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Azole Resistance Profile of Amino Acid Changes in Aspergillus fumigatus CYP51A Based on Protein Homology Modeling

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Molecular studies have shown that the majority of azole resistance in Aspergillus fumigatus is associated with amino acid substitutions in the cyp51A gene. To obtain insight into azole resistance mutations, the cyp51A gene of 130 resistant and 76 susceptible A. fumigatus isolates was sequenced. Out of 130 azole-resistant isolates, 105 contained a tandem repeat of 34 bp in the promoter region and a leucine-to-histidine substitution in codon 98 (designated TR/L98H). Additionally, in 12 of these TR/L98H resistant isolates, the mutations S297T and F495I were found, and in 1 isolate, the mutation F495I was found. In eight azole-resistant isolates, known azole resistance mutations were detected in codon G54, G138, or M220. In three azole-susceptible isolates, the mutation E130D, L252L, or S400I was found and in 13 azole-susceptible isolates but also in 1 azole-resistant isolate, the mutations F46Y, G98G, M172V, N248T, D255E, L358L, E427K, and C454C were found. All of the nonsynonymous mutations, apart from the mutations in codons G54, G138, and M220 and L98H, were located at the periphery of the protein, as determined by a structural model of the A. fumigatus Cyp51A protein, and were predicted neither to interact with azole compounds nor to affect structural integrity. Therefore, this wide diversity of mutations in the cyp51A gene in azole-susceptible A. fumigatus isolates is not correlated with azole resistance. Based on the Cyp51A protein homology model, the potential correlation of a mutation to azole resistance can be predicted.

Aspergillus fumigatus is the etiological agent of a range of clinical syndromes, most notably invasive aspergillosis (IA), which is associated with significant morbidity and mortality. Advances in the management of IA have been made in recent years by imaging techniques, by the use of non-culture-based diagnostic tools, by improvement in the management of patients with IA, and by the use of more effective antifungal agents, especially azole compounds (2). Azole resistance in invasive aspergillosis (IA), and by the use of more effective antifungal agents, is associated with significant morbidity and mortality. Clinical syndromes, most notably invasive aspergillosis (IA), have been described for azole-resistant A. fumigatus clinical isolates, as well as for laboratory-induced azole-resistant A. fumigatus mutants (5). Mutations at codon G54 are related to cross-resistance to the azoles itraconazole and posaconazole (4). Also, different mutations in codon M220 have been described in clinical strains that are correlated with itraconazole resistance combined with different patterns of elevated MICs of the other azole drugs (12). Azole-resistant A. fumigatus isolates have been found that showed a glycine-to-cysteine substitution in codon 138 and exhibited a pan-azole resistance phenotype (8). In codon 488, a mutation from glycine to serine was correlated with resistance to voriconazole and itraconazole (1). A recent survey of MAR clinical isolates in the Netherlands showed over 90% dominance of a resistance mechanism consisting of a tandem repeat of 34 bp in the promoter region combined with a leucine-to-histidine substitution at codon 98 (TR/L98H) (11, 17, 18, 20, 23).

The cyp51A sequence of Mycobacterium tuberculosis shows 28% sequence identity over 464 residues with the cyp51A sequence of A. fumigatus. Therefore, it was possible to derive the structure of the wild-type CYP51A protein of A. fumigatus from the crystal structure of M. tuberculosis by homology modeling (6, 26). The carefully optimized and checked structure of the protein was used to characterize the mutations in the CYP51A homology model. Two ligand access channels were previously identified in the model which probably not only accommodate the natural substrates but are also used by the azole compounds for docking (6, 26). The aims of our study

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A. fumigatus isolates cultured between 1994-2008

Ability to grow on ITZ-containing agar

- 130 (+)
- 2,795

Confirmation Azole-resistant phenotype (CLSI M38-A)

Selection of control isolates Criteria:
- matched on underlying disease
- temporal relationship to ITZ+ isolate
- sample type

Phenotype (CLSI M38-A)

Cyp51A sequencing

130

Cyp51A sequencing

76

RESULTS AND DISCUSSION

A total of 206 A. fumigatus isolates, 130 ITZ+ and 76 ITZ-, were analyzed for mutations in the cyp51A gene. A wide variety of mutations was found in the cyp51A gene of ITZ+ and ITZ- isolates, both known and not known from the literature to be correlated with azole resistance (Table 1). In 113 ITZ- isolates, cyp51A mutations known to be correlated with azole resistance were found. In 105 ITZ+ isolates, a tandem repeat of 34 bp in the promoter region and a leucine-to-histidine substitution at codon 98 (TR/L98H) were found, and in 8 ITZ+ isolates, other known mutations were found (11).

