathologia*.2017;182(34):285-295.

Figures

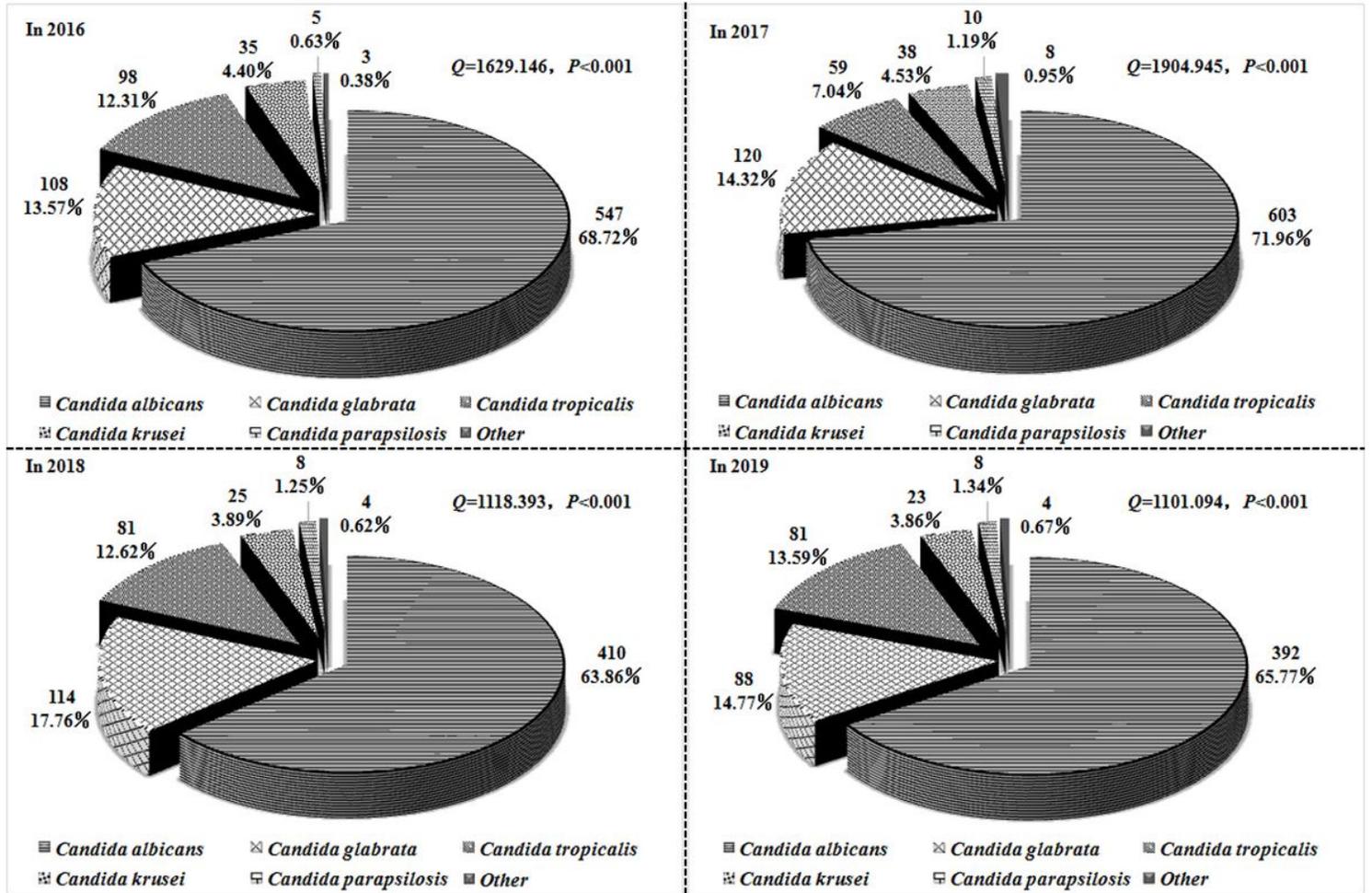


Figure 1

Composition of *Candida* species detected from 2016 to 2019. The composition ratios (cases and percentage) of *Candida* detected in 2016, 2017, 2018, and 2019.

