

Table 1.- Nucleotide and amino acids substitutions in *cyp51A* and *cyp51B* genes from *Aspergillus fumigatus* clinical isolates.

Isolate/Origin	Base changes in <i>cyp51A</i> gene ^(a)		Base changes in <i>cyp51B</i> gene ^(a)					(MICs (µg/ml))			
	Codon 54	Codon 236	Codon 35	Codon 42	Codon 187	Codon 387	Codon 394	ITC	VRZ	FCZ	KTZ
CM- 237	GGG	ATG	TCT	CAG	TTC	GAT	CCT	0.25	0.5	640	8.0
AF-1119	GGG	ATG	TCT	CAG	TTC	GAT	CCT	0.5	0.5	640	8.0
CM-1369	GGG	ATG	TCT	CAG	TTC	GAT	CCT	0.25	0.5	640	8.0
AF- 72	¹⁶¹ GAG [*]	ATG	TCT	¹²⁵ CTG	⁶⁶⁴ TTT	GAT	CCT	> 8.0	0.25	160	1.0
AF-1237	¹⁶⁰ AGG ^{***}	ATG	TCT	CAG	TTC	GAT	CCT	> 8.0	0.5	160	2.0
CM- 796	¹⁶¹ GTG ^{**}	ATG	¹⁰⁵ TCC	CAG	TTC	GAT	CCT	> 8.0	1.0	640	8.0
CM-1910	GGG	ATG	¹⁰⁵ TCC	CAG	TTC	GAT	CCT	> 8.0	4.0	3200	> 8.0
AF- 91	GGG	⁷²⁹ GTG [*]	¹⁰⁵ TCC	CAG	TTC	GAT	CCT	> 8.0	1.0	3200	> 8.0
AF- 90	GGG	⁷²⁹ GTG [*]	¹⁰⁵ TCC	CAG	TTC	GAT	CCT	> 8.0	1.0	3200	> 8.0
AF1422	GGG	⁷²⁹ GTG [*]	¹⁰⁵ TCC	CAG	TTC	GAT	¹²⁸⁵ CCG	> 8.0	1.0	3200	> 8.0
F/6919	GGG	⁷³⁰ AAG ^{**}	TCT	CAG	TTC	GAT	CCT	> 8.0	2.0	3200	8.0
F/7075	¹⁶¹ GAG [*]	ATG	TCT	CAG	TTC	GAT	¹²⁸⁵ CCG	> 8.0	0.5	320	2.0
Br130	¹⁶¹ GAG [*]	ATG	TCT	¹²⁵ CTG	⁶⁶⁴ TTT	GAT	¹²⁸⁵ CCG	> 8.0	0.5	160	1.0
Br181	¹⁶¹ GTG ^{**}	ATG	TCT	CAG	TTC	GAT	CCT	> 8.0	0.25	160	2.0
SO/3829	GGG	⁷³⁰ ACG ^{***}	TCT	CAG	TTC	¹²⁶⁴ GAA	¹²⁸⁵ CCA	> 8.0	1.0	1600	8.0
T-21	¹⁶¹ GAG ^{**}	ATG	TCT	CAG	TTC	GAT	CCT	> 8.0	0.5	160	1.0
T-23	¹⁶¹ GAG ^{**}	ATG	TCT	CAG	TTC	GAT	CCT	> 8.0	0.25	80	1.0
Amino acid substitution	(G54E) ^{**} (G54V) ^{***} (G54R)	(M236V) ^{**} (M236K) ^{***} (M236T)	(S35S)	(Q42L)	(F187F)	(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) MIC: Minimal Inhibitory Concentration of itraconazole (ITC), voriconazole (VRZ), fluconazole (FCZ) and ketoconazole (KTZ) in µg/ml