In 19 isolates that contained the TR/L98H mutations, additional mutations in the cyp51A gene (S297T, F495I, S52T, Q88H, N125I, Q141H, A284A, and L339L) were found. In one ITZ+ isolate, the mutations F46Y, G98G, M172V, N248T, D255E, L358L, E427K and C454C were found, and in one ITZ+ isolate, no mutations were found in the cyp51A gene. In 13 ITZ+ isolates, combinations of the mutations F46Y, G98G, M172V, N248T, D255E, L358L, E427K, and C454C were found, and in three ITZ- the mutations, E130D, L252L, and S400L were found. In 60 ITZ+ isolates, no mutations were found in the cyp51A gene.

ITZ+ isolates, (i) Cyp51A mutations known to be correlated with azole resistance. In eight ITZ+ isolates, mutations changing amino acid G54, G138, or M220 in the cyp51A-encoded protein were detected (Table 1). These mutations were all known to be correlated with azole resistance (4, 8, 12). The amino acids in codons G54, G138, and M220 were all located in close proximity to the opening of one of the two ligand access channels of the protein (Fig. 2). The ligand access channels are thought to be used by the azole compounds to enter the active site of the protein, and alterations of these openings of these channels due to amino acid changes probably disturb the docking of azole molecules. The G138C mutation was...
located in a helix of channel 1 close to the heme cofactor, and isolates harboring this mutation show a pan-azole resistance phenotype (Fig. 2). This was also described previously for G138R, in which the arginine was predicted to clash with neighboring residues (26). Amino acids G54 and M220 are one of the heme’s side chains and with the side chains of the residue, it might sufficiently close the entrance of access channel 2 to disturb the docking of large molecules such as those of itraconazole and posaconazole. The long tails of itraconazole and posaconazole need to make interactions along the entrance surface of the channel. Therefore, changes in residues in codon 54, which is located at the entrance of the channel, do not affect voriconazole but do have a dramatic effect on the docking of itraconazole and posaconazole. Furthermore, the G54E mutation produced only an itraconazole resistance phenotype. The main difference in structure between posaconazole and itraconazole is the presence of the hydroxyl group at the end of the long tail of posaconazole that may create a hydrogen bond interaction on the surface of the protein. Moreover, it is not clear whether an additional oxygen atom in the core scaffold of itraconazole plays any role in the recognition of azole molecules. Moreover, it is not clear whether the presence of the G54E mutation. Therefore, not only the specific location of an amino acid change is important but the amino acid replacement is of at least the same importance for the binding. Therefore, it is of interest to examine the interactions of azole and posaconazole with the G54E mutant. Therefore, although there are two ligand
access channels present, the change of an amino acid in the opening in one channel is already sufficient for certain azole resistance phenotypes. It seems that the structural changes in one channel affect the docking of certain azole compounds for the whole protein.

Out of 130 azole-resistant isolates, 105 contained the TR/L98H mutations. It was shown that leucine 98 is not located close to either the active heme center or any of the two ligand access channels but is located on a loop that partly forms an arch-like structure that is highly conserved among the members of the CYP51 family of proteins (Fig. 2). In a preliminary study, we have used molecular dynamic simulations changing the leucine to histidine in codon 98. In these studies, we observed that the flexibility of this arch-like structure increased considerably, thereby narrowing the diameter of the entry of the ligand access channels (data not shown). These changes may result in the MAR phenotype by affecting the ligand access channels important for the docking of azole compounds.

(ii) ITZ* isolates with other cyp51A mutations. In each of six isolates with the TR/L98H mutations, an additional mutation was found, four nonsynonymous mutations, namely, S52T, Q88H, N125I, and Q141H, and two synonymous mutations, L339L and A284A (Table 1). Introduction of these mutations into the CYP51A homology model showed that these mutations were not located in conserved regions of the protein but were all distributed on the periphery of the protein, except for two, S52T and N125I (Fig. 2). S52 was located at the entrance of channel 2; however, the serine is replaced with an only slightly larger threonine that is similar to serine, an alcoholic residue with intermediate hydrophobicity. The N125I mutation represents a change from electrophilic asparagine to a large nonpolar isoleucine and may have a larger impact on resistance. However, as the isolates all contain the TR/L98H mutations and exhibit the MAR phenotype, these additional nonsynonymous mutations probably play only a minor or no role at all in the azole resistance phenotype and no differences in MIC values were observed between these isolates and those containing only the TR/L98H mutations. It is important to correlate changes in the structural integrity of the protein with susceptibility to azole compounds because structural changes could affect the docking of the azole molecules, with azole resistance as a possible consequence. The amino acid residues on the periphery of the protein generally have a lower conservation level and are not essential for the functionality of the protein; therefore, amino acid changes in these residues will not influence structural integrity. The structural integrity of the Cyp51A protein is not changed by the two synonymous mutations L339L and A284A, since the amino acids are not changed. However, the possibility of changes at the RNA structural level due to silent mutations cannot be excluded, as synonymous mutations in RNA regulatory elements might alter transcription, splicing, and other regulatory processes, although there is no evidence that they may actually play a role in *A. fumigatus* (21, 25).

