Multiple amino acid substitutions in lanosterol 14α-demethylase contribute to azole resistance in Candida albicans

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Lanosterol 14α-demethylase (14DM) is the target of the azole antifungals, and alteration of the 14DM sequence leading to a decreased affinity of the enzyme for azoles is one of several potential mechanisms for resistance to these drugs in Candida albicans. In order to identify such alterations the authors investigated a collection of 19 C. albicans clinical isolates demonstrating either frank resistance (MICs ≥32 µg ml⁻¹) or dose-dependent resistance (MICs 8–16 µg ml⁻¹) to fluconazole. In cell-free extracts from four isolates, including the Darlington strain ATCC 64124, sensitivity of sterol biosynthesis to inhibition by fluconazole was greatly reduced, suggesting that alterations in the activity or affinity of the 14DM could contribute to resistance. Cloning and sequencing of the 14DM gene from these isolates revealed 12 different alterations (two to four per isolate) leading to changes in the deduced amino acid sequence. Five of these mutations have not previously been reported. To demonstrate that these alterations could affect fungal susceptibility to azoles, the 14DM genes from one sensitive and three resistant C. albicans strains were tagged at the carboxyl terminus with a c-myc epitope and expressed in Saccharomyces cerevisiae under control of the endogenous promoter. Transformants receiving 14DM genes from resistant strains had fluconazole MICs up to 32-fold higher than those of transformants receiving 14DM from a sensitive strain, although Western blot analysis indicated that the level of expressed 14DM was similar in all transformants. Amino acid substitutions in the 14DM gene from the Darlington strain also conferred a strong cross-resistance to ketoconazole. In conclusion, multiple genetic alterations in C. albicans 14DM, including several not previously reported, can affect the affinity of the enzyme for azoles and contribute to resistance of clinical isolates.

Keywords: azoles, fluconazole resistance, Candida albicans, lanosterol 14α-demethylase

INTRODUCTION

Candida albicans, an asexual, diploid and dimorphic fungus, is the most common opportunistic fungal pathogen of humans (Rinaldi, 1993). Immunocompromised patients are particularly susceptible to infection by C. albicans and more than 80% of AIDS patients suffer from oropharyngeal candidiasis during the course of their illness. The most commonly used antimycotic to prevent or combat mucosal and systemic candidiasis is fluconazole, because of its favourable bioavailability and safety profile (Feczko, 1992). The primary target of the azole antimycotics is lanosterol 14α-demethylase (14DM), a key enzyme in the ergosterol biosynthesis pathway (Hitchcock, 1993; Vanden Bossche & Koymans, 1998). 14DM is a P450 haem thiolate protein which catalyses, in the presence of NADPH reductase, the oxidative removal of the 14α-methyl group (C-32) from lanosterol (Aoyama et al., 1989). 14DM is inhibited by azoles in a competitive manner. The imidazole or triazole moiety of azoles replaces water in the sixth coordination position of the haem in the active site,
while substituent groups interact directly with the protein backbone (Hitchcock, 1993; Hitchcock et al., 1990; Vanden Bossche & Marichal, 1992; Vanden Bossche & Koymans, 1998; Yoshida & Aoyama, 1985).

The prolonged and repeated periods of treatment needed by AIDS patients have led to the increasing occurrence of candidiasis resistant to fluconazole therapy. Drug susceptibility testing of *C. albicans* isolated from these patients revealed in many cases that the organism had acquired resistance to fluconazole (Denning et al., 1997; Law et al., 1994; Rex et al., 1995; Tumbarello et al., 1996; White et al., 1998). Several mechanisms, independent of 14DM, have been reported which could contribute at least partially to fluconazole resistance in *Candida* species, including increased ergosterol biosynthesis (Vanden Bossche et al., 1992), a lesion in Δ5,6 sterol desaturase (Kelly et al., 1997), and lower intracellular accumulation of the drug (Marichal et al., 1995; Parkinson et al., 1995; Sanglard et al., 1995; Vanden Bossche et al., 1992; Venkateswarlu et al., 1996, 1997). This last mechanism seems to be the most common and is associated with the overexpression of two types of multidrug transporters, the ABC-binding cassette (ABC) transporters (Albertson et al., 1996; Miyazaki et al., 1998; Moran et al., 1998; Prasad et al., 1995; Sanglard et al., 1995, 1996, 1997; van Veen & Konings, 1998, White, 1997a) and the major facilitators (Albertson et al., 1996; Goldway et al., 1995; Moran et al., 1998; Sanglard et al., 1995, 1996; White, 1997a). Recently, additional *C. albicans* genes able to directly or indirectly confer resistance to fluconazole when expressed in *Saccharomyces cerevisiae* have been identified (Alarco et al., 1997; Sanglard et al., 1997).

