

REVIEW

Has the era of individualised medicine arrived for antifungals? A review of antifungal pharmacogenomics

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Treatment or prophylaxis of invasive fungal infection in recipients of haemopoietic SCT (HSCT) may require management of coexistent malnutrition, organ dysfunction and GVHD, all of which create added potential for inter- and intra-patient variations in drug metabolism as well as drug interactions. Polymorphism is common in genes encoding pathway components of antifungal drug metabolism such as enzymes (cytochrome *P450* (CYP450), glutathione *S*-transferase, *N*-acetyltransferase and uridine 5'-diphospho-glucuronosyltransferase), uptake transporters (organic cationic transporter, novel organic cationic transporter, organic anion transporter protein (OATP), organic anion transport (OAT), and peptide transporter) and efflux transporters (breast cancer resistance protein, bile salt export pump (BSEP), multidrug and toxin extrusion type transporter, multidrug resistance protein (MRP), OAT, permeability glycoprotein (P-gp), and urate transporter). Specific polymorphisms may be generalised throughout a population or largely confined to ethnic groups. CYP450 enzymes, especially 2C9 and 2C19, exhibit extensive polymorphism and are central to the metabolism of azole antifungals and their interactions with other drugs including calcineurin inhibitors, cytotoxics and benzodiazepines. Polymorphism may ultimately affect drug efficacy: CYP2C19 variation leads to a fivefold variation in voriconazole levels between individuals. Anticipated routine provision of pharmacogenomic data in the future for new drugs, together with accumulating knowledge about established agents, challenge physicians to assimilate and apply that information to drug prescribing. Increasing availability of pharmacogenomic data may strengthen demand for rapid turnaround therapeutic drug monitoring of antifungal agents in HSCT recipients.

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Introduction

Achievements such as the Human Genome Project provide sound foundations for the development of 'individualised medicine'. Therapy tailored to individual genotype may enable prediction of efficacy and adverse events.¹ The Food and Drugs Administration clearly anticipates such developments and encourages the inclusion of pharmacogenomic data for new drugs² such as voriconazole, one of the first to include these data. Hence, it is timely to review current knowledge of pharmacogenomics of antifungal drugs and consider whether we might soon individually tailor therapy based on our understanding of genotypic variability in patients.

Absorption, distribution and metabolism of drugs

Table 1 presents an overview of factors affecting drug absorption, distribution and metabolism.

Gastric pH varies markedly within the population, with up to tenfold interindividual variation.³ The impact of gastric pH on absorption of antifungal drugs is most clinically relevant for itraconazole and posaconazole.

Several antifungals are extensively protein bound, rendering them susceptible to variations in the levels of serum proteins, particularly albumin. Recipients of haemopoietic SCT (HSCT) are prone to malnutrition,⁴ with consequent reduction in serum proteins. At least in the case of itraconazole, this results in increased levels of unbound drug.⁵

Structural variation in plasma proteins, such as is seen in the genetic variants of albumin,^{6,7} may affect substrate binding,⁸ but no relevant data are yet available as to whether this affects antifungal drugs.

Most cellular uptake of drugs occurs by passive diffusion, but some drugs are actively imported, requiring specific transporters (see Table 2) and energy expenditure. Most of the transporters exhibit genetic variants, the relative frequency of which varies with ethnicity.^{9–11} This may be reflected in differing transport characteristics and drug levels among ethnic groups.¹¹ This is relevant to antifungal therapy as several antifungals are substrates or inhibitors of these transporters. The effect of genetic variability of transporters on the cyclodextrin carrier used to solubilise some antifungal drugs is currently unknown.

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Table 1 Factors affecting the absorption, distribution and metabolism of drugs

Process	Factors affecting the process	Comments
<i>Absorption (affects orally administered drugs)</i>		
Dissolution in stomach	Gastric pH Presence of food	Gastric pH: lower and more acidic (enhances some drug absorption, e.g., <i>itraconazole capsules</i>) in men than women ¹²⁴ in critically ill patients ¹²⁵ Gastric pH: increased and less acidic (reduces some drug absorption, e.g., <i>posaconazole</i>) during fasting ¹²⁶ use of H ₂ -receptor agonists proton pump inhibitors ¹²⁷
Uptake from GI tract	Passive diffusion (no energy expenditure) Active transport (requires expenditure of energy)	Affected by chemical composition of drug: Lipophilic drugs diffuse across cell membrane (e.g., <i>itraconazole, posaconazole</i>); hydrophilic drugs cross via aqueous channels (e.g., <i>fluconazole</i>) Other drugs, e.g., <i>amphotericin B</i> ; presence and activity of active transporters (e.g., <i>P-glycoprotein and itraconazole</i>)
<i>Distribution</i>		
Protein binding	Distribution to tissues affected by extent of protein binding of the drug in serum	<i>Fluconazole</i> and <i>voriconazole</i> are less protein bound, resulting in more extensive tissue penetration, such as central nervous system
Drug transporters	Presence and activity of transporters varies in different tissues (see Table 2)	SNPs in transporters may lead to reduced affinity for their substrates, ¹²⁹ although there are currently no data for antifungal drugs
<i>Metabolism</i>		
First-pass metabolism (for orally administered drugs) and metabolism of many drugs	Distribution and activity of cytochrome P450 enzymes and P-glycoprotein in the liver and GI tract. Activity of CYP450 enzymes varies with age, ¹³⁰ gender ¹³¹ and ethnicity ¹⁷	Intestinal CYPs: 3A (80%), 2C9 (~14%) ¹³² Liver CYPs: 3A4/5 (29%), 2C (18%), 1A2 (13%) ¹³³ Highest levels of 3A in duodenum and middle jejunum, declining in the distal jejunum and ileum ¹³⁴ <i>Voriconazole</i> and <i>itraconazole</i> have extensive interactions via the CYP system

