

Members of Glycosyl-Hydrolase family 17 of *A. fumigatus* differentially affect morphogenesis

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Table S1. Primers used in the present study.

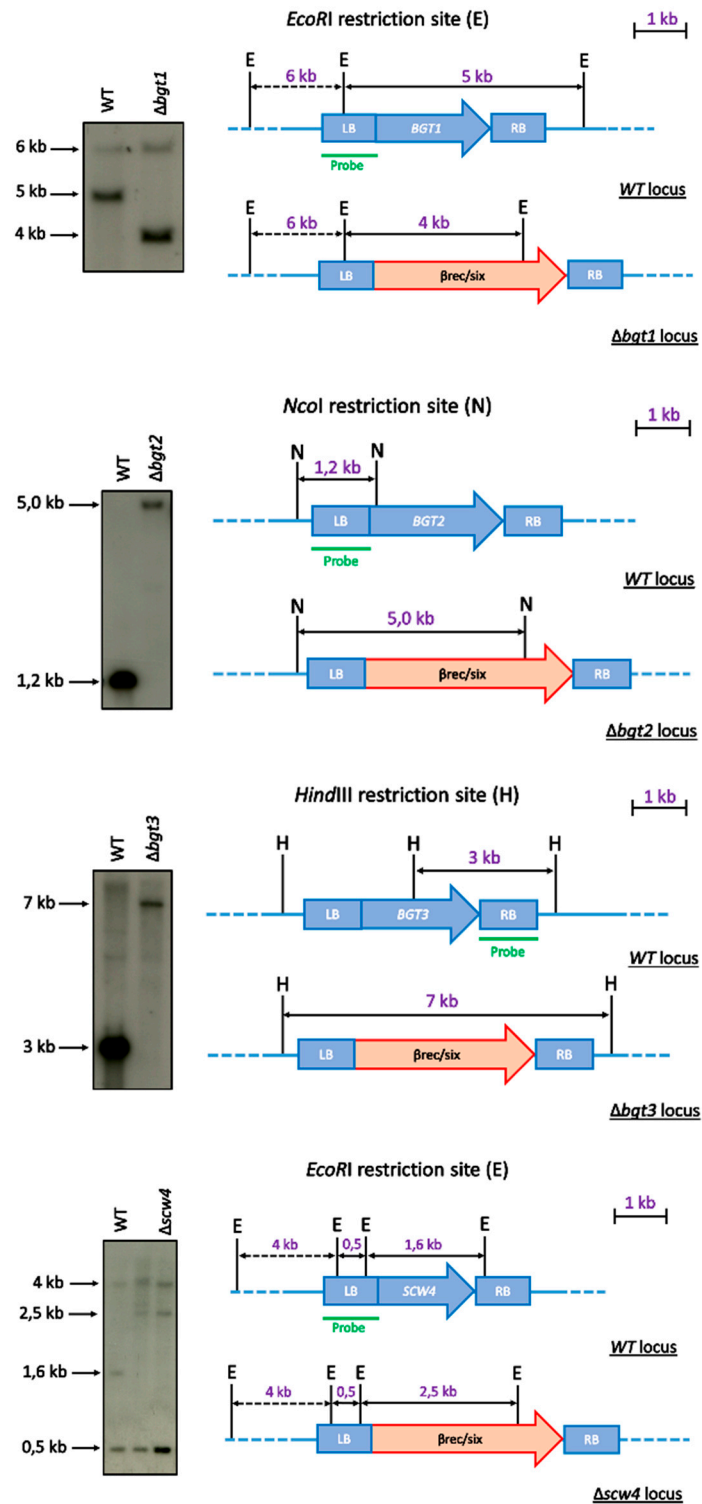
Primers	Sequences	Restriction site
BGT1_forw1	AATTCGAGCTCGGTACGATATCTAATGAGCCCTGAAGGCAGA	<i>EcoRV</i>
BGT1_rev1	GGACCTGAGTGATGCGGGCAATGTTAGCAACCTA	
BGT1_forw2	TGGTCCATCTAGTGCCCCGAAGTGCTCTACCGAAAG	
BGT1_rev2	GCCAAGCTTGCATGCCGATATACCCAAATCCCATCAAATCCA	<i>EcoRV</i>
BGT2_forw1	AATTCGAGCTCGGTACTGCGCACTCGGAGCAATCAAATCCAT	<i>FspI</i>
BGT2_rev1	GGACCTGAGTGATGCTGGAAGTACGGGTAGCCATC	
BGT2_forw2	TGGTCCATCTAGTGCCCAAGACCTACTGGGACGAG	
BGT2_rev2	GCCAAGCTTGCATGCCITGCGCAATCGGGGCTATTAGCAGGAC	<i>FspI</i>
BGT3_forw1	AATTCGAGCTCGGTACTGCGCACGGATCAATTGACTCGACCT	<i>FspI</i>
BGT3_rev1	GGACCTGAGTGATGCAGCAATGACAGCGGAGAACT	
BGT3_forw2	TGGTCCATCTAGTGCTTCGATAGCTCTTGGCACCT	
BGT3_rev2	GCCAAGCTTGCATGCCITGCGCAGTCGATTGCTGCGATCAGTA	<i>FspI</i>
SCW4_forw1	AATTCGAGCTCGGTACCCCGGGGAGACCGTTTCTCAAGTG	<i>SmaI</i>
SCW4_rev1	GGACCTGAGTGATGCCGTTGAATCTTCTGGGCAAT	
SCW4_forw2	TGGTCCATCTAGTGCGTCCTGTGGAGGTTAGCTG	
SCW4_rev2	GCCAAGCTTGCATGCCCCCGGGGAGTCTGGTACTCCCACCA	<i>SmaI</i>
SCW11_forw1	AATTCGAGCTCGGTACGATATCTATTGCCTCCCAGTCCAAAG	<i>EcoRV</i>
SCW11_rev1	GGACCTGAGTGATGCGATCTGATTCGGTCGCAACT	
SCW11_forw2	TGGTCCATCTAGTGCAACATCCACCCCTTCTTCAA	
SCW11_rev2	GCCAAGCTTGCATGCCGATATCAGGATAACTGCCGCGATGT	<i>EcoRV</i>
BGT1qa	AGAATCCAGCAGGTCCAGAAGG	
BGT1qb	CCGTGCCATCAGCGAACTTG	
BGT2qa	CGGTATCGTCGGCAGCACTC	
BGT2qb	GGCGGCGGAGGAAGAAGAAG	
BGT3qa	ATCCTGGCTTTCATCATCATTGGG	
BGT3qb	CTTCGGTGGCTGTTTGTGTGG	
SCW4qa	TCGCTTCGGCATCACCTACTC	
SCW4qb	TGCTCAATGTCCTGGTTTATCTGG	
SCW11qa	TCGTCGTCGGTAATGAGGCTATC	
SCW11qb	GGCGGACTTGGCAGAGGAG	
TEFqa	CCATGTGTGTCGAGTCCTTC	
TEFqb	GAACGTACAGCAACAGTCTGG	

