

Table 1.- Nucleotide and amino acids substitutions in *cyp51A* and *cyp51B* genes and MICs for azole drugs of *A. fumigatus* clinical and mutant isolates.

Isolate / strain N.	<i>cyp51A</i> gene ^(a)		<i>cyp51B</i> gene ^(a)			MICs (µg/ml)			
	Codon 54	Codon 220	Codon 35	Codon 387	Codon 394	ITC	VRC	RVC	POS
CM- 237	GGG	ATG	TCT	GAT	CCT	0.25	0.5	0.5	0.06
CM-2739	GGG	ATG	TCT	GAT	CCT	0.50	0.5	0.5	0.06
CM-1369	GGG	ATG	TCT	GAT	CCT	0.25	0.5	0.5	0.06
CM-1245 (AF-91)	GGG	⁷²⁹ GTG *	¹⁰⁵ TCC	GAT	CCT	> 8.0	1.0	2.0 - 4.0	0.5 -1.0
CM-1252 (AF-90)	GGG	⁷²⁹ GTG *	¹⁰⁵ TCC	GAT	CCT	> 8.0	1.0	1.0 - 2.0	0.5
CM-2158 (AF/1422)	GGG	⁷²⁹ GTG *	¹⁰⁵ TCC	GAT	¹²⁸⁵ CCG	> 8.0	1.0	2.0 - 4.0	0.5 -1.0
CM-2159 (F/6919)	GGG	⁷³⁰ AAG **	TCT	GAT	CCT	> 8.0	1.0 - 2.0	1.0 - 2.0	2.0
CM-2164 (SO/3829)	GGG	⁷³⁰ ACG ***	TCT	¹²⁶⁴ GAA	¹²⁸⁵ CCA	> 8.0	0.5 - 1.0	1.0 - 2.0	0.25 - 0.5
T - XII	GGG	⁷²⁹ GTG *	TCT	GAT	CCT	> 8.0	1.0	2.0	0.5
T - III	GGG	⁷³⁰ AAG **	TCT	GAT	CCT	> 8.0	1.0	1.0	2.0
T - IV	GGG	⁷³⁰ AAG **	TCT	GAT	CCT	> 8.0	1.0	1.0	1.0
T - VII	GGG	⁷³⁰ AAG **	TCT	GAT	CCT	> 8.0	1.0	1.0	1.0
T - XI	GGG	⁷³⁰ AAG **	TCT	GAT	CCT	> 8.0	1.0	1.0	1.0
T - XXII	GGG	⁷³⁰ ACG ***	TCT	GAT	CCT	> 8.0	0.5 - 1.0	1.0	0.12 - 0.25
Amino acid substitution	(G54)	(M220V) * (M220K) ** (M220T) ***	(S35S)	(D387E)	(P394P)				

(a) Nucleotides are numbered from the translation start codon ATG of *cyp51A* and *cyp51B*.

(b) The numbers indicate the position at which a base change occurs (in bold)

(c) MICs: Minimal Inhibitory Concentrations of itraconazole (ITC), voriconazole (VRC), ravuconazole (RVC), and posaconazole (POS) in µg/ml.

(d) Transformants T-III, T-VI, T-VII, and T-XI (replacement of mutated *cyp51A* gene copy from CM-2159), T-XII (*cyp51A* from CM-1252) and T-XXII (*cyp51A* copy from CM-2164)