Candida albicans drug resistance – another way to cope with stress

Richard D. Cannon,1 Erwin Lamping,1 Ann R. Holmes,1 Kyoko Niimi,1 Koichi Tanabe,2 Masakazu Niimi2 and Brian C. Monk1

1Department of Oral Sciences, University of Otago, Dunedin 9054, New Zealand
2Department of Bioactive Molecules, National Institute of Infectious Diseases, Tokyo, Japan

There are relatively few classes of antifungal drugs. This restricts clinicians’ therapeutic choices and these choices are further reduced by the emergence of drug resistance. Exposure to antifungal drugs represents an environmental stress for the fungal pathogen Candida albicans. The immediate response of C. albicans to antifungals may be drug tolerance, which can lead to drug resistance. This article examines C. albicans drug resistance from the perspective of it being a stress response and investigates how commonality with other stress-response pathways gives insights into the prospects for overcoming, or preventing, drug resistance.

Introduction

Antimicrobial drug resistance is an important biological phenomenon that has a considerable impact on animal and human health. The prevalence of clinical drug resistance has increased in recent decades with the greater use, and abuse, of otherwise efficacious antimicrobial agents. This has been a significant problem for bacterial pathogens, where resistance to multiple antibiotics severely limits therapeutic options. Antimicrobial resistance is not restricted to bacteria, however, and in the 1990s fluconazole treatment failure emerged due to the development of resistance by the fungal pathogen Candida albicans (White et al., 1998). Antifungal resistance is particularly problematic as initial diagnosis of systemic fungal infection can be delayed and there are few antifungal drugs available. The development of antimicrobial drug resistance is not a new phenomenon – micro-organisms have been responding to toxic environmental stresses for millennia (Wright, 2007). Indeed it is likely that the mechanisms utilized to confer resistance to ‘novel’ synthetic drugs have been selected from an extensive repertoire that has enabled micro-organisms to survive for so long in changing environments.

Exposure to antifungal drugs is, for C. albicans, another environmental stress that stimulates responses to mitigate the harmful effects of the drugs and permit continued growth. The antifungal stress is transduced through signalling pathways that induce stress responses and affect the growth and virulence of the organism. Stress-response signalling and its interrelation with C. albicans morphogenesis and virulence are complex and beyond the scope of this mini-review. Signalling pathways, and their role in virulence, have been excellently reviewed by Quinn & Brown (2007), Monge et al. (2006) and Roman et al. (2007). Although little is known about stress responses in non-albicans Candida species, the stress-response pathways in the model yeasts Saccharomyces cerevisiae and Schizosaccharomyces pombe have been well studied (Roman et al., 2007). Despite extensive congruence in the fungal stress-response networks, there are significant differences in the stress responses of C. albicans (Enjalbert et al., 2006). Therefore, although major differences in the stress responses of other fungi will be noted, this review will focus specifically on how C. albicans responds to antifungal stress and how the development of resistance is a component of the stress-response network of C. albicans.

Antifungal drug targets in C. albicans

There are four main antifungal drug targets in C. albicans (Fig. 1a). The fluorinated pyrimidine analogue 5-fluorocytosine (5-FC) causes aberrant RNA synthesis and interferes with DNA replication (Akins, 2005; Sanglard & Bille, 2002). A significant proportion of C. albicans isolates are resistant to 5-FC, limiting its utility. The polyenes, such as amphotericin B and nystatin, are heterocyclic amphipathic molecules that insert into lipid bilayers, bind to sterols, and aggregate in annuli to form pores. These pores disrupt plasma membrane integrity and permit the efflux of cations such as K+, which is fungicidal for C. albicans. Polyenes are also thought to cause oxidative damage (Sanglard & Bille, 2002). The azole antifungals, such as the triazole fluconazole, interfere with sterol biosynthesis (Fig. 1a). They inhibit the cytochrome P450 14z-lanosterol demethylase, encoded by the ERG11 gene, which is part of the ergosterol biosynthetic pathway. Inhibition of Erg11p