An obvious mechanism for resistance to azoles would be alteration of their primary target, 14DM. Based on indirect biochemical evidence, both overexpression and mutation of 14DM have been suggested to explain acquired resistance to azoles in several fungi (Ishida et al., 1988; Joseph-Horne et al., 1995; Lamb et al., 1995; Orozco et al., 1998; Vanden Bossche et al., 1990, 1992, 1994; Venkateswarlu et al., 1997; White, 1997a, b). In *S. cerevisiae*, overexpression of 14DM encoded by *ERG11* leads to resistance to azoles, but the amplitude of resistance is rather weak, not exceeding fivefold (Doignon et al., 1993; Kalb et al., 1986; Kelly et al., 1993). Several studies have supported the concept that azole resistance can be due to mutation(s) in 14DM (Lamb et al., 1997; Loeffler et al., 1997; White, 1997b).

Substitution of the highly conserved residue T315A in the *C. albicans* 14DM gene (*CaERG11*, also called *ERG16* and *CYP51A1*) conferred a fivefold resistance to azoles when this gene was expressed in *S. cerevisiae* (Lamb et al., 1997). Sequencing of *CaERG11* from a number of clinical isolates revealed the existence of numerous amino acid substitutions in the gene amplified from resistant isolates, suggesting a possible link with the resistant phenotype (Loeffler et al., 1997). Lower sensitivity of sterol biosynthesis to fluconazole in cell-free extracts from a fluconazole-resistant *C. albicans* isolate correlates with the amino acid substitution R467L in *CaERG11* at both loci in the diploid genome resulting from a loss of allelic variation (White, 1997b).

Very recently, Sanglard et al. (1998) have formally demonstrated that several mutations in *CaERG11* can confer azole resistance upon *S. cerevisiae*. Interestingly, a single point mutation does not seem to drastically affect azole sensitivity of *CaERG11* but combinations of point mutations, principally G129A with G464S, Y132H with S405F, or Y132H with G484S, have cooperative effects (Sanglard et al., 1998).

The present study was performed as part of an ongoing project to develop novel approaches to overcoming fungal drug resistance. Using a collection of fluconazole-resistant clinical isolates, we first identified potentially altered 14DM by measuring sensitivity to azole of sterol synthesis in cell-free extracts. Cloning and sequencing of *CaERG11* from the four isolates from which cell-free sterol synthesis was insensitive to fluconazole revealed the presence of several amino acid substitutions in each of them. Five of the 12 identified amino acid substitutions have not been previously reported and all their combinations are novel. Finally, we show that expression of altered *CaERG11* in *S. cerevisiae* resulted in increased resistance to fluconazole and, to a variable extent, also to ketoconazole.

**METHODS**

**Strains.** Azole-resistant clinical isolates were from patients who had failed therapy with fluconazole and were obtained from clinical centres in Europe, North America and Australia. The Darlington strain, ATCC 64124, originally isolated from a patient suffering from chronic mucocutaneous candidiasis and treated with ketoconazole (Ryley et al., 1984), was obtained from the American Type Culture Collection. Species were identified using the API 20C test (bioMérieux), as well as CHROMagar (Mast Diagnostica) and Albicans ID (bioMérieux). The *S. cerevisiae* strains INV5C2 (MATα his3-Δ200 ured-167) and HR1 (ura3-52 trp1 leu2 his3-Δ200) were obtained from Invitrogen and Anneliese Karwan (Vienna), respectively.

**MIC determinations.** Fluconazole, itraconazole and ketoconazole were prepared by Novartis Pharmaceuticals. Drug susceptibility testing of *Candida* species was performed in a broth macrodilution assay slightly modified from the NCCLS system (Galgiani et al., 1995), as previously described (Ryder et al., 1998). Drugs were prepared according to the recommendations of the NCCLS method. MIC was defined as the lowest drug concentration causing 80% inhibition of fungal growth. The assay was validated with the standard drugs fluconazole, amphoterin B (Bristol-Myers Squibb) and 5-flucytosine (Sigma) in three reference strains of *C. albicans*: ATCC 90028, ATCC 90029 and ATCC 24433 (Galgiani et al., 1995). The reference strains of *C. krusei* (ATCC 6258) and *C. parapsilosis* (ATCC 22019) were used to validate the assay with itraconazole and ketoconazole (Rex et al., 1996). To ensure reproducibility, strain ATCC 24433 was run in parallel with each set of assays; MICs with this strain never varied by more than one dilution.

A microdilution assay using a 96-well plate with a flat bottom and low-evaporation lid (Costar) was developed to test drug susceptibility of *S. cerevisiae*. Under the same conditions, the
micro assay gave similar results to those initially obtained with the macro assay. Briefly, to 200 µl per well of a cell suspension at 2.5 x 10^5 c.f.u. ml^{-1}, prepared in the same medium as for the macro assay but supplemented with 18% glucose (final concn 2%) and 0.2 mg adenine ml^{-1} (as well as 0.2 mg uracil ml^{-1} for untransformed cells), 2 µl of a serial twofold dilution of fluconazole or ketoconazole in DMSO was added. The plate was shaken for 10 min at 900 r.p.m. and incubated for 48 h at 32 °C in maximum relative humidity. Growth was monitored spectrophotometrically at 620 nm with a Digiscan microtitre plate reader (Asys Hitech) after having shaken the plates for 30 min at 900 r.p.m. MICs were defined as the minimal drug concentration reducing growth by ≥ 80%, in comparison with solvent controls.

