

# Molecular epidemiology and azole resistance mechanism study of *Candida guilliermondii* from a Chinese surveillance system

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## 1. Introduction

### 1.1 Incidence

The incidence of candidaemia cases due to *C. guilliermondii* is low, ranging from 1% to 3%.

### 1.2 Poor clinical outcomes

Poor clinical outcomes in immunocompromised patients

### 1.3 Higher resistance rates

*C. guilliermondii* were more resistant to antifungal agents compared to other *Candida* species

### 1.4 Limited studies

Little is known about the mechanism of fluconazole resistance in *C. guilliermondii*.

## 2. Materials and methods

### 2.1 Bacterial isolates

164 toxigenic isolates from 37 hospitals distributed in 18 provinces across China. Study period 2010-2014

### 2.2 Identification

Species identification was performed using the ITS gene sequencing.

### 2.3 Antifungal susceptibility testing

fluconazole, voriconazole, broth microdilution method.

### 2.4 Sequencing of ERG11

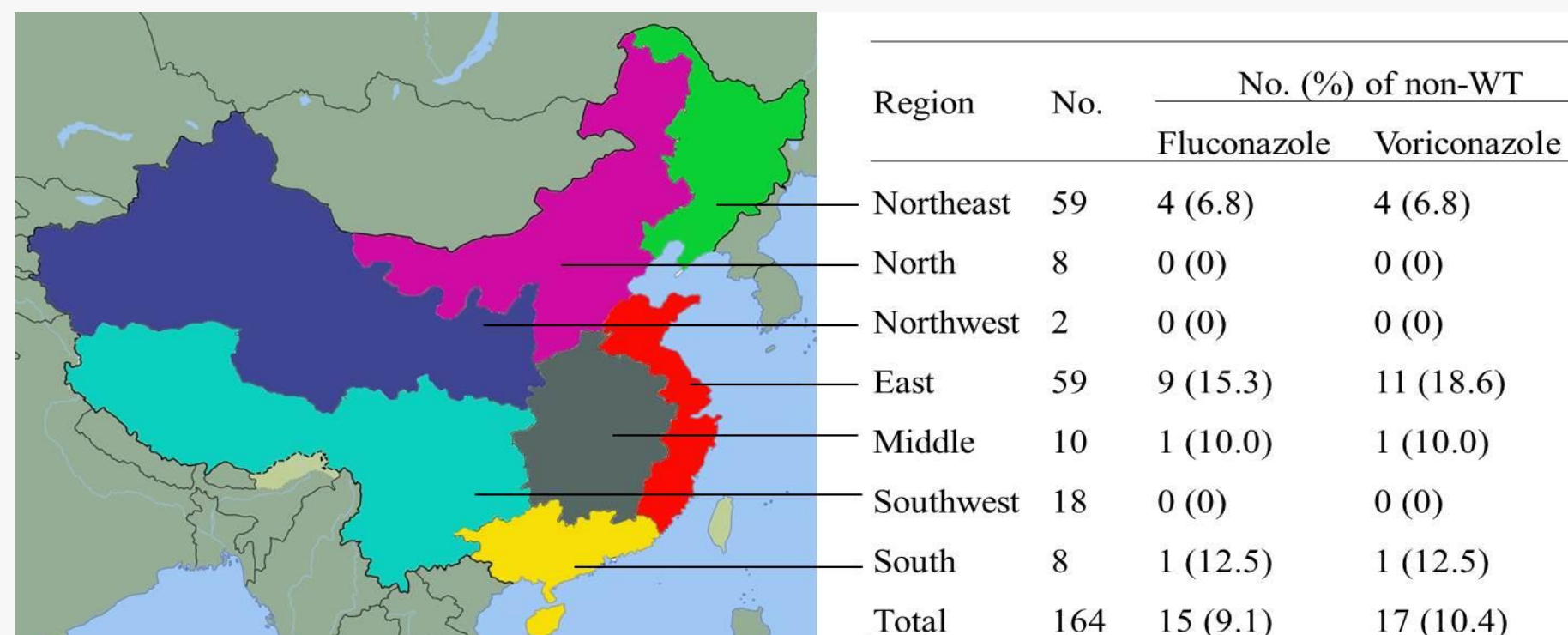
2.5 Microsatellite amplification and analysis three short tandem repeat (STR) markers (sc15, sc32 and sc72)