Abbreviations: 5-FC, 5-fluorocytosine; ABC, ATP-binding cassette; CsA, cyclosporin A; Cyp1p, cyclophilin A; HOG, high-osmolarity glycerol; Hsp90, heat-shock protein 90; MAPK, mitogen-activated protein kinase; MFS, major facilitator superfamily; PKA, protein kinase A.
depletes the ergosterol content of membranes and results in the accumulation of toxic sterol pathway intermediates which inhibit growth (Akins, 2005; Sanglard & Bille, 2002). Azoles are thus usually fungistatic for *C. albicans*. The most recently developed class of antifungals are the cyclic lipopeptides the echinocandins. These were originally obtained from soil fungi, but semi-synthetic derivatives have been developed such as caspofungin, micafungin and anidulafungin. These drugs are thought to interfere with wall biosynthesis by inhibiting (1,3)-d-β-glucan synthase (Fig. 1a), and are fungicidal for yeasts such as *C. albicans*. Thus the current antifungal drugs that are effective against *C. albicans* primarily affect cell wall and cell membrane composition and integrity and thereby induce stress responses.

**Stress response in *C. albicans***

*C. albicans* can be isolated from a number of environments, but is usually found in association with mammals, particularly humans. It can colonize a variety of ecological niches on humans (Cannon & Chaffin, 1999) and will experience a range of environments that will cause physiological stress. These stresses include temperature changes, ionic stress, changes in osmolarity, and oxidative stress such as that experienced in the phagosomes of neutrophils. Stresses are transduced through a variety of membrane receptors but elicit responses through conserved signalling pathways, one of the most important being the MAP kinase (MAPK) signal transduction network (Monge et al., 2006). Although individual components of these pathways are conserved between fungal species there are some distinct features of the *C. albicans* stress-response network. *C. albicans* has a smaller set of core stress responses than *S. cerevisiae* or *S. pombe*, and is relatively resistant to oxidative and heat stress (Enjalbert et al., 2006). *C. albicans* has parallel stress-response pathways (Fig. 2). The divergence of their regulation from that in other fungi, and *C. albicans*’ specialized stress responses, may be due to the different types and amounts of stresses experienced on and within the human host (Quinn & Brown, 2007). Two important components of the MAPK network are the high-osmolarity glycerol (HOG; Hog1p) pathway and the protein kinase C

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**Fig. 1.** (a) Targets of current antifungal drugs in *C. albicans*. (b) Mechanisms of resistance to antifungal drugs in *C. albicans*. Grey lettering indicates mutated proteins; bold lettering indicates protein overexpression. 5-FU, 5-fluourouracil; 5-FUMP, 5-fluourouridine monophosphate.

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**Fig. 2.** Stress-response network in *C. albicans*. Grey lines indicate stresses; black lines indicate stress responses. PKA, protein kinase A (TPK2/TPK1).
cell wall integrity (Mkc1p) pathway (Fig. 2), which respond to oxidative, osmotic and heavy metal stress (Quinn & Brown, 2007; Roman et al., 2007). The response to oxidative stress can be transduced via both Mkc1p and Hog1p and involves increased expression of antioxidants such as catalase, superoxide dismutase and glutathione (Fig. 2). The cell wall integrity pathway regulates glucan synthesis and cell wall repair (Navarro-Garcia et al., 1998), which can be protective in response to echinocandins. Despite the involvement of the MAPK pathway, oxidative stress induces responses mainly via transcription factor Cap1p. Cap1p is also involved in multidrug resistance. Activation of Cap1p by a C-terminal truncation of the protein results in upregulation of the major facilitator superfamily (MFS) transporter gene MDR1 (Alarco & Raymond, 1999). Hog1p is mainly responsible for the activation of core stress-response genes that are induced by osmotic or heavy metal stress. Osmotic stress results in glycerol uptake and synthesis, and exposure to heavy metal ions results in upregulation of genes involved in glutathione synthesis (Enjalbert et al., 2006). Although there are similarities in the responses of *Candida glabrata* and *S. cerevisiae* to osmotic stress, *C. glabrata* lacks a HOG signalling branch, and the *C. glabrata* HOG pathway also responds to weak acid stress (Gregori et al., 2007). In *C. albicans*, Hog1p represses filamentation through the Cek1 signalling pathway (Monge et al., 2006), although the formation of hyphae can be an oxidative-stress response.