Abbreviations: CYP = cytochrome P450; GI = gastrointestinal; SNP = single-nucleotide polymorphism.

Table 2 Key uptake and efflux transporters

Uptake transporters	Efflux transporters	Comments
OCT ^{135,136}	BCRP ^{142,143}	Relative distribution of each transporter varies in intestines, kidney, liver and brain Genetic variants have been described for almost all the transporters listed here (references describing genetic variants are in bold). As several antifungals interact with these transporters <i>in vitro</i> , potentially they may interact <i>in vivo</i> .
OCTN ^{137,138}	BSEP ^{144,145}	
OATP ^{139,140}	MATE ¹⁴⁶	
OAT ^{137,140}	MRP ^{142,147}	
PEPT ^{137,141}	OAT ^{148,149}	
	P-glycoprotein ^{150,151}	
	URAT ^{148,152}	

Abbreviations: BCRP = breast cancer resistance protein; BSEP = bile salt export pump; MATE = Multidrug and toxin extrusion type transporter; MRP = multidrug resistance protein; OAT = organic anion transporter; OATP = organic anion transport protein; OCT = organic cation transporter; OCTN = novel organic cation transporter; PEPT = peptide transporter; URAT = urate transporter.

The cytochrome P450 (CYP450) enzyme system carries out phase I oxidative metabolism of a vast range of endogenous and exogenous substrates, including 75% of all drugs.¹² Drugs metabolised by the same CYP enzymes often interact,^{13,14} and several websites detail the role of CYP enzymes in drug interactions (for example, <http://bioinformatics.charite.de/supercyp/index.php?site=home>, <http://medicine.iupui.edu/clinpharm/ddis/> and <http://www.drugbank.ca/>). CYP expression varies with site and age (see Table 1) and, in addition, there may be up to 20-fold variability in CYP3A4 activity between individuals.¹⁵ Thus, the same drug given orally to two patients may be subject to different levels of first-pass metabolism and hence achieve very different levels in the circulation. A further

complication is the overlapping substrate specificities of CYP3A4 and permeability glycoprotein (P-gp).¹⁶

Interindividual variability of CYP450 enzyme activity is influenced by the frequent presence of allelic single-nucleotide polymorphisms (SNPs), some of which result in reduction or ablation of their metabolic activity. CYP2C19 has over 20 polymorphisms that result in truncated or inactive enzyme¹⁷ and one that causes enhanced activity.¹⁸ Other polymorphic cytochromes involved in antifungal drug metabolism include CYP2C9^{19,20} and CYP3A4/5.^{21,22} The prevalence of these polymorphisms varies in different populations and hence the likelihood of expressing a particular genotype/phenotype varies with ethnicity. In Caucasians, ~80% will have wild-type 2C9 alleles and ~20% the

commonly occurring variants, resulting in alterations in their substrate affinity.²³ For 2C19, the incidence of the 'poor metaboliser' phenotype associated with inactive 2C19 protein production is 2–6% in Caucasians, but 15–20% in Asians.¹⁷

Phase II metabolic processes, or conjugation reactions, are catalysed by a range of enzymes, including glutathione *S*-transferase, *N*-acetyltransferase and uridine 5'-diphosphoglucuronosyltransferase (UGT). These enzymes are genetically polymorphic,^{24–26} with some of the resultant enzymes having decreased activity.^{26,27} The CYP enzymes are central to the metabolism of azole antifungals, but some of the phase II enzymes have also been shown to be important for certain antifungal drugs.

Absorption, distribution, metabolism and elimination of antifungal drugs

Polyenes

Amphotericin B deoxycholate and the lipid formulations of amphotericin B. Amphotericin B deoxycholate is a polyene antifungal first licensed in the late 1950s, but now little used in its original formulation because of its toxicity. It binds to ergosterol in the fungal cell membrane, resulting in pore formation and leakage of cell constituents.²⁸

The therapeutic advantages provided by the broad spectrum of activity, including yeasts and moulds, are offset by infusion-related toxicity and nephrotoxicity. In contrast, lipid formulations of amphotericin B maintain similar efficacy and are generally associated with fewer toxicities, but are significantly more expensive.²⁹ None of the amphotericin B preparations is absorbed orally and they must be given i.v. Amphotericin B is extensively protein bound in serum to lipoproteins via cholesterol,³⁰ serum albumin and human α 1-acid glycoprotein,³¹ but liposomal amphotericin largely remains within the liposomes in serum and hence does not appear to be significantly protein bound (Table 3).³¹

The metabolic pathway of amphotericin B and liposomal amphotericin is largely unknown,^{28,32} rendering assessment of the impact of genetic variation somewhat speculative. In the case of amphotericin B deoxycholate, most of the drug is excreted unchanged in urine or faeces with >90% recovered within 7 days, suggesting that little metabolic breakdown occurs.³³ In contrast, <10% of liposomal amphotericin B is excreted unchanged within 7 days,³³ possibly reflecting slow tissue release.³⁴ No metabolites have been detected from either drug.