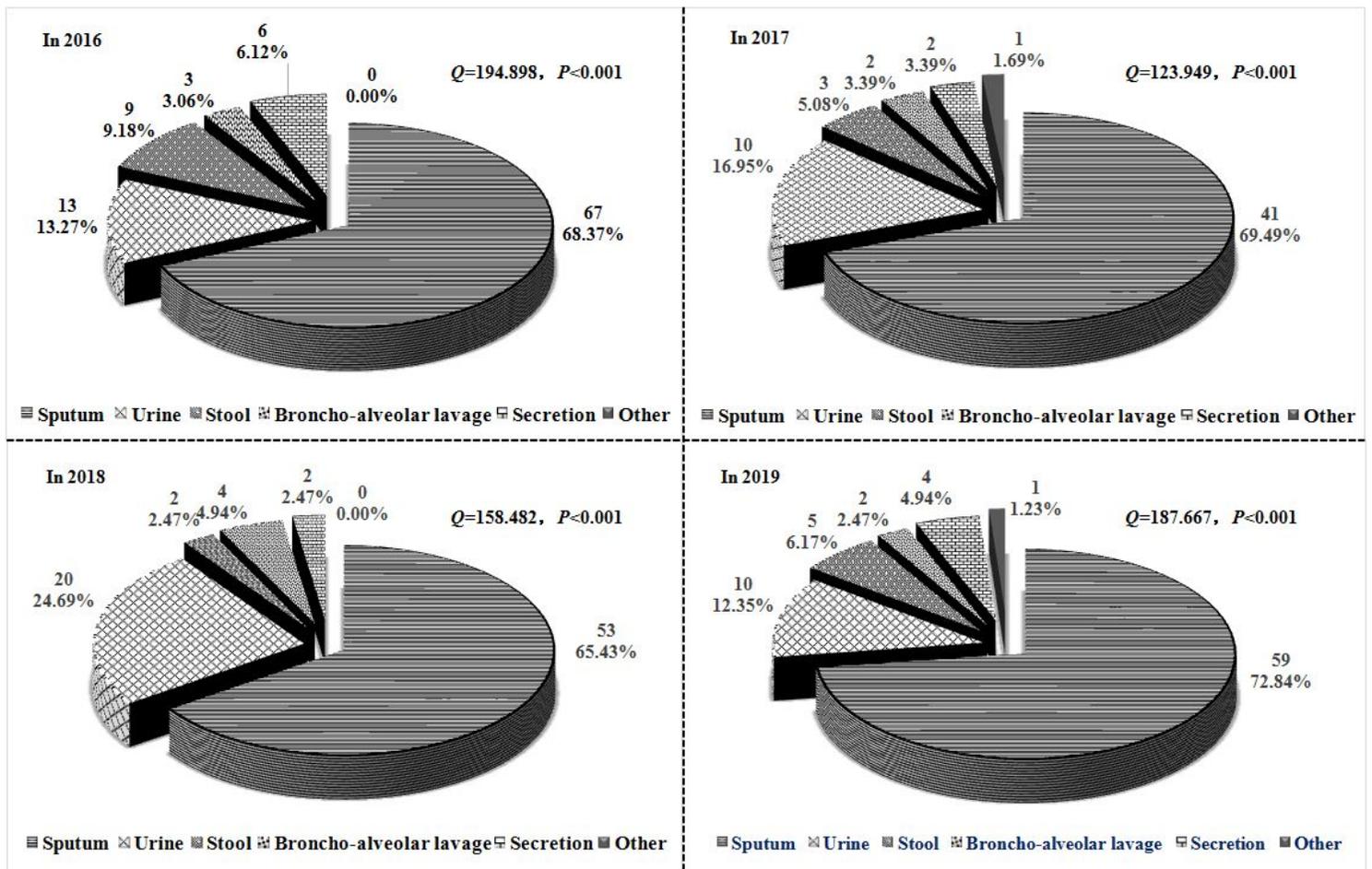


Figure 2

Sample composition of *C. tropicalis* from 2016 to 2019. The sample sources (cases and percentage) of *C. tropicalis* detected in 2016, 2017, 2018, and 2019.