The cAMP-PKA (protein kinase A) signal transduction pathway is involved in *C. albicans*’ response to antifungal stress (Fig. 2); adenylate cyclase (*CDC35*) mutants no longer respond to azoles with upregulation of *CDR1* (Jain et al., 2003). Azoles also cause a membrane stress that induces Mkc1p expression (J. Pla, personal communication). Membrane stress can also mediate a response through calmodulin (Fig. 2). Interestingly, exposure of cells to the heavy metal Ca^{2+} induces expression of heat-shock protein 90 (Hsp90), which stabilizes a number of proteins, including calcineurin.

The serine/threonine protein phosphatase calcineurin is highly conserved in eukaryotes and is activated in response to several stresses. It has important physiological roles in *C. albicans*, and is essential for survival during membrane stress (Cruz et al., 2002). *C. albicans* calcineurin is a heterodimer composed of a catalytic subunit A (encoded by *CMP1* [CNA1]) and a regulatory subunit B (encoded by *CNB1*) (Fig. 3). The phosphatase activity of calcineurin is activated when it binds calmodulin in the presence of calcium ions and it affects gene expression via transcriptional regulators such as Crz1p. Calcineurin mediates tolerance to a variety of stresses, including salt and high pH in addition to membrane stress (Steinbach et al., 2007) (Fig. 2). Calcineurin is essential for survival in serum (Bader et al., 2006) and it is the calcium component of serum that is toxic for *C. albicans* in the absence of functional calcineurin (Blankenship & Heitman, 2005). Calcineurin also plays an important role in the tolerance of *C. albicans* to certain antifungal drugs (see below).

### Antifungal drug resistance

The mechanisms by which *C. albicans* can become resistant to antifungal drugs have been reviewed by Sanglard & Bille (2002) and Akins (2005) and are summarized in Fig. 1(b). Resistance of clinical isolates to 5-FC most often correlates with mutations in the enzyme uracil phosphoribosyltransferase (Fur1p) that prevent the conversion of 5-fluorouracil to 5-fluorouridine monophosphate. Resistance of *C. albicans* to polycenes is rare and can be caused by a reduction in the amount of plasma membrane ergosterol, to which polycenes bind (Fig. 1b). Mutations in *ERG3*, which lower the concentration of ergosterol in the membrane, cause amphotericin B resistance and also confer resistance to azoles.

There are multiple mechanisms that can give rise to azole resistance in *C. albicans* (Fig. 1b). The drug target, Erg11p, can be overexpressed or can develop point mutations that reduce fluconazole binding (Akins, 2005; Sanglard & Bille, 2002; White et al., 1998). Azole-induced *C. albicans* growth inhibition is caused by reduction in the ergosterol content of membranes, and also by the accumulation of toxic ergosterol precursors such as 14α-methylgergosta-8,24(28)-dien-3β,6α-diol. If Erg3p is inactivated by mutation, in the