There are few data on the interaction of amphotericin B with the CYP system or drug transporters (see Table 4). Amphotericin B was associated with reduced levels of hepatic CYP3A4 in patients seropositive for HIV but this may have been because of nonspecific hepatocyte damage.³⁵ There are currently no data on the interaction of liposomal amphotericin and the CYP enzymes or drug transporters.

Amphotericin B deoxycholate reduces oral bioavailability of ciclosporin, an effect observed clinically.³⁶ This is mediated via increased expression of the multidrug resistance gene *MDR1* in the duodenum causing increased levels of the *MDR1* gene product P-gp,³⁶ but it is not known if liposomal amphotericin has a similar effect. This results

in increased efflux of ciclosporin and reduced plasma levels. Interestingly, ciclosporin is itself an inhibitor of P-gp. The *MDR1* gene is polymorphic, raising the possibility of variation in the interaction with amphotericin B. These data suggest a possible interaction between amphotericin B deoxycholate and P-gp, and hence with the genetic polymorphisms seen in this transporter.

Overall, however, there is little evidence to support a clinically significant impact of pharmacogenomic variation upon the therapeutic effects of amphotericin B or its lipid formulations.

Triazole antifungals

The azoles have a common mode of action, inhibiting biosynthesis of ergosterol, critical to the integrity of the fungal cell membrane. Specifically, they inhibit 14 α -sterol demethylase, an enzyme in the conversion pathway of lanosterol to ergosterol;³⁷ this demethylase is a member of the CYP450 superfamily found in fungi, designated CYP51A1.

Azoles are both inhibitors and substrates of various human CYP enzymes (Table 4). This may explain, in part, the plethora of drug interactions between azoles and several other groups of drugs, many of which are clinically relevant to the HSCT recipient.³⁸

Fluconazole. Fluconazole is a triazole antifungal, with activity against *Cryptococcus* and many species of *Candida*, often with reduced activity against *Candida glabrata* and none against *Candida krusei*. It is not active against *Aspergillus*.

Available as oral and i.v. formulations, the oral bioavailability of fluconazole exceeds 90%,³⁹ and is unaffected by gastric pH,⁴⁰ food intake or gastrointestinal disease.⁴¹

It is hydrophilic with minimal protein binding and therefore achieves good tissue penetration into cerebrospinal fluid, saliva, sputum, vagina, skin⁴¹ and brain tissue.⁴² Elimination of fluconazole is predominantly renal with no circulating metabolites.⁴³

Fluconazole inhibits, but is not a substrate of, several CYP enzymes (Table 4). It inhibits 2C9, 2C19 and to a lesser extent 3A4,^{44,45} but not CYP1A2,⁴⁶ 2A6 or 2E1. Its ability to inhibit 2C9 and 2C19 causes potential drug interactions particularly relevant to HSCT recipients; for example, the interaction with CY may result in increased formation of toxic metabolites,⁴⁷ although others have noted a protective effect of co-administration.⁴⁸

Fluconazole is both a substrate⁴⁹ and an inhibitor⁵⁰ of the UGT isoform, UGT2B7, the enzyme involved in its metabolism to the urinary metabolite fluconazole glucuronide.⁴³ It also inhibits UGT2B4, hence inhibiting, for example, the glucuronidation of codeine that may potentiate codeine-induced analgesia.⁵¹

The limited involvement of CYP and drug transporters in the uptake and metabolism of fluconazole means that their genetic variation has relatively little impact on fluconazole pharmacokinetics.

Itraconazole. Itraconazole is a triazole antifungal, with activity against *Candida* species (including some fluconazole-

Table 3 Licensed indications, absorption, distribution, metabolism and elimination of antifungal drugs