**Sterol biosynthesis assay in whole cells or cell-free extracts.** Whole-cell ergosterol biosynthesis was measured by incorporation of [1,2,14C]acetate into nonsaponifiable lipids as described previously (Ryder, 1985; Ryder et al., 1984). Sterol synthesis in cell-free extracts, prepared as in Favre & Ryder (1997b) and Ryder (1987), was assayed in a final volume of 300 µl, consisting of 30 mM sodium/potassium phosphate pH 7.4, 0.5 mM DTT, 1 mM NAD, 1 mM NADP, 0.1 mM FAD, 3 mM glucose 6-phosphate, 5 mM ATP, 3 mM glutathione, 2.7 mM MnCl₂, 4 mM MgCl₂, and 0.5 µg l^{-1} (1.85 x 10^8 Bq) [RS]-[2,14C]mevalonate, supplemented with 1.25 mg protein from cell-free extracts and the appropriate concentration of antymycotic, added from a 50-fold concentrated stock prepared in DMSO. After 2 h incubation at 30 °C in a shaking water bath, reactions were terminated by the addition of 1 ml 15% KOH in 90% ethanol. Nonsaponifiable lipids were extracted and analysed by TLC (Ryder, 1985; Ryder et al., 1991). The [1,2,14C]acetate into nonsaponifiable lipids as

**Cloning and sequencing of CaERG11.** Genomic DNA from *C. albicans* was isolated according to Philippens et al. (1991). PCR amplification of *CaERG11* from genomic DNA was performed with the forward primer 5'-CTCGGATCCTATATATAAGATTCTTTTTC-3' and the reverse primer 5'-CCGAAATCATCGAGAAATGTCGTCGCTTTA-3', including a BamHI site, and an EcoRI site, respectively. PCR was conducted using the polymerases mixture Expand High Fidelity (Boehringer Mannheim) and an annealing temperature of 55 °C under standard conditions. For direct sequencing, the PCR amplicons were purified with the PCR product purification kit from Qiagen. For cloning, PCR products were digested with BamHI and EcoRI and ligated into the vector pBS (Stratagene). Sequencing on both strands of two independent clones or PCR amplicons was performed with a Li-Cor automatic sequencer, model 4000, using primers labelled with the infrared dye IRD40 (MWG Biotech) and Thermosequenase (Amersham).

**Expression of c-myc-tagged CaERG11 in S. cerevisiae.** An Ncol site containing the translational initiation codon was introduced at the 5' end, whereas a c-myc tag sequence and an XbaI site were inserted at the 3' end of *CaERG11* ORF by two PCR amplifications from the cloned genes in pBS, using the forward primer 5'-AACGTGCCATGCTATTTTGTTGAAA-

CTGCTATTG-3' and sequentially the following reverse primers: (1) 5'-CTTCAAAATAAGTTTTTCTTCAACATACAAAATTCTTCATTTTCCC-3' and (2) 5'-GGTCTAGATATAGATCTTTCAGAAAATTTGTGTT-TCC-3'. A similar strategy was applied to introduce the same c-myc sequence at the 5' end of *CaERG11* ORF, between the translational initiation codon ATG and the triplet encoding the second amino acid. The promoter of *S. cerevisiae* *ERG11* was PCR-amplified from genomic DNA isolated from the strain HRI with the following forward and reverse primers, which contain an XbaI and an Ncol site, respectively: 5'-CTCTAGAGCAATAAACCAACTTCCTTCC-3' and 5'-CTTGGTACAGGGCATGTTGTATACGTGTTG-3'. The identity of the amplified fragment was confirmed by restriction analysis and partial sequencing. The terminator of *S. cerevisiae* *CYC1* was amplified by PCR from the plasmid pYES2 (Invitrogen) with the forward and reverse primers, which contain an XbaI and a XhoI site, respectively: 5'-ATGCATCTAGAGGGCGCATC-3' and 5'-CACCTGTCGAGGGCCGAAATTTAAAGCCTTG-3'. Amplified *CaERG11* genes, digested with Ncol and XbaI, and the *CYC1* terminator, digested with XbaI and XhoI, were subcloned together into the plasmid Litmus 28 (BioLabs). Finally, the *ERG11* promoter, digested with XbaI and Ncol, and the previous insert in Litmus 28, isolated by digesting the plasmid with Ncol and XhoI, were cloned into the vector pRS416 (Stratagene). For each final construct of c-myc-tagged *CaERG11* in pRS416, the ORF was completely sequenced to make sure that no mutation had been introduced by the PCR amplifications and the various cloning steps.

The triplet 70°CGT in *CaERG11* ORF (encoding Ser in *C. albicans*: Santos & Tuite, 1995) was replaced by the triplet GCG in the QuickChange site-directed mutagenesis kit (Stratagene) using the primer 5’-CTTTATGAGGAAATTTAATCAGAAC-3’, amplified *CaERG11* genes, digested with Ncol and XbaI, and its reverse primer, which contain an XbaI site. To preserve the amino acid substitution E266D, in *CaERG11* from the strain NFI 2007, the same primers as above, except for the substitution A2717→C, were used, whereas the standard primers were applied to suppress the alteration. After site-directed mutagenesis, *CaERG11* ORFs were again completely sequenced to confirm the replacement of 5’-CGT by TCT (identified by restriction analysis with XbaI) and to ensure that no other mutations had been introduced.