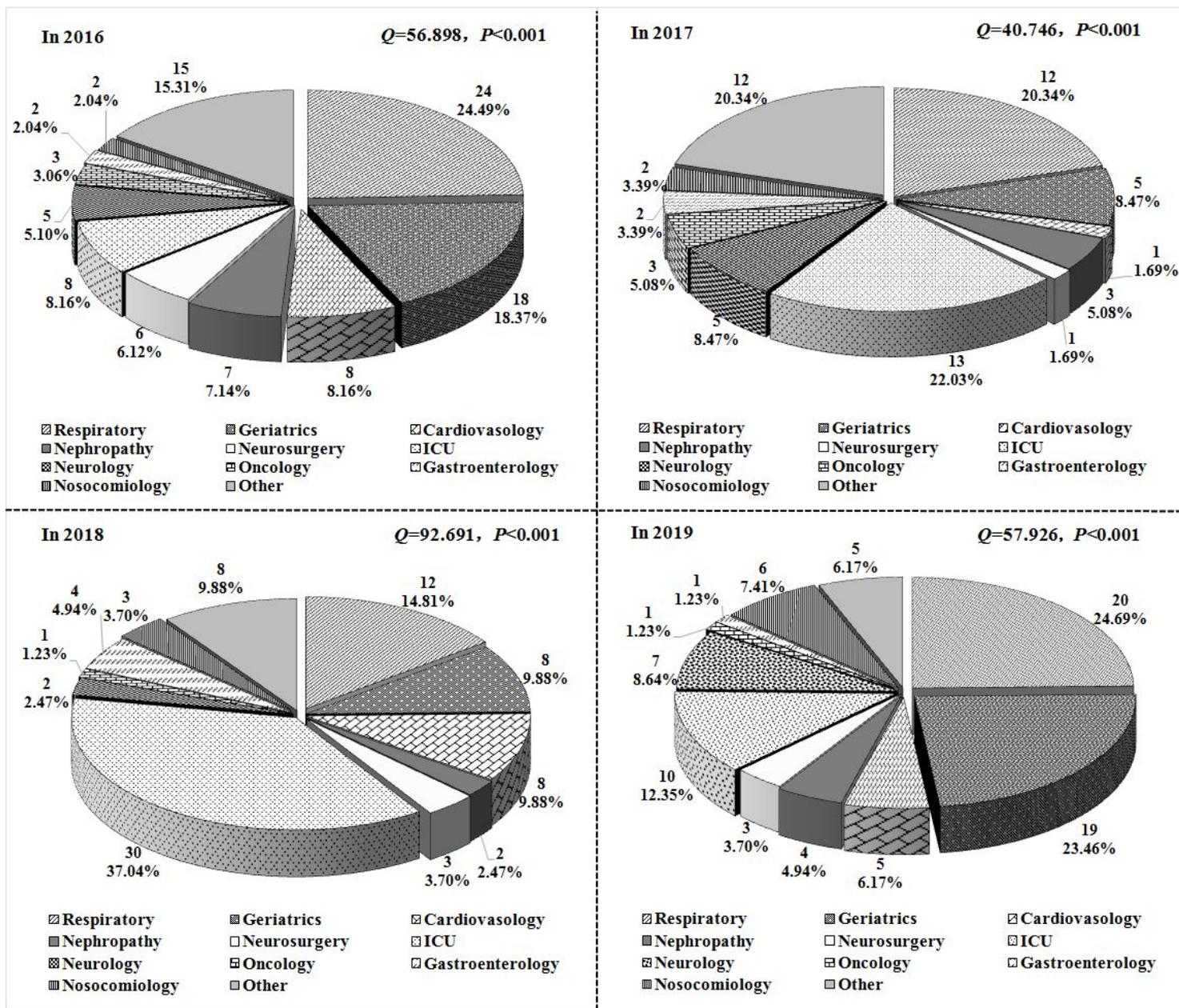


Figure 3

Distribution of *C. tropicalis* in different departments from 2016 to 2019. The distribution of *C. tropicalis* in different departments (cases and percentage) in 2016, 2017, 2018, and 2019.