	Licensed indications ^a	Absorption	Distribution	Metabolism	Elimination	Comments
Amphotericin B deoxycholate	Systemic or deep mycoses; suspected or proven infection in febrile neutropenic patients	Poor oral bioavailability, hence i.v. only—complete absorption	95% protein bound ³⁰	Very little metabolic breakdown ³³	Largely unchanged in urine (21%) and bile (43%) ³³	Less often used clinically because of nephrotoxicity
Liposomal amphotericin B	Systemic or deep mycoses; suspected or proven infection in febrile neutropenic patients	Poor oral bioavailability, hence i.v. only—complete absorption	Most remains associated with the liposomes ³¹	Very little metabolic breakdown ³³	Slow elimination: after 7 days only 5% excreted in urine and 4% in faeces—remaining drug thought to be in the tissues ³³	Complete elimination from tissues may take several weeks. ³³ Aerosolised liposomal amphotericin B has shown promise in preventing aspergillosis ⁵³ Dose adjustment in renal impairment or use alternative antifungal agent In renal impairment dosage adjustment is required and may be required in hepatic impairment ¹⁵⁴
Fluconazole	Invasive candidiasis; treatment and prophylaxis of cryptococcosis; prophylaxis in immunocompromised patients	Good oral bioavailability > 90% ³⁹	11–20% protein bound ³⁹	Limited metabolism ³⁹	Largely unchanged in urine (80%) with 11% metabolites ³⁹	
Itraconazole	Oral and oesophageal candidiasis in immunocompromised patients; prophylaxis in haematology patients and HSCT recipients who are likely to become neutropenic	Gastric pH important; oral bioavailability better with solution than capsules ^{52,55}	99% protein bound ⁵⁷	Extensive hepatic metabolism via CYP3A4. ⁵⁷ Hydroxy-itraconazole is an active metabolite	As metabolites via urine (35%) and faeces (54%); only 3–18% as parent drug detected in faeces ⁵⁷	The i.v. prep not recommended in severe renal impairment or haemodialysis; consider dose reduction in hepatic impairment
Voriconazole	Invasive aspergillosis; candidaemia in non-neutropenic patients; fluconazole-resistant invasive candidiasis; serious infections caused by <i>Scedosporium</i> and <i>Fusarium</i> .	Good oral bioavailability > 90% ⁶¹	58% protein bound ¹⁵⁵	Largely hepatic. CYP2C19 and 3A4 are most important. ⁷³ Higher incidence of 'poor metabolisers' in Asian, ¹⁷ SE Asian ¹⁵⁶ and Pacific islander ¹⁵⁷ populations	As metabolites in urine (78%) and faeces (23%); only 2% unchanged drug excreted in faeces ⁶⁵	The i.v. preparation not recommended in severe renal impairment or haemodialysis; dosage adjustment in hepatic impairment
Posaconazole	Prophylaxis in neutropenic patients undergoing chemotherapy for AML or MDS; patients who have received a HSCT and have GVHD. Invasive aspergillosis in patients intolerant of or refractory to amphotericin B or itraconazole.	Absorption is enhanced by concomitant fatty food intake ⁸⁰ and acidic gastric environment ⁸⁵	99% protein bound ⁸⁷	Mainly via the UGT enzyme pathway, limited role for CYP ⁸⁹	66% excreted unchanged in faeces. Metabolites excreted in faeces (11%) and urine (14%) ⁸⁹	Cautions in hepatic impairment
Caspofungin	Invasive candidiasis, aspergillosis in patients refractory to or intolerant of amphotericin or itraconazole; empiric therapy in febrile neutropenic patients	Poor oral bioavailability, hence i.v. only—complete absorption	> 90% protein bound, mainly to albumin ⁹⁵ but varies between healthy individuals and patients	Peptide hydrolysis and <i>N</i> -acetylation ⁹⁸	Metabolites eliminated in urine (41%) and faeces (35%), with little drug excreted unchanged ⁹⁸	Dosage adjustment in hepatic impairment
Micafungin	Oesophageal and invasive candidiasis; prophylaxis in adults undergoing allogeneic HSCT who are expected to become neutropenic; invasive candidiasis; prophylaxis in children and adolescents	Poor oral bioavailability, hence i.v. only—complete absorption	99.8% protein bound, mainly to albumin and less to α 1-acid glycoprotein ¹⁰⁴	Metabolised in liver, but not by CYP ¹⁰³	Metabolites excreted in faeces (> 90%) and urine (8%); < 1% of unchanged drug excreted in urine ¹⁰³	Avoid in severe hepatic impairment
Anidulafungin	Invasive candidiasis in non-neutropenic patients	Poor oral bioavailability, hence i.v. only—complete absorption	> 99% protein bound ¹⁵⁸	Slow chemical degradation, limited hepatic metabolism ¹¹⁰	Mainly as metabolites in faeces (> 90%) with ~ 10% excreted as unchanged drug ¹¹⁰	No dosage adjustment required for renal or hepatic impairment

Abbreviations: CYP = cytochrome P450; HSCT = haemopoietic SCT; MDS = myelodysplastic syndrome; UGT = uridine 5'-diphospho-glucuronosyltransferase.
^aAll licensed indications and dosage adjustments are as in the British National Formulary, March 2011 (<http://bnf.org/bnf/index.htm>), or Ashley and Currie.¹⁵⁹

Table 4 Interactions of antifungals with cytochrome P450 enzymes and transporters