*S. cerevisiae* INVSC2 was transformed with pRS416 containing or not containing *CaERG11* using the lithium acetate method (Becker & Guerente, 1991). Two colonies from each transformation were isolated and independently analysed.

**Antibodies and Western blotting.** Whole-cell extracts were prepared according to Favre & Ryder (1997a). Cell lysates from *S. cerevisiae* transformants were prepared from cultures grown in conditions as similar as possible to those for MIC determinations (medium, temperature and cell density) in 250 ml Erlenmeyer flasks containing 100 ml medium for 24 h with agitation, harvested by centrifugation, washed with phosphate-buffered saline and either immediately processed or frozen at −70 °C. Protein concentration was determined with the Bradford reagent and detergent-compatible (DC) protein assay (Bio-Rad), for samples without and with detergents, respectively. Western blot analysis with the monoclonal anti-c-myc antibodies (clone 9E10, Boehringer Mannheim), 10 µg ml^{-1}, was performed as previously described (Favre & Ryder, 1997a). Membranes were exposed to Hyperfilm ECL (Amersham).
RESULTS

Selection of C. albicans isolates with enzymic resistance to fluconazole

Out of the 23 C. albicans isolates obtained from patients who had failed azole therapy, only 19 demonstrated either dose-dependent or frank resistance to fluconazole in vitro (MIC range 8 to > 128 mg ml⁻¹), as determined by the NCCLS method (Galgiani et al., 1995; Ghannoum et al., 1996). In order to identify strains which might express altered 14DM genes among these 19 isolates, we measured the sensitivity to fluconazole of the incorporation of (RS)-[2-¹⁴C]mevalonate into sterols in cell-free extracts. Disruption of the cell membrane should eliminate the effect of multidrug transporters on the sensitivity of sterol synthesis to fluconazole, whereas other mechanisms of resistance, independent of cell integrity, such as overexpression or mutation of 14DM, should still be effective. In four isolates, Darlington strain) and itraconazole, although to various extents (Table 1).

Table 1. Susceptibility to fluconazole (FLU), ketoconazole (KETO) and itraconazole (ITRA) of the four selected azole-resistant C. albicans isolates in comparison with that of four sensitive strains

<table>
<thead>
<tr>
<th>Strain</th>
<th>MIC (µg ml⁻¹)</th>
<th>FLU</th>
<th>KETO</th>
<th>ITRA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Darlington</td>
<td>&gt; 128</td>
<td>32</td>
<td>&gt; 4</td>
<td></td>
</tr>
<tr>
<td>NFI 2007</td>
<td>32</td>
<td>1</td>
<td>0.25</td>
<td></td>
</tr>
<tr>
<td>NFI 2013</td>
<td>&gt; 128</td>
<td>0.5</td>
<td>&gt; 4</td>
<td></td>
</tr>
<tr>
<td>NFI 2021</td>
<td>&gt; 128</td>
<td>0.25</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Normal†</td>
<td>0.25–0.5</td>
<td>0.06–0.12</td>
<td>0.02–0.12</td>
<td></td>
</tr>
</tbody>
</table>

† Range of values obtained with the sensitive strains NFI 0124, ATCC 90028, ATCC 90029 and ATCC 24433.

In parallel to MIC determinations, the sensitivity of sterol synthesis to inhibition by fluconazole, ketoconazole and itraconazole was determined both in whole cells and in cell-free extracts. In whole cells, inhibition of [1,2-¹⁴C]acetate incorporation by the antimycotics correlated with increasing MICs, with a few exceptions which might be due to the different experimental conditions used for each of the two assays. In contrast, sensitivity of sterol synthesis in cell-free extracts to the various antimycotics did not correlate with MICs (Tables 1 and 2). This suggests that at least two distinct mechanisms were responsible for the observed resistance to azoles: one at the enzymic level, mainly affecting fluconazole and sometimes ketoconazole, and a second, which influenced the action of all azoles including itraconazole and was suppressed by disruption of the cell membrane, suggesting the involvement of membrane transporters.

Biological and biochemical characterization of four selected azole-resistant isolates

Susceptibility of the four selected fluconazole-resistant strains to several azoles was measured and compared with that of a set of four control strains, known to be susceptible to these drugs (NFI 0124, ATCC 90028, ATCC 90029 and ATCC 24433). Most of the fluconazole-resistant strains showed some degree of cross-resistance to ketoconazole (especially, as expected, the Darlington strain) and itraconazole, although to various extents (Table 1).