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**Fig. 3.** Involvement of calcineurin in the azole tolerance of *C. albicans*. Dots on calcineurin subunit A represent active-site residues. CsA, cyclosporin A; Cyp1p, cyclophilin A. 1, Fox & Heitman (2002); 2, Cowen & Lindquist (2005); 3, Bruno & Mitchell (2005); 4, Karababa et al. (2005); 5, Onyewu et al. (2005); 6, Sanglard et al. (2003).
presence of fluconazole these cells accumulate the non-toxic sterol 14α-methylfecosterol. High-level azole resistance correlates with overexpression in the plasma membrane of the MFS drug pump Mdr1p, or the ATP-binding cassette (ABC) pumps Cdr1p or Cdr2p (Perea et al., 2001; White et al., 1998). These proteins have been found to pump a variety of substrates, including the azoles (Lamping et al., 2007), but they do not pump the echinocandins (Niimi et al., 2006). Little clinical resistance to the echinocandins has been reported so far. This may reflect its limited use to date, or that resistance events are rare. Echinocandin-resistant C. albicans isolates have point mutations in (1,3)-β-glucan synthase subunit Gsc1p (Baïench et al., 2007).

One way to discover antifungal drug resistance mechanisms is to compare resistant clinical isolates with their susceptible parents (Perea et al., 2001; White, 1997). Another way is to select for resistance in vitro (Albertson et al., 1996; Anderson, 2005; Cowen et al., 2000). These studies have shown distinct patterns in the type and combinations of mechanisms that evolve in C. albicans populations to confer azole resistance. Often the patterns of mechanisms that evolve mimic those seen in clinical isolates, described above, validating this approach (Anderson, 2005). Interestingly, there is often a fitness gain associated with the development of azole resistance and so resistant isolates may persist in the population after the cessation ofazole therapy (Anderson, 2005). In vitro studies have also demonstrated a role for Hsp90, a molecular chaperone for calcineurin, in promoting the rapid acquisition of fluconazole resistance by C. albicans (Cowen & Lindquist, 2005; Cowen et al., 2006).

### Antifungal drug resistance is a stress response

The exposure of C. albicans to antifungal drugs will induce stress responses that are dependent on the dose and the nature of the drug. For fungicidal drugs such as echinocandins and polyenes at concentrations above the minimum growth-inhibitory concentration (MIC), the responses fail to prevent cell death. With fungistatic drugs, such as the azoles, at the MIC growth is inhibited but the cells are not killed – a phenomenon referred to in this context as drug tolerance (Sanglard et al., 2003).

Most of the established antifungal resistance mechanisms are due to genetic mutation – usually point mutations in genes encoding drug targets or enzymes in metabolic pathways, or transcription factors leading to gene overexpression. Such mutations are stable, take time to be acquired, and can be thought of as long-term stress responses. Likewise, azole resistance can be caused by genetic rearrangements (Perepnikhatka et al., 1999) or aneuploidy (Selmecki et al., 2006) affecting the expression of drug targets, pumps or transcription factors. Antifungal drugs also, however, stimulate classic immediate stress responses. These can be thought of as reversible phenotypic responses that do not involve mutation or chromosomal rearrangement. Phenotypic switching and biofilm formation are other phenotypic responses that can increase drug resistance (Akins, 2005). The short-term phenotypic stress responses that lead to drug tolerance are important because they may allow C. albicans cells to develop long-term stable resistance mechanisms that could also confer a fitness gain.

An insight into the immediate stress responses induced by antifungals can be gained by transcript profiling cells exposed to drugs at, or below, their MIC. Liu et al. (2005) examined the effect of exposing C. albicans to 5-FC, amphotericin B, ketoconazole or caspofungin at concentrations equating to their IC50s (concentrations that inhibit growth by 50%). Exposure of cells to 5-FC resulted in increased expression of genes involved in purine and pyrimidine biosynthesis, including the gene implicated in resistance, FUR1, and the drug target CDC21 (Liu et al., 2005). Ketoconazole induced expression of genes involved in ergosterol biosynthesis, including ERG3 and the target ERG11, the ABC drug efflux pumps CDR1 and CDR2, and a putative sphingolipid flippase RTA3. The response of cells to amphotericin B was upregulation of genes involved in Ca2+, K+, Na+, Zn2+ and sulphate transport and downregulation of phosphate, H+, citrate, Cu2+ and Fe2+ transporters. In addition, there was upregulation of oxidative stress-response genes such as AOX1, SOD2 and GSH1, consistent with amphotericin B causing oxidative damage (Sanglard & Bille, 2002). Caspofungin exposure induced the expression of several genes involved in cell wall maintenance, including the gene encoding the (1,3)-β-glucan synthase subunit GSL1 (GSL22).