	<i>Interaction</i>	<i>Comments</i>
Amphotericin B	No inhibition of CYP3A4 ¹⁶⁰ or of P-gp <i>in vitro</i> .	Interaction with other transporters unknown.
Fluconazole	Potent inhibitor of CYP2C9 and CYP2C19, ^{44,45} and less so for CYP3A4. ¹⁶⁰	Interaction with ciclosporin via CYP inhibition causes increased ciclosporin levels, especially with oral fluconazole. ^{164,165}
Itraconazole	No inhibition of P-gp ^{160–162} or BCRP. ¹⁶³ Substrate for CYP3A4; ⁵⁷ potent inhibitor of CYP3A4 ¹⁶⁰ and less so for CYP2C9, CYP2C19. ⁴⁵	CYP3A4 inhibition will affect metabolism of a variety of drugs to increase their levels (e.g., BU, ¹⁷¹ dexamethasone, ¹⁷² midazolam, ¹⁷³ ciclosporin, ¹⁷⁴ tacrolimus, ¹⁷⁴ methyl-prednisolone ¹⁷⁵) or the levels of their metabolites. (e.g., CY ⁴⁷).
Voriconazole	Substrate ¹⁶⁶ and inhibitor of P-gp. ^{160,161,167} Conflicting data as to inhibitory effect on OATP. ^{168,169} Inhibitor of multidrug resistance protein 3. ¹⁷⁰ Inhibitor of BCRP. ¹⁶³ No inhibition of NTCP or BSEP. ¹⁷⁰	Inhibition of P-gp and, therefore P-gp-mediated cellular efflux, may cause increased VCR toxicity, ¹⁷⁶ increased ciclosporin, tacrolimus and sirolimus levels, ¹⁷⁷ reversal of resistance to vinblastine, DNR and doxorubicin. ¹⁷⁸
Posaconazole	Substrate for CYP2C19, CYP 3A4, CYP2C9. ⁷³ Inhibitor of CYP2C9, CYP2C19, CYP3A4 and CYP2B6. ¹⁷⁹ No inhibition of BCRP. ¹⁶³	CYP interaction probably accounts for the interaction of voriconazole with many drugs, causing increased levels of tacrolimus, ¹⁸⁰ ciclosporin, ¹⁸¹ increased VCR neurotoxicity ¹⁸² and reduced clearance of midazolam, ¹⁸³ particularly the oral formulation of midazolam. Concomitant use of rifabutin, ¹⁸⁴ an inducer of CYP and especially of CYP3A4, causes significant reduction in voriconazole levels.
Caspofungin	Inhibitor of CYP3A4, but not a substrate of CYP. ¹⁸⁵ Inhibitor and substrate of P-gp. ⁸⁶	Inhibition of CYP3A4 ¹⁸⁵ results in increased levels of ciclosporin, tacrolimus ¹⁸⁶ and midazolam. ¹⁸⁵ Genetic polymorphisms of P-gp did not affect posaconazole exposure in healthy individuals. ⁸⁶
Micafungin	Inhibitor of CYP3A4 ⁵⁸ and NCTP. ⁹⁶ Not a substrate for CYP1A2, 2A6, 2C9, 2C19, 2D4 or 3A4. No inhibition of P-gp ⁹⁶ Substrate and inhibitor of OAT1B1. ⁹⁶ Slight inhibition of CYP3A4. ¹⁶⁰	CYP3A4 inhibition by caspofungin causes a 76% decrease in the metabolism of cytarabine. ¹⁸⁷ CYP inducers (e.g., rifampin, nevirapine, efavirenz, carbamazepine, dexamethasone and phenytoin) induce the metabolism of caspofungin. ¹⁰⁶ Rifampin may inhibit caspofungin tissue penetration via OATP1. ⁹⁹ Micafungin inhibition of CYP3A4 increases ciclosporin levels in ~20% of patients, ¹⁸⁸ but not tacrolimus. ¹⁸⁹
Anidulafungin	No inhibition of P-gp. ¹⁶⁰ No inhibition of CYP or OATP. ¹⁰⁹	Currently, no drug interactions are recorded.

Abbreviations: BCRP = breast cancer resistance protein; BSEP = bile salt export pump; CYP = cytochrome P450; NTCP = Na-taurocholate cotransporting polypeptide; OAT = organic anionic transporters; OATP = organic anionic transporting polypeptide; P-gp = permeability glycoprotein.

resistant species), *Aspergillus*, *Cryptococcus* and a range of other clinically important fungi.

Itraconazole is available as capsules, an oral solution and an i.v. infusion. The bioavailability of the capsules and oral solution varies significantly with dietary intake. Itraconazole capsules are maximally absorbed with food⁵² and acidic drinks (for example, cola⁵³ or vitamin C drink⁵⁴) at low gastric pH. Oral itraconazole solution has increased bioavailability (~30–35%) compared with the capsules, but in contrast to the capsules, is maximally absorbed during fasting.⁵⁵ Variations in gastric acidity and the widespread use of proton pump inhibitors in HSCT recipients may decrease absorption of itraconazole. Therefore, use of itraconazole oral solution in these patients, which produces higher serum trough concentrations,⁵⁶ is preferred.

Itraconazole is also a substrate or inhibitor of several drug transporters (Table 4).

Itraconazole is extensively protein bound, mainly to albumin,⁵⁷ and is predominantly metabolised in the liver, mainly by CYP3A4, for which it is both a substrate and an inhibitor.⁵⁸ More than 30 metabolites are formed,⁵⁷ including hydroxy-itraconazole,^{59,60} all of which are inhibitors of CYP3A4 and have a higher affinity for CYP3A4 than itraconazole itself. This may explain the potency of CYP3A4 inhibition seen with itraconazole.⁵⁹

Recently, itraconazole was shown to be a substrate for the phase II enzyme UGT1A4, with an affinity similar to

that of the imidazole antifungal agents, and it may also be an inhibitor of UGT1A4.⁴⁹

Itraconazole interacts with several genetically variable drug transporters and CYP enzymes, thus implicating them in the observed variability of itraconazole levels. Moreover, because CYP3A4 and P-glycoprotein also play a crucial role in the metabolism of many other drugs used in HSCT patients, this effect is likely to be compounded. Enhanced understanding of the pharmacogenomics of itraconazole will optimise itraconazole dosing as well as prediction of toxicities with other drugs.