Table 2. Sensitivity of sterol synthesis to inhibition by azoles determined in whole cells and cell-free extracts from the four selected azole-resistant C. albicans isolates, in comparison with that of four sensitive strains

<table>
<thead>
<tr>
<th>Strain</th>
<th>IC₅₀ (µM)</th>
<th>Fluconazole</th>
<th>Ketoconazole</th>
<th>Itraconazole</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Cells</td>
<td>Cell-free</td>
<td>Cells</td>
<td>Cell-free</td>
</tr>
<tr>
<td>Darlington</td>
<td>&gt; 300</td>
<td>2.6</td>
<td>2.8</td>
<td>0.067</td>
</tr>
<tr>
<td>NFI 2007</td>
<td>&gt; 100</td>
<td>0.8</td>
<td>0.1</td>
<td>0.003</td>
</tr>
<tr>
<td>NFI 2013</td>
<td>&gt; 300</td>
<td>0.5</td>
<td>3.3</td>
<td>0.010</td>
</tr>
<tr>
<td>NFI 2021</td>
<td>&gt; 1000</td>
<td>0.9</td>
<td>0.2</td>
<td>0.029</td>
</tr>
<tr>
<td>Normal†</td>
<td>3</td>
<td>0.007</td>
<td>0.03</td>
<td>0.002</td>
</tr>
</tbody>
</table>

† Mean of values obtained with the four sensitive strains NFI 0124, ATCC 90028, ATCC 90029 and ATCC 24433. The standard deviation did not exceed 50% of the mean value.
Table 3. Analysis by TLC of the distribution of incorporated [1,2-**14**C]acetate into squalene and sterols in whole cells of the four selected azole-resistant *C. albicans* isolates, in comparison with that of four sensitive strains

<table>
<thead>
<tr>
<th>Strain</th>
<th>Incorporation of radioactivity (% of total)</th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>4-Desmethyl sterol</td>
<td>4-Methyl sterol</td>
<td>Lanosterol</td>
<td>Squalene</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Mean</td>
<td>SD*</td>
<td>Mean</td>
<td>SD*</td>
<td>Mean</td>
</tr>
<tr>
<td>Darlington</td>
<td>49.7</td>
<td>± 9.2</td>
<td>48</td>
<td>± 0.8</td>
<td>26.4</td>
</tr>
<tr>
<td>NFI 2007</td>
<td>42.6</td>
<td>± 9.8</td>
<td>62</td>
<td>± 14</td>
<td>26.8</td>
</tr>
<tr>
<td>NFI 2013</td>
<td>30.9</td>
<td>± 4.7</td>
<td>50</td>
<td>± 0.6</td>
<td>56.3</td>
</tr>
<tr>
<td>NFI 2021</td>
<td>88.4</td>
<td>± 3.5</td>
<td>28</td>
<td>± 0.6</td>
<td>5.3</td>
</tr>
<tr>
<td>Normal†</td>
<td>81.5</td>
<td>± 4.3</td>
<td>41</td>
<td>± 0.9</td>
<td>5.6</td>
</tr>
</tbody>
</table>

* n ≥ 4.
† Mean of the values obtained with the four sensitive strains NFI 0124 and ATCC 90028, ATCC 90029 and ATCC 24433.

Analysis of the distribution of the radioactivity incorporated from the precursor [1,2-**14**C]acetate into squalene and sterols by TLC revealed that in strains Darlington, NFI 2007 and NFI 2013, a larger proportion of radioactivity was associated with squalene and especially lanosterol in comparison with that from sensitive strains or the fluconazole-resistant strain NFI 2021 (Table 3). Similar results were obtained from the analysis of sterol synthesis in cell-free extracts with (RS)-[2-**14**C]mevalonate as the sterol precursor (data not shown). These results suggest that fluconazole resistance in strains Darlington, NFI 2007 and NFI 2013 is associated with a defective 14DM activity, implying that alterations of CaERG11 affect both the enzymic activity and the affinity for azoles of the protein. This dual effect is in fact expected since azoles bind to the active site of 14DM (Hitchcock *et al*., 1990; Hitchcock, 1993; Vanden Bossche & Koymans, 1998; Vanden Bossche & Marichal, 1992; Yoshida & Aoyama, 1985). In contrast, strain NFI 2021, while resistant to fluconazole, incorporated [1,2-**14**C]acetate in a manner similar to fluconazole-sensitive strains, both qualitatively and quantitatively (Table 3).

Amino acid substitutions in CaERG11 from the four selected azole-resistant strains

In order to identify the molecular basis for the azole insensitivity of 14DM from the four selected azole-resistant isolates, we proceeded to clone and completely sequence their CaERG11 genes. As a control, we also sequenced CaERG11 cloned from the sensitive strain NFI 0124. All of the sequences contained at least one cryptic nucleotide variation (not affecting the protein sequence; data not shown) when compared to the published sequence of *CaERG11* (Lai & Kirsch, 1989). In addition, all *CaERG11* genes from the azole-resistant strains contained two to four additional variations leading to amino acid substitutions in the protein sequence (Table 4). No variation leading to amino acid substitutions was found in NFI 0124 CaERG11. Since PCR amplification could lead to the introduction of random mutations and cloning of PCR products can fortuitously select the mutated sequences, CaERG11 from all five strains was PCR-amplified a second time from genomic DNA and the sequences directly determined without prior cloning. Exactly the same variations as shown in Table 4 were again found, indicating that they were not artificially introduced during the PCR amplification.