In 12 isolates with the TR/L98H mutations, the nonsynonymous mutations S297T and F495I were found, and in 1 isolate with the TR/L98H mutations, only the F495I mutation was found (Table 1). Interestingly, although both mutations are located close to the active site of the protein, they do not seem to affect resistance, as the TR/L98H mutations already produce the MAR phenotype and no differences in MIC values were observed between these isolates and those containing only the TR/L98H mutations. Apart from that, although threonine is slightly larger than serine and both residues contain a hydroxyl group, in the case of the second observed mutation, F495I, the hydrophobic phenylalanine is replaced with a hydrophobic though not aromatic isoleucine. The slight differences are not expected to influence the binding of the external ligands, and therefore these additional mutations do not seem to affect protein function either (brown, Fig. 2).

(iii) ITZ* isolates without cyp51A mutations. In 16 azole-resistant isolates, no mutations were found in the cyp51A gene. Azole-resistant *A. fumigatus* isolates without mutations in the cyp51A gene have been reported previously in the literature,
which suggests that alternative mechanisms of azole resistance exist (7). The upregulation of efflux pumps has been described as a mechanism of azole resistance in Candida albicans previously; however, for clinical A. fumigatus strains, this possibility has only been described once (3, 16). A selection of two of these ITZ™ isolates did not show any significant increase in the mRNA expression levels of the ABC transporter AtfR or the multidrug resistance protein MDR3 or MDR4 compared to ITZ™ isolates (unpublished observations). Therefore, in these isolates, an as-yet-unknown mechanism of azole resistance must be present. Possibly, the cyp51A gene could be upregulated, although no changes in the promoter region of the cyp51A gene were present. Further investigation is warranted to characterize the alternative mechanisms of resistance in these isolates.

**ITZ™ isolates.** In 60 of 76 azole-susceptible isolates, no mutations were found in the cyp51A gene. However, in 3 susceptible isolates, either the nonsynonymous mutation E130D or S400I or the synonymous mutation L252L was found. E130D and S400I are both located on the periphery of the protein and, indeed, do not seem to interact with azole compounds. Also, in different combinations, five nonsynonymous mutations, F46Y, M172V, N248T, D255E, and E427K, and three synonymous mutations, G98G, L358L, and C454C, were found in 13 azole-susceptible isolates. These mutations were also found in one azole-resistant isolate without any other known mutation in the cyp51A gene related to azole resistance. These same exact mutations have been described previously in the literature to be found in both azole-resistant and susceptible isolates (7, 14). Therefore, amino acid changes found in the protein encoded by the cyp51A gene are not exclusively correlated with the development of azole resistance. Introducing the nonsynonymous amino acid alterations in the CYP51A homology model shows that these amino acid changes are all distributed at the periphery of the protein, not close to any of the two ligand access channels (Fig. 2), and are not located in any of the conserved regions of the CYP51A protein. Therefore, no effect on the biological activity of the CYP51A protein or the docking of the azole compounds in the ligand access channels is expected.

Due to the importance of CYP51 in antifungal drug studies, many CYP51 homology models have been made, e.g., C. albicans, Cryptococcus neoformans, Penicillium digitatum, and Saccharomyces cerevisiae, by using the crystal structure of M. tuberculosis CYP51 as a template (10, 15, 26, 27). Although this approach has several limitations, functionally important regions are conserved among the members of this fungal CYP51 family. A wide diversity of amino acid changes probably not correlated with resistance has been described by others (7, 14). In this study, we showed that the use of a CYP51A homology model can be very informative in predicting the effects of these amino acid changes. Specific residues in the CYP51A protein are of importance for azole docking, and identifying the location of a mutation in the CYP51A protein can help to predict whether a mutation can be considered a polymorphism or whether it has a potential correlation with azole resistance. Taking into account the diversity of cyp51A mutations, new mutations found in the cyp51A gene in azole-resistant isolates should be interpreted with care. By using a CYP51A protein homology model, a mutation can be investigated for a correlation with azole resistance. Subsequently, by placing the mutation into a wild-type strain by recombinant analysis, the impact of a mutation can be studied at the protein level to make a conclusive correlation with azole resistance.

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