Voriconazole. Voriconazole is a triazole antifungal, available as i.v. and oral formulations, with excellent oral bioavailability⁶¹ and highly variable nonlinear pharmacokinetics.^{62–64}

Excretion of voriconazole occurs predominantly via metabolites in the urine, with limited faecal excretion.⁶⁵

Voriconazole has moderate plasma protein binding, but there are limited data on the interaction of voriconazole with the various drug transporters. Voriconazole may interact with CaMdr1p,⁶⁶ the yeast homologue of P-gp, and by implication human P-gp.

Genetic polymorphism in CYP2C19 accounts for 49% of the variance in clearance of voriconazole,⁶⁷ with recognition of 'poor metaboliser' and 'extensive metaboliser' phenotypes.¹⁷ Levels of voriconazole in poor metabolisers

can be 4 to 5 times higher than those in extensive metabolisers.⁶⁸ A rapid metaboliser 2C19 phenotype has been described,¹⁸ resulting in levels of voriconazole that are significantly lower than either the extensive or poor metaboliser phenotypes.⁶⁹ Interestingly, the coexistence of multiple CYP polymorphisms in the same patient do not necessarily have an additive effect on the metabolism of voriconazole.^{70–72}

Metabolism of voriconazole results in several metabolites, the major circulating metabolite being the *N*-oxide of voriconazole,⁶⁵ formed predominantly by CYP3A4 and 2C19, with a smaller contribution from 2C9.⁷³ Production of the methyl hydroxylated metabolite is due solely to CYP3A4.⁷⁴ CYP450-mediated metabolism of voriconazole is responsible for ~75% of its oxidative metabolism. The remainder is due to flavin-containing mono-oxygenases⁷⁵ that also exhibit genetic polymorphism with resultant variations in catalytic activity.⁷⁶ Voriconazole is also a low-affinity substrate for UGT1A4 *in vitro*.⁴⁹

An understanding of how genetic polymorphism affects voriconazole metabolism has been pivotal in explaining the pharmacokinetic variability observed in patients. The occurrence of genetic variants in the CYP alleles (Table 4) has a significant impact on the levels of drug achieved in those patients and probably upon the therapeutic efficacy of voriconazole.^{77–79}

Posaconazole. Posaconazole is a triazole antifungal, currently only available as an oral suspension. Its bioavailability is significantly improved when taken with food (168% compared with the fasting state), especially if the food is high in fat (290% compared with the fasting state).⁸⁰ Doses up to 800 mg/day result in dose-proportional pharmacokinetics, but absorption is saturated at 800 mg/day.⁸¹ Absorption of posaconazole is further improved by splitting the dose (200 mg four times daily compared with 400 mg twice daily) and administering with an acidic beverage or a nutritional supplement.^{82,83} Concomitant dosing with cimetidine⁸⁴ or omeprazole⁸² both decrease posaconazole serum trough levels, probably because of reduced gastric acidity, an effect likely to be seen with other H₂ receptor agonists or proton pump inhibitors.⁸⁵

Data on interactions with transporters demonstrate that posaconazole is both a substrate and an inhibitor of P-gp.⁸⁶ The effect of SNPs in P-gp alleles was studied in 28 black and 28 Caucasian healthy volunteers dosed with 400 mg posaconazole twice daily after a meal. Individuals with a SNP resulting in reduced expression of P-gp (*n* = 13) demonstrated no difference in the area under the curve compared with those with normal levels of P-gp (*n* = 43). Therefore, the expression of SNPs in P-gp alleles had no effect on posaconazole pharmacokinetics in healthy individuals,⁸⁶ but whether this is also true in HSCT recipients, many of whom may have other issues related to absorption and reduced food intake, is not known. There are as yet no data on the interaction of posaconazole with other transporters in the setting of HSCT.

Posaconazole is extensively bound by plasma proteins mainly by serum albumin.⁸⁷

In contrast to the other triazoles, posaconazole interacts with fewer CYP enzymes (Table 4), possibly explaining its narrower drug interaction range.

Posaconazole is excreted largely unchanged; there are no active metabolites⁸⁸ and the metabolites seen in urine are glucuronide conjugates,⁸⁹ produced by UGT1A4.⁹⁰ Genetic variants occur in the alleles for this enzyme,⁹¹ some of which cause reduced catalytic activity.⁹² Drug interactions may also occur via the UGT metabolic pathway, including that between posaconazole and phenytoin.⁹³

Overall, it is likely that the effect of genetic variation on posaconazole pharmacokinetics is relatively small and more related to absorption than metabolism or elimination.