Expression of CaERG11 with amino acid substitutions in *S. cerevisiae* confers resistance to fluconazole

To formally demonstrate that the identified amino acid substitutions in *CaERG11* from fluconazole-resistant strains could confer resistance to the antifungal in an intact yeast cell, *CaERG11* genes from fluconazole-resistant and -sensitive clinical isolates were expressed in *S. cerevisiae*. It has been shown that *C. albicans* 14DM is active when expressed in *S. cerevisiae* (Sanglard *et al*., 1998; Shyadehi *et al*., 1996), and 14DM from *C. albicans* and *S. cerevisiae* exhibit similar affinities for several azoles (Hitchcock *et al*., 1989, 1990; Vanden Bossche & Marichal, 1992; Yoshida & Aoyama, 1985). Therefore, normal expression of *CaERG11* from a fluconazole-sensitive isolate in an *erg11*^±^ *S. cerevisiae* strain should not dramatically affect the susceptibility of the cells to fluconazole. To avoid overexpression of *CaERG11*, which could have led to a resistant phenotype (Doignon *et al*., 1993; Kalb *et al*., 1986) and affected membrane biogenesis (Vergeres *et al*., 1993; Zimmer *et al*., 1997), we put the expression of the gene under the control of the *ERG11* promoter (−1036 to −3; see Methods). To monitor the expression of *C. albicans* 14DM in *S. cerevisiae* we introduced a c-myc tag (30 nucleotides long, encoding the decapetide EQLK-SEEDL) into its sequence. The *CaERG11* ORFs from NFI 0124 and Darlington were initially tagged either at the 5’ end or at the 3’ end. These tagged genes were then
Table 4. Nucleotide variations leading to amino acid substitutions identified in CaERG11 cloned from the four selected azole-resistant isolates in comparison with the sequence from sensitive strains SC5314 (Lai & Kirsch, 1989) and NFI 0124

<table>
<thead>
<tr>
<th>Strain</th>
<th>Amino acid substit.</th>
<th>DNA sequence*</th>
<th>Protein sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Fluconazole-sensitive</td>
<td>Fluconazole-resistant</td>
</tr>
<tr>
<td>Darlington</td>
<td>1</td>
<td>TTC</td>
<td>CTC</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>TAT</td>
<td>CAT</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>GGG</td>
<td>GAG</td>
</tr>
<tr>
<td>NFI 2007</td>
<td>1</td>
<td>TTC</td>
<td>TTA</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>GAA</td>
<td>GAC</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>TCT</td>
<td>TTT</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>GTT</td>
<td>ATT</td>
</tr>
<tr>
<td>NFI 2013</td>
<td>1</td>
<td>GAT</td>
<td>GAA</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>TAT</td>
<td>CAT</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>TTT</td>
<td>CTT</td>
</tr>
<tr>
<td>NFI 2021</td>
<td>1</td>
<td>AAA</td>
<td>GAA</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>ACC</td>
<td>GCC</td>
</tr>
</tbody>
</table>

* Nucleotides are numbered from the translation start codon ATG of CaERG11 ORF (Lai & Kirsch, 1989).

Table 5. Increased resistance to fluconazole and ketoconazole in S. cerevisiae strain INVSC2 transformed with CaERG11 genes cloned from azole-resistant strains

<table>
<thead>
<tr>
<th>Transformants expressing CaERG11 from</th>
<th>Position of c-myc tag</th>
<th>Expression of residue 263 as</th>
<th>MIC (µg ml&lt;sup&gt;−1&lt;/sup&gt;)&lt;sup&gt;a&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Fluconazole</td>
</tr>
<tr>
<td>Untransformed</td>
<td>–</td>
<td>–</td>
<td>64</td>
</tr>
<tr>
<td>Vector alone</td>
<td>–</td>
<td>–</td>
<td>64</td>
</tr>
<tr>
<td>NFI 0124</td>
<td>N</td>
<td>Leu</td>
<td>128</td>
</tr>
<tr>
<td>NFI 0124</td>
<td>C</td>
<td>Leu</td>
<td>256</td>
</tr>
<tr>
<td>NFI 0124</td>
<td>C</td>
<td>Ser</td>
<td>128</td>
</tr>
<tr>
<td>Darlington</td>
<td>N</td>
<td>Leu</td>
<td>1024</td>
</tr>
<tr>
<td>Darlington</td>
<td>C</td>
<td>Leu</td>
<td>4096</td>
</tr>
<tr>
<td>Darlington</td>
<td>C</td>
<td>Ser</td>
<td>4096</td>
</tr>
<tr>
<td>NFI 2007</td>
<td>C</td>
<td>Ser</td>
<td>4096</td>
</tr>
<tr>
<td>NFI 2021</td>
<td>C</td>
<td>Ser</td>
<td>4096</td>
</tr>
</tbody>
</table>

* Values obtained in two or three out of three independent determinations. Variations did not exceed a twofold dilution step.

cloned into the centromere vector pRS416 in between the ERG11 promoter and the terminator of S. cerevisiae CYC1.