## 3. Results

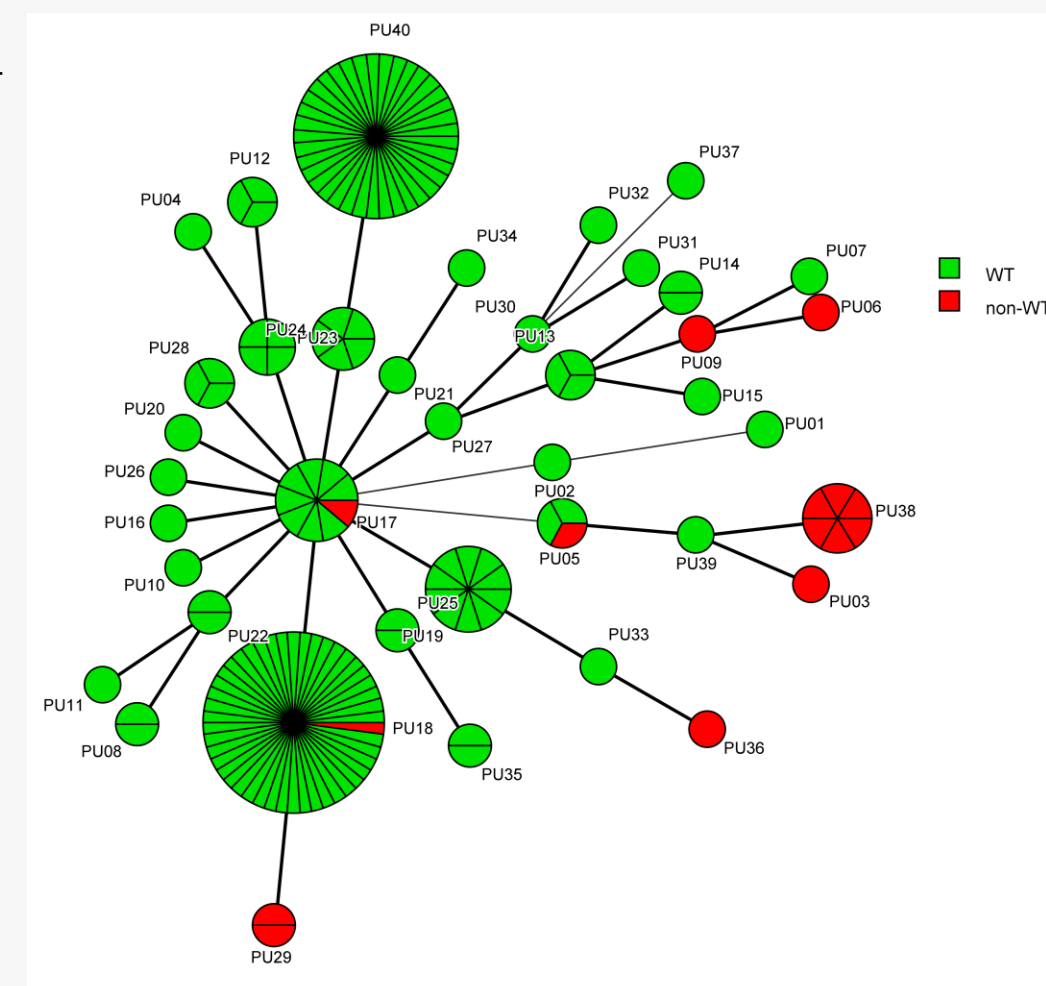
### 3.1 Results of in vitro azole susceptibility testing and 16 ERG11 sequence type analysis for 164 isolates

Sequence type	No.	%	No. (%) of non-WT isolates		Non-synonymous mutations of <i>ERG11</i>
			Fluconazole	Voriconazole	
1	65	39.6	1 (1.5)	1 (1.5)	Reference sequence
2	45	27.4	0 (0)	0 (0)	W37C
3	25	15.2	0 (0)	0 (0)	P518R
4	6	3.7	0 (0)	0 (0)	P430Q
5	3	1.8	0 (0)	0 (0)	D492N, P518R
6	1	0.6	0 (0)	0 (0)	W37C, P518R
7	1	0.6	0 (0)	0 (0)	Y41F, L328T, S346T, V410M, S420T, N485K
8	3	1.8	1 (33.3)	3 (100)	Y41F, L328T, S346T, V410M, S420T
9	4	2.4	4 (100)	4 (100)	Y41F, Y132F, L328T, S346T, V410M, S420T
10	1	0.6	1 (100)	1 (100)	G16S, Y41F, Y132F, M332I, S346T, S420T
11	2	1.2	0 (0)	0 (0)	G16S, F39L, R247K, L328I, S346T, S420T
12	2	1.2	2 (100)	2 (100)	Y41F, L328T, S346T, V410M, S420T, G459S
13	2	1.2	2 (100)	2 (100)	Y132F
14	2	1.2	2 (100)	2 (100)	K143R, P518R
15	1	0.6	1 (100)	1 (100)	Q469K
16	1	0.6	1 (100)	1 (100)	I303V
Total	164	100	15 (9.1)	17 (10.4)	

### 3.2 Geographical distribution *C. guilliermondii* in China



### 3.3 The association between microsatellite genotypes and antifungal susceptibility patterns of fluconazole of *C. guilliermondii*



## 4. Conclusions

4.1 This is the first molecular epidemiology and azole resistance mechanism study of *C. guilliermondii* in China.

4.2 The rate of non-WT isolates to fluconazole and voriconazole were high and the accurate contribution of ERG11 gene mutations to azole resistance need be confirmed by further studies.

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