Echinocandins

The echinocandins inhibit β 1,3-glucan synthetase, an enzyme involved in fungal cell wall synthesis, leading to increased cell wall permeability and fungal cell lysis. The lack of β 1,3-glucan synthetase and cell wall in human cells explains the corresponding lack of toxicity seen with the echinocandins.⁹⁴

Caspofungin. Caspofungin is an echinocandin antifungal that is dosed i.v. and is extensively protein bound in plasma, mainly to albumin. Its plasma profile is determined primarily by its rate of distribution from plasma into tissues, rather than by metabolism or excretion.⁹⁵ Uptake occurs into hepatocytes via an initial rapid reversible adsorption to the cell surface and a second slow phase of transport across the cell membrane,^{95,96} mediated by organic anion transporter protein 1B1 (OATP1B1).⁹⁶ Interactions with other transporters are detailed in Table 4.

Biotransformation of caspofungin occurs primarily through hydrolysis, rather than by oxidative metabolism.⁹⁷ An initial open-ring metabolite is found in plasma, with subsequent peptide degradation resulting in low MW products found in urine. Within 4 weeks, 41% of the dose is excreted in urine and 35% in faeces⁹⁸ as metabolites.

Caspofungin is the echinocandin with most interaction with the CYP450 system (see Table 4).

Rifampin may inhibit the uptake of caspofungin into the tissues via OATP1, with trough levels 14–31% lower after multiple rifampin doses.⁹⁹ Genetic polymorphisms of OATP1B1¹⁰⁰ may affect the efficiency of uptake of caspofungin into the liver. However, there are no other known points at which genetic variability affects caspofungin, and hence pharmacogenomic analysis will be of minor importance in optimising use of this antifungal drug.

Micafungin. Micafungin is an echinocandin antifungal that is dosed i.v. It is mainly to bound to albumin and binding is independent of micafungin concentration.¹⁰¹ Hepatocyte uptake is mediated by both active and passive mechanisms. Na–taurocholate cotransporting polypeptide (NTCP) is most important in uptake, whereas secretion across the canalicular hepatocyte membrane is mediated largely by BSEP (bile salt export pump). MRP3 (multidrug resistance protein 3) mediates transport of micafungin across the sinusoidal hepatocyte membrane. Biliary excretion rather than hepatic uptake is thought to be the rate-

limiting step in hepatic elimination of micafungin in humans.¹⁰² Active transport is utilised for both uptake and excretion of micafungin and may be susceptible to genetic variability, as all the transporters involved in the process are known to be polymorphic.

Metabolism of micafungin occurs mainly in the liver, with inactive metabolites excreted in bile and urine.¹⁰³ Arylsulfatase is involved in micafungin metabolism,¹⁰⁴ and polymorphisms have been described.¹⁰⁵

In general, however, pharmacogenomic analysis seems unlikely to add much to the clinical use of micafungin.

Anidulafungin. Anidulafungin is an echinocandin antifungal that is dosed i.v. Importantly, anidulafungin has no interactions described with any drug yet studied,¹⁰⁶ including rifampin.¹⁰⁷

Anidulafungin is extensively bound by plasma proteins¹⁰⁸ and undergoes biotransformation, rather than metabolism, undergoing a slow, nonenzymatic degradation to inactive peptides.⁹⁷ Neither phase 1 nor phase 2 hepatic metabolism is involved in elimination of anidulafungin, nor is it a substrate, inducer or inhibitor of CYP450. At physiologically relevant concentrations it does not inhibit OATP.¹⁰⁹

Elimination of anidulafungin is via bile in the faeces, with <10% of the drug excreted unchanged in the faeces and <1% in urine.^{107,110}

Table 5 Assessment of laboratory service for provision of therapeutic drug monitoring (TDM)

Assay is fully validated ^{190,191} and is:
Selective
Accurate
Sensitive
Robust
Stable
Performs well in relevant quality assurance schemes
Small sample volume required
Clinical range defined
Assay performed regularly (ideally daily) and results communicated quickly
Cost per test appropriate to allow regular testing
Staff available to provide advice on interpretation of results and suggest corrective action if necessary

Genetic variation of CYP or phase II enzymes or the hepatic transporters is unlikely to affect anidulafungin pharmacokinetics, given their lack of interaction with anidulafungin, and hence pharmacogenomic analysis will not inform clinical use.

Therapeutic drug monitoring (TDM)

TDM is considered necessary for drugs with (1) unpredictable population pharmacokinetics, (2) a narrow therapeutic index and (3) a defined therapeutic range.¹¹¹ Amphotericin B, its lipid formulations and the echinocandins demonstrate predictable pharmacokinetics, and hence TDM is not required. The triazoles are the main agents where TDM is considered helpful in optimising treatment.^{111–113} Although levels of fluconazole can vary significantly between patients, the variability is largely due to renal function, and hence doses are best adjusted according to creatinine clearance.¹¹⁴ There is increasing evidence to support TDM in routine use of itraconazole, voriconazole and posaconazole.