S. cerevisiae INVSC2 was transformed with the vector containing CaERG11, or with vector alone, and then tested for susceptibility to fluconazole and ketoconazole (this strain was primarily resistant to itraconazole) (Table 5). Expression of CaERG11 from the Darlington strain conferred an increased resistance to fluconazole in comparison with that from NFI 0124. However, the position of the c-myc tag influenced the susceptibility of the transformants to both fluconazole and ketoconazole whatever the source of CaERG11 (Table 5). Western blotting with anti-c-myc tag antibody revealed that this variation in susceptibility correlated with the apparent level of expression of 14DM. Proteins tagged at the carboxyl (C) terminus were more abundant than those tagged at the amino (N) terminus (Fig. 1; compare lanes 2–7 with lanes 8 and 9). The c-myc tag at the N-terminus might interfere with the targeting of 14DM to the membrane of the endoplasmic reticulum, which depends on a transmembrane domain and also probably on clusters of positively charged residues, both situated toward the N-terminus of P450 proteins (Boscott & Grant, 1994; Chen et al., 1988; Sanglard et al., 1993). CaERG11 from NFI 2007 and NFI 2021 were therefore exclusively tagged at the C-terminus. A cryptic alter-
cloning into the expression vector, which was based on position 409 of the ORF (data not shown), precluding its expression of codon CUG is decoded as Ser in S. cerevisiae. 

![Image](57x604 to 296x734)

**Fig. 1.** Western blot analysis of the expression of c-myc-tagged CaERG11 from whole homogenates (30 μg protein) of S. cerevisiae INVC2 transformed with the vector or plasmid containing CaERG11 cloned from several C. albicans strains with anti-c-myc tag antibodies (see Methods for details). The strain from which CaERG11 was derived, the position [amino (N) or carboxyl (O) of the c-myc tag, and the designated amino acid residue at position 263 in the expressed protein are indicated above the Western blot. Molecular mass markers (kDa) are shown on the left. The band corresponding to c-myc-tagged C. albicans 14DM is arrowed. The results are representative of two independent experiments.

ation of NFI 2013 CaERG11 introduced an XbaI site at position 409 of the ORF (data not shown), precluding its cloning into the expression vector, which was based on a strategy involving two digestions with XbaI. Since codon CUG is decoded as Ser in C. albicans instead of Leu (Santos & Tuite, 1995), expression of CaERG11 in S. cerevisiae introduces the substitution S263L. To ensure that this would not influence the sensitivity of 14DM to inhibitors, the triplet TGT was systematically replaced by TCT (a Ser codon) in CaERG11 tagged at the 3’ end. Results obtained with these last plasmids are presented in Table 5. The substitution S263L in CaERG11 gene from the sensitive strain NFI 0124 resulted in a slight decrease (one step dilution) in fluconazole and ketoconazole resistance. Transformants expressing the CaERG11 genes from fluconazole-resistant strains were 32-fold more resistant to fluconazole than transformants expressing CaERG11 from the sensitive strain (Table 5). The identity of residue 263, Ser or Leu, did not affect MICs to fluconazole of transformants expressing the CaERG11 genes from resistant strains (data not shown). The amino acid substitutions present in the Darlington CaERG11 gene simultaneously conferred a potent cross-resistance to ketoconazole (16-fold more than the control), in the other cases cross-resistance to ketoconazole was weak (4-fold) (Table 5).

Transformants expressing NFI 2007 CaERG11 without the amino acid substitution E266D were indistinguishable from those expressing CaERG11 containing all four amino acid substitutions identified in this gene (not shown).

Western blot analysis of extracts from transformants with anti-c-myc antibodies showed that 14DM from fluconazole-sensitive or -resistant C. albicans strains were equally abundant, ruling out that increased expression or stability of altered proteins could account for increased MICs (Fig. 1).

**DISCUSSION**

In this study we have demonstrated for three C. albicans clinical isolates that lower susceptibility to fluconazole could be at least partly due to the presence of amino acid substitutions in CaERG11, since expression of the altered genes in S. cerevisiae led to a resistant phenotype when compared to transformants expressing CaERG11 from a sensitive strain. In all three cases altered sensitivity of sterol synthesis to fluconazole in cell-free lysates was a good screening tool to identify altered CaERG11, which can confer fluconazole resistance upon a yeast cell. Therefore, it is most probable that the amino acid substitutions identified in NFI 2013 CaERG11, and that detected by White (1997b), R467K, are in the same way responsible for the observed biochemical insensitivity to fluconazole, and contribute to the overall fluconazole resistance of these strains. However, it remains to be investigated whether under- or overexpression of NADPH P450 reductase or cytochrome b₅ reductase, which alters the susceptibility of S. cerevisiae to azoles (Sutter & Loper, 1989; Truan et al., 1994), has a similar effect on the affinity of 14DM for azoles in C. albicans cell extracts, and whether this mode of resistance occurs in Candida isolates. It cannot therefore be concluded without reserve that lower sensitivity of sterol synthesis to azoles in cell-free extracts is invariably associated with mutation(s) of CaERG11.