While it is not surprising that exposure to antifungals induced upregulation of drug targets and genes already identified as contributing to resistance, what is noteworthy is the number of other genes that were differentially expressed: 439 for 5-FC; 256 for amphotericin B; 82 for ketoconazole; and 480 for caspofungin exposure (Liu et al., 2005). This in itself is also not surprising as the stresses will activate response networks involving transcriptional regulators with multiple substrates, as described above. It does raise the prospect, however, of identifying other potential drug targets including components of the stress-response pathways.

### Antifungal drug tolerance

As already noted, the azoles are fungistatic and can be tolerated to a certain degree. If C. albicans calcineurin activity is inhibited, however, the azoles become fungicidal. The immunosuppressants cyclosporin A (CsA) and FK506 have been found to act synergistically with fluconazole (Sanglard et al., 2003) and this is because they bind with either cyclophilin A (Cyp1p) or Rbp1p, respectively, and inhibit calcineurin by binding at the subunit A and B interface (Fig. 3), possibly restricting access of substrate to the active site (Cruz et al., 2002; Sanglard et al., 2003). Synergism of FK506 with fluconazole was also seen with Candida tropicalis and Candida parapsilosis but not with S. cerevisiae or Candida krusei (Cruz et al., 2002). Calcineurin
is activated, following an increase in intracellular Ca$^{2+}$, by
the binding of Ca$^{2+}$-calmodulin. As in S. cerevisiae, one of
the major substrates of C. albicans calcineurin is transcription
factor Crz1p (Karababa et al., 2006). Crz1p is required
for both calcium-induced transcription of GSC1, which may
play a role in the repair of cell wall damage, and increased
transcription of the gene encoding vacuolar Ca$^{2+}$- P-ATPase
pump Pmc1p (Sanglard et al., 2003). This may provide
feedback control of calcineurin activity (Figs 2 and 3). Disruption of CRZ1, however, did not completely remove
azole tolerance, suggesting that the tolerance is mediated by
other substrates of calcineurin (Karababa et al., 2006; Onyewu et al., 2004). Protein kinase Cka2p is involved in
fluconazole susceptibility, possibly by inhibiting CDR1 and
CDR2 expression (Bruno & Mitchell, 2005). In a CKA2
knockout strain CDR1, CDR2 and RTA3 were over-
expressed. Although calcineurin contributes to Cka2p-
mediated fluconazole sensitivity, Crz1p is not the Cka2p
substrate (Fig. 3). Thus the precise mechanism of calcine-
urin-dependent azole tolerance remains to be discovered.
Calcineurin responds to changes in calcium ion concentra-
tion (Figs 2 and 3) and it is possible that exposure to azoles
causes an intracellular calcium spike that induces the
calcineurin tolerance pathway (Sanglard et al., 2003).