The methods available for the measurement of drug levels include bioassays, high-performance liquid chromatography and liquid chromatography–mass spectrometry. Bioassays are inherently unreliable in patients receiving more than one antifungal drug, where the assay will usually only measure total antifungal activity and cannot separate out the activity due to each drug.¹¹⁵ The presence of the microbiologically active metabolite of itraconazole, hydroxy-itraconazole, results in artificially elevated results in itraconazole bioassays.¹¹² Most laboratories now use either high-performance liquid chromatography or liquid chromatography–mass spectrometry as they are more sensitive, specific and have reduced analytical times. When properly validated, they are capable of measuring the level of an individual drug even in the presence of others. Assessment of a laboratory service for provision of TDM should ensure that the assays are performed regularly and results are communicated in a timely manner to ensure that they are relevant to patient management (see Table 5). The therapeutic ranges used vary between laboratories, but data are accumulating to suggest what the optimal ranges should be.

Table 6 Therapeutic drug monitoring ranges for itraconazole, voriconazole and posaconazole (pre-dose or trough levels)

Antifungal	Target during prophylaxis (mg/L)	Target during treatment (mg/L)	Upper limit of nontoxic range (mg/L)	Studies from which levels are derived
Itraconazole	0.5	0.5	4–5	Outcome better in aspergillosis, ¹⁹² cryptococcosis ¹⁹³ and oral candidosis ¹⁹⁴ with higher serum trough levels. In neutropenic patients, fewer breakthrough infections during prophylaxis with levels >0.5 mg/L ¹⁹⁵
Voriconazole	1–2	1–2	5–6	In invasive aspergillosis, favourable outcome correlated with levels >2.05 mg/L. ⁷⁷ Improved outcome and lower fungal infection-related mortality with trough levels >2.2 mg/L ⁷⁹ Liver toxicity seen in patients with levels >6 mg/L ⁶³ and neurotoxicity seen in patients with levels >5.5 mg/L ⁷⁸
Posaconazole	0.7	1.25	Unknown	In prophylaxis, levels above 0.7 mg/L were associated with reduced clinical failure ¹⁹⁶ In salvage therapy for invasive aspergillosis, response rate increased with increasing serum levels and in patients with average levels above 1.25 mg/L response rate was 75% ¹⁹⁷

Table 7 Suggested indications for therapeutic drug monitoring (TDM) of itraconazole, voriconazole and posaconazole*Indications for TDM*

At 5–7 days after initiation of therapy or dose adjustment
 If an interacting drug is started or stopped^a
 During prophylaxis if a breakthrough infection occurs
 Uncertain drug compliance
 Patient exhibits signs or symptoms of toxicity
 Lack of response during treatment
 Reduced oral absorption, for example, diarrhoea
 Patient has inadequate oral nutrition^b

^aPrecise timings of assay will be determined by the individual drug and concomitant medication.

^bNot usually applicable for voriconazole because absorption is independent of gastric pH.

Table 6 summarises therapeutic ranges for itraconazole, voriconazole and posaconazole, and Table 7 lists the suggested indications for TDM.

Use of TDM is becoming more widespread and data from reference laboratories indicate that therapeutic levels are not achieved in a significant proportion of routine samples.^{116–118} In compliant patients who have levels persistently out of range, there is an argument to support pharmacogenomic analysis of CYPs, for example, 2C19 in the case of voriconazole. In fact, some clinical laboratories are already providing this service.

The inability to predict serum levels from triazole drug doses, the significant potential for drug interactions, the effects of genetic variation on pharmacokinetics and the correlation between improved outcomes with higher serum levels all add to the weight of evidence supporting TDM in HSCT recipients.

Conclusions and future perspectives

Antifungal efficacy in invasive fungal infection is dependent on systemic drug exposure; therefore, maximising the absorption and distribution of antifungals to relevant tissues is essential for favourable treatment outcomes. The potential for genetically induced variation in metabolism of antifungal drugs, and the knock-on effect on drug interactions, remains largely theoretical, pending systematic laboratory evaluation. Such experience will clarify the relative importance of specific polymorphisms. However, there is already ample evidence of clinically relevant pharmacogenetic influence in the case of the azoles, particularly voriconazole. In contrast, its role in the use of amphotericin B and the echinocandins may be less important, because of their distinct metabolic and elimination pathways.

Genetic variation affects susceptibility to fungal infection,¹¹⁹ metabolism and drug interactions of antifungals and, it is now emerging, the development of resistance to the azoles in *Aspergillus fumigatus*.^{120,121} Unsurprisingly, mutations of fungal CYP51, a prime target of the triazoles, seem to mediate the predominant resistance pathways.¹²²

Large-scale screening for SNPs in relevant human genes, using next-generation sequencing techniques,¹²³ is now feasible. As scientists unravel the journey of antifungal

drugs through the body and the many enzymes and transporters encountered *en route*, we will benefit from a better understanding of how genetic variation affects pharmacokinetics. An individual will have a unique profile of susceptibility to invasive fungal infection,¹¹⁹ metabolic handling of and response to antifungal therapy. Meaningful analysis of this genomic profile is a tantalising prospect on the horizon, if not quite within our grasp. The transition from horizon to clinic will depend upon a better understanding of the costs and benefits, particularly in the current economic climate.

Conflict of interest

HRA has received speakers fee, travel support or research funding from Pfizer, Gilead UK and Merck Ltd. MHG has received speakers fees or travel support from Pfizer, Gilead UK and Merck Ltd.

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