Sixteen different mutations leading to amino acid substitutions have previously been identified in CaERG-11 from fluconazole-resistant isolates (Loeffler et al., 1997; Sanglard et al., 1998; White, 1997b). We report here five new, previously undescribed substitutions, to give a total of 21 which are now known. This multiplicity of mutations in CaERG11 potentially leading to fluconazole resistance, and their widespread distribution along the primary structure, might be surprising at first glance. However, a molecular model for C. albicans 14DM has been derived from the crystallographic structure of bacterial (Pseudomonas putida) soluble P450 camphor hydroxylase (P450cam) (Boscott & Grant, 1994; Poulos et al., 1987) (see also Loeffler et al., 1997; Sanglard et al., 1998). The active site of P450 proteins is buried in the core of the protein and is constituted by a complex three-dimensional arrangement of various secondary structures involving several parts of the linear protein sequence. It is thus not surprising that several amino acid substitutions along the primary structure of 14DM can affect the affinity of azoles, which act as competitive inhibitors by binding to the active site.

Fourteen of these 21 known amino acid substitutions involve residues which are conserved in all the yeast 14DM genes which have been sequenced so far. Six of these are located in a segment spanning residues 126–147, three are clustered at positions 448–450, and
isolates by Loeffler et al. for azoles. For instance, substitution E266D found in mutations are important for conferring reduced affinity (1998; our work). It is unclear as yet whether all identified mutations usually have a synergistic effect over single mutations. For instance, Lys143, substituted by Glu in CaERG11 from isolate NFI 2021, is thought to be important for resistant strains (Loeffler et al. 1997) seems to be irrelevant in CaERG11 from strains Darlington, NFI 2007 or NFI 2021 were up to 32-fold more resistant to fluconazole than those expressing CaERG11 from a sensitive strain that double point mutations in azole-resistant CaERG11, probably do not constitute the sole mechanism of resistance to antifungals present in any of the four strains examined. In contrast to NFI 2021 discussed above, strains Darlington, NFI 2007 and NFI 2013 negatively affected not only the specificity toxicity so that the real extent of resistance induced by mutations in CaERG11 might well be higher than 32-fold. Mutations in CaERG11 from strains Darlington, NFI 2007 and NFI 2013 seem to be important for membrane binding and the correct entrance of the substrate (Boscott & Grant, 1994; Loeffler et al., 1997). Amino acid substitutions between residues 405 to 450 are located in the ‘helix-poor’ domain connecting helices K to L, which are involved in the substrate-binding site in P450cam (Boscott & Grant, 1994; Poulos et al., 1987). Surprisingly, despite the selectivity of fluconazole for fungal versus mammalian 14DM, 10 out of the 14 residues substituted in CaERG11 from azole-resistant isolates are conserved in both fungal and mammalian 14DMs (Fig. 2). The occurrence of two or more amino acid substitutions appears to be common in CaERG11 from fluconazole-resistant strains (Loeffler et al. 1997; Sanglard et al., 1999; our work). It is unclear as yet whether all identified mutations are important for conferring reduced affinity for azoles. For instance, substitution E266D found in CaERG11 from NFI 2007 and four fluconazole-resistant isolates by Loeffler et al. (1997) seems to be irrelevant in CaERG11 from NFI 2007 for conferring resistance to either fluconazole or ketoconazole. Sanglard et al. (1998) found by introducing some amino acid substitutions in CaERG11 from a sensitive strain that double point mutations usually have a synergistic effect over single amino acid substitution, explaining the apparent natural occurrence of more than one mutation in azole-resistant CaERG11. S. cerevisiae transformants expressing CaERG11 from strains Darlington, NFI 2007 or NFI 2021 were up to 32-fold more resistant to fluconazole than those expressing CaERG11 from a fluconazole-sensitive strain. Moreover, at the high concentration of 4096 µg ml⁻¹ (13 mM), fluconazole might exert non-specific toxicity so that the real extent of resistance induced by mutations in CaERG11 might well be higher than 32-fold.

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assays (Table 2). For example, NFI 2013 is strongly resistant to itraconazole but its sterol synthesis in cell-free extracts is very sensitive to the same azole. Therefore, these three strains probably also express one or more transporters which reduce the intracellular concentration of the antifungals. In support of this, reduced cellular accumulation of fluconazole was observed in strains Darlington, NFI 2007 and NFI 2013, but not in NFI 2021 (authors’ unpublished data). A similar diversity of resistance mechanisms expressed in a single isolate has previously been observed (Lopez-Ribot et al., 1998; Sanglard et al., 1998; White, 1997a).

In conclusion, azole resistance in C. albicans is a complex phenomenon which can involve several different mechanisms. In addition to overexpression of the target enzyme or drug transporters, which have been widely reported, mutations in CaERG11 can significantly contribute to a clinically occurring resistant phenotype induced by long-term treatment of patients with azoles. Our data suggest that amino acid substitutions in 14DM may contribute to resistance in about 20% of fluconazole-resistant C. albicans strains. The diversity of the mutations able to influence the affinity of 14DM for azoles precludes any simple analysis to detect them. Moreover, selection of more than one resistance mechanism by prolonged treatment with azoles also seems to be very common (Lopez-Ribot et al., 1998; Sanglard et al., 1998; White, 1997a), excluding a simple therapeutic approach to combat azole resistance. Combination of antifungals with different modes of action, for example azole and allylamine (Barchiesi et al., 1998; Ryder & Favre, 1997), is one potential approach to this problem.

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Mutations in C. albicans 14α-demethylase gene

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