Prospects of overcoming drug resistance

Clinically significant C. albicans drug resistance has only
been observed to date with immunocompromised individ-
uals prescribed long courses of azole antifungals. For the
mechanisms resulting in high-level clinical resistance, described above, two strategies for overcoming the
resistance are evident – inhibition of drug efflux pumps
and other, indirect, ways of chemosensitizing cells to the
azoles. Drug efflux pumps have been studied by hetero-
logous expression in S. cerevisiae, where they confer
increased resistance to azoles (Lamping et al., 2007;
Nakamura et al., 2001; Niimi et al., 2005; Schuetzer-
Muehlbauer et al., 2003). This not only allows an analysis
of pump function (Lamping et al., 2007) but also provides
a system to screen for pump inhibitors that chemosensitize
the strains overexpressing pumps to fluconazole (Monk et al.,
2002; Niimi et al., 2004; Schuetzer-Muehlbauer et al.,
2003). While FK506 has been demonstrated to be a pump inhibitor
using this approach (Schuetzer-Muehlbauer et al., 2003) its
other effects in the cell, such as inhibiting calcineurin-
mediated azole tolerance, may complicate interpretation of
chemosensitization susceptibility tests. Also, to be an effective
azole chemosensitizer, pump inhibitors must be specific for
the pumps causing resistance and not adversely affect human
transporters. Inhibition of calcineurin-mediated azole
tolerance has been proposed as a novel therapeutic approach
(Steinbach et al., 2007). While FK506 and CsA chemosensi-
tize C. albicans cells to azoles, and can render the azoles
fungidal, they are also immunosuppressive, which could be
problematic for candidosis patients, many of whom are
already immunocompromised. Therefore the search needs
to be widened to related chemosensitizers that are not
immunosuppressants. The calcineurin stress-response path-
way is extensive and provides other potential targets, such as
Hsp90, although again inhibitors would have to be specific for
C. albicans Hsp90.

Conclusions

Exposure of C. albicans to antifungal drugs induces
immediate phenotypic stress responses that may permit
drug tolerance. This tolerance allows the selection, or
evolution, of stable stress responses that confer higher
levels of resistance. All micro-organisms contain a plethora
of genes that can potentially confer resistance to new
environmental stresses (Wright, 2007). C. albicans is a
diploid fungus with several gene families that have
probably arisen by gene duplication. We have discovered
that alleles of CDR1 and CDR2 within the same strain differ
functionally and that CDR2 alleles are continuing to evolve
(Holmes et al., 2006). Thus there are a large number of
pumps with different substrate specificities that, if over-
expressed or mutated, could confer resistance to ‘novel’
antifungals with intracellular targets.

This perspective on antifungal drug resistance suggests
several possible ways of overcoming, or preventing, drug
resistance. Combination therapy can be used to attack two
different targets simultaneously with a low probability that
resistance to both drugs will arise, or to attack a drug target
and its resistance mechanism (cf. augmentin). While
combination therapy sounds attractive, and it has been
reported that antimicrobial combinations can actually
select against the development of resistance (Chait et al.,
2007), clinical results are variable and there are increased
efficacy testing requirements.

Another prospect for resistance prevention is to abrogate
the initial stress response that permits tolerance and the
development of resistance. Calcineurin, Hsp90 and other
stress-response components provide a range of targets. A
suitable tolerance inhibitor may render the azole flucona-
azole more potent and fungidical, thus creating a wider
window of therapeutic efficacy. Other potential targets
include biofilm formation or transcriptional regulators of
efflux pumps such as Tac1p, Upc2p or Mcm1p (Coste et
al., 2006; Riggle & Kumamoto, 2006; Silver et al., 2004).
Provided host toxicity is not a problem, selection of
resistance can also be precluded clinically by simply
prescribing high doses of antifungals.

A third strategy is to choose drug targets and select drug
candidates more carefully. Rapidly acting fungidical drugs
are better, theoretically, than fungistatic drugs as they do
not allow the selection of resistant variants. Therefore
essential gene products make better targets than non-
essential gene products. Extracellular targets are also better
than intracellular targets as the intracellular action of drugs
provides more options for drug inactivation, sequestration
and efflux-pump-mediated resistance. Drug candidates
should be screened as potential substrates of known drug
pumps (Niimi et al., 2006), and the in vitro mutagenesis of the target, or selection of resistant host cells, could be used to give an indication of the likelihood of resistance developing (Anderson, 2005).

In summary, in order to ensure that novel antifungals are not merely additional stresses to which C. albicans will respond with tolerance and resistance, it is imperative to elucidate the biology, physiology and underlying stress responses of this important fungus.

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