

Table S1: Virulence related genes identified in *A. fumigatus* LMB35Aa genome, considering the clinical strain *A. fumigatus* Af293 as reference.

Gene ID	Gene name	Gene location	Similarity with <i>A. fumigatus</i> Af293 strain
AFUA_6G06900 (ID 3508842)	<i>rho1</i>	scaffold15_size1369881	99%
AFUA_3G00910 (ID 3506018)	<i>ags1</i>	scaffold5_size439689	99%
AFUA_3G07870 (ID: 3512474)	<i>agd3</i>	scaffold2_size2524342	99%
AFUA_3G12690 (ID: 3512175)	<i>glfA</i>	scaffold30_size544622	99%
AFUA_1G17250 (ID: 3510125)	<i>robB</i>	scaffold22_size414029	99%
AFUA_3G09690 (ID: 3511970)	<i>calA</i>	scaffold24_size814358	99%
AFUA_1G12690 (ID: 3510389)	<i>mdr4</i>	scaffold2_size2524342	99%
AFUA_6G04360 (ID: 3505316)	<i>atrF</i>	scaffold26_size551250	99%
AFUA_6G09630 (ID: 3508157)	<i>gliZ</i>	scaffold15_size1369881	98%
AFUA_5G02330 (ID:3505541)	<i>aspF1</i>	scaffold6_size935784	99%
AFUA_3G00590 (ID: 3505795)	<i>aspHs</i>	scaffold31_size151726	99%
AFUA_8G00170 (ID: 3504405)	<i>ftmA</i>	scaffold42_size84196	99%
AFUA_1G14660 (ID: 3509858)	<i>laeA</i>	scaffold53_size69050	99%
AFUA_2G01900 (ID: 3506941)	<i>rtfA</i>	scaffold13_size1331972	99%
AFUA_2G13260 (ID: 3513134)	<i>medA</i>	scaffold3_size965284	99%

Table S2: Primer sequences for gene expression analysis through qPCR for main virulence related genes found in *A. fumigatus* LMB-35Aa genome.

Gene name	Primers sequences (5'- 3')	Amplicon size (bp)
<i>rho1</i>	F: GATCTCCGAGGTTCTTCACTTC R: GCAGCTCCTCAATGGTCTT	98
<i>ags1</i>	F: CCAACACCTGGAAGATGACC R: AACACCGACCGATAGAAGGA	139
<i>agd3</i>	F: CGAGCAACACCAAGGAGAT R: GGTGGCAAAGCCAATGAAG	125
<i>glfA</i>	F: GCTTCGGTGAGAAGGGTAAG R: GCTTCTTGTAGCCGATGGT	90
<i>rodB</i>	F: CCAGAACAAGTGCGGTGA R: TCAGGAGGCCGTAGTTGA	92
<i>calA</i>	F: TCCGGTGACACCATCTACT R: GACGGTGAAGCCGAACTT	81
<i>mdr4</i>	F: CGTTCGGCAGAGGATGAA R: CTCTGGGCGATGTGGATAAG	111
<i>atrF</i>	F: CAGCCCTCGTCGATGTTAAT R: GCCAACTGGACCGAAATAGA	87
<i>gliZ</i>	F: AGCCTAACCGCTCGAGATA R: CAGTGGGAACAGTGGTAGAAG	98
<i>aspF1</i>	F: TACCCGCACTGGTTCCTAA R: GACGGTCACAGTCGGCTT	94
<i>aspHs</i>	F: AGTCCACTGGGACTGTCCAT R: GCACCACCTACTTGTTCCTA	108
<i>ftmA</i>	F: CCACGATGGCCCTATGTTT R: GGATGTGCCGTAGAGGAATG	131
<i>laeA</i>	F: GTCTCGGACGGACTGATCTA R: CGACGAAGGCTTCTGGATAC	118
<i>rtfA</i>	F: CTGAGGCCATTGAGGCATAC R: CTTACCAGCAGCCATATCC	87
<i>medA</i>	F: CGAAACATTGAAAAGGATGTG R: CTGAGGGAAATCTGAAGGAAG	107