

S1 Table. *Aspergillus* strains and oligonucleotides used in this study.

STRAINS		
Name	GENOTYPE	SOURCE
NRRL3357	Wild-type	Fungal Genetic Stock Center
3357.5	<i>pyrG</i> ⁻	[1]
TMY1	$\Delta wetA::AfupyrG^+; pyrG^-$	This study
TMY2	$\Delta wetA::AfupyrG^+; pyrG^-; wetA$	This study

OLIGONUCLEOTIDES		
Name	SEQUENCE (5'→3')	PURPOSE
oMY-19	ggagagcagattagcacctg	5' flanking of <i>wetA</i>
oMY-20	ttacctcgacatgccacag	3' flanking of <i>wetA</i>
oMY-21	ccatgcatggttactggagg	5' nested of <i>wetA</i>
oMY-22	atgcgaccacgaatgcatcc	3' nested of <i>wetA</i>
oMY-51	gggtgaagagcattgtttgaggcacgatggtggtccaagctcagctgctc	5' <i>wetA</i> with <i>AfupyrG</i> tail
oMY-52	tcagtgcctcctctcagacagaatatcgggtgttctgatggatccggagtc	3' <i>wetA</i> with <i>AfupyrG</i> tail
oMY-25	gaccactcgttcaacaacgatg	5' <i>wetA</i>
oMY-26	cgtactgcattaagtgcgg	3' <i>wetA</i>
oJH-84	gctgaagtcatacagggccaaa	5' <i>AfupyrG</i> marker
oJH-85	atcgtcgggaggtattgtcgtcac	3' <i>AfupyrG</i> marker

1. He Z-M, Price MS, Obrian GR, Georgianna DR, Payne GA. Improved protocols for functional analysis in the pathogenic fungus *Aspergillus flavus*. BMC Microbiol. BioMed Central; 2007;7: 104. doi:10.1186/1471-2180-7-104