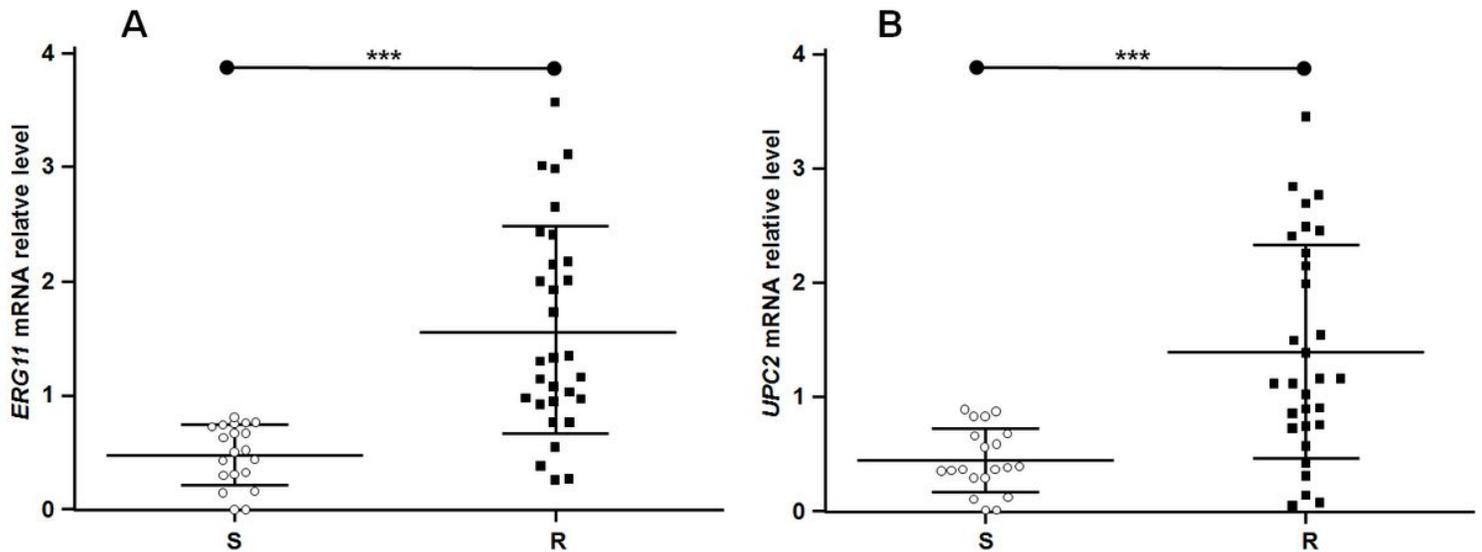


Figure 4

ERG11 and UPC2 expression levels in *C. tropicalis*. (A-B) Relative mRNA expression levels of ERG11 (A) and UPC2 (B) were analyzed and compared between the sensitive group (20 strains) and the resistant group (30 strains). $P < 0.001$. S, the fluconazole-sensitive group of *C. tropicalis*; and R, the fluconazole-resistant group of *C. tropicalis*.

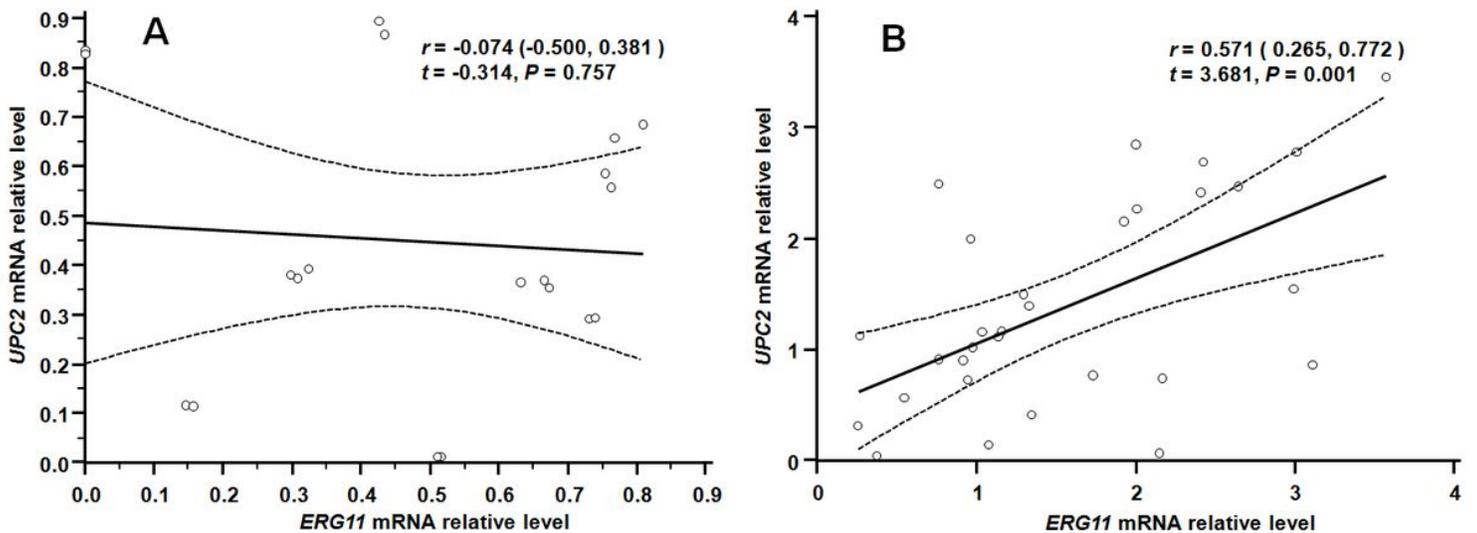


Figure 5

Correlation analysis between UPC2 and ERG11 expression levels. (A-B) The correlation between the UPC2 and ERG11 expression levels in the fluconazole-sensitive (A) and -resistant (B) groups of *C. tropicalis*. $P < 0.05$.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- FigS1.jpg
- FigS2.jpg
- FigS3.jpg