Table S2. Single and multiple deleted strains used and constructed in this study.

Strain Names	Genotype	Source
Parental strain (WT)	A1163 ^{ku80Δ}	Da Silva Ferreira <i>et al.</i> , 2006
<i>Δbgt1</i>	A1163 ^{ku80Δ} <i>Δbgt1::hygroR</i>	Gastebois A. <i>et al.</i> , 2010
<i>Δbgt2</i>	A1163 ^{ku80Δ} <i>Δbgt2::hygroR</i>	Gastebois A. <i>et al.</i> , 2010
<i>Δbgt3</i>	A1163 ^{ku80Δ} <i>Δbgt3::six-β-rec-hygroR-six</i>	This Study
<i>Δscw4</i>	A1163 ^{ku80Δ} <i>Δscw4::six-β-rec-hygroR-six</i>	This Study
<i>Δscw11</i>	A1163 ^{ku80Δ} <i>Δscw11::six-β-rec-hygroR-six</i>	This Study
<i>Δscw4Δscw11 (Δ2)</i>	A1163 ^{ku80Δ} <i>Δscw4::six/Δscw11::six-β-rec-hygroR-six</i>	This Study
<i>Δscw4Δscw11Δbgt3 (Δ3)</i>	A1163 ^{ku80Δ} <i>Δscw4::six/Δscw11::six/Δbgt3::six-β-rec-hygroR-six</i>	This Study
<i>Δscw4Δscw11Δbgt3Δbgt2 (Δ4)</i>	A1163 ^{ku80Δ} <i>Δscw4::six/Δscw11::six/Δbgt3::six/Δbgt2::six-β-rec-hygroR-six</i>	This Study
<i>Δscw4Δscw11Δbgt3Δbgt2Δbgt1 (Δ5)</i>	A1163 ^{ku80Δ} <i>Δscw4::six/Δscw11::six/Δbgt3::six/Δbgt2::six/Δbgt1::six-β-rec-hygroR-six</i>	This Study

Table S3. Percentages of identities between the different proteins of the *A. fumigatus* GH17 family.

	Bgt2p	Bgt3p	Scw4P	Scw11P
Bgt1p	26	25	20	16
Bgt2p		10	14	9
Bgt3p			12	14
Scw4P				28



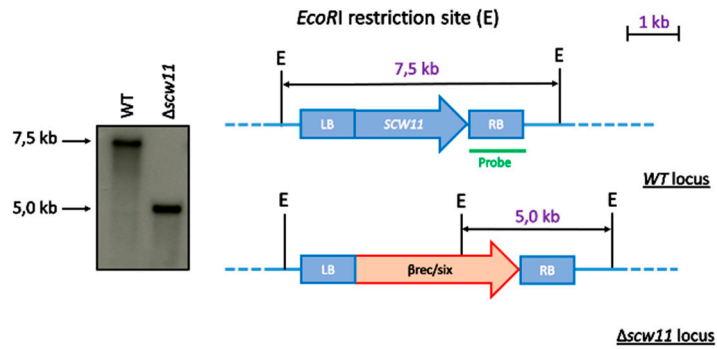


Figure S1. Construction of the deletion strains. Subsequent deletion of the GH17 genes family and verification by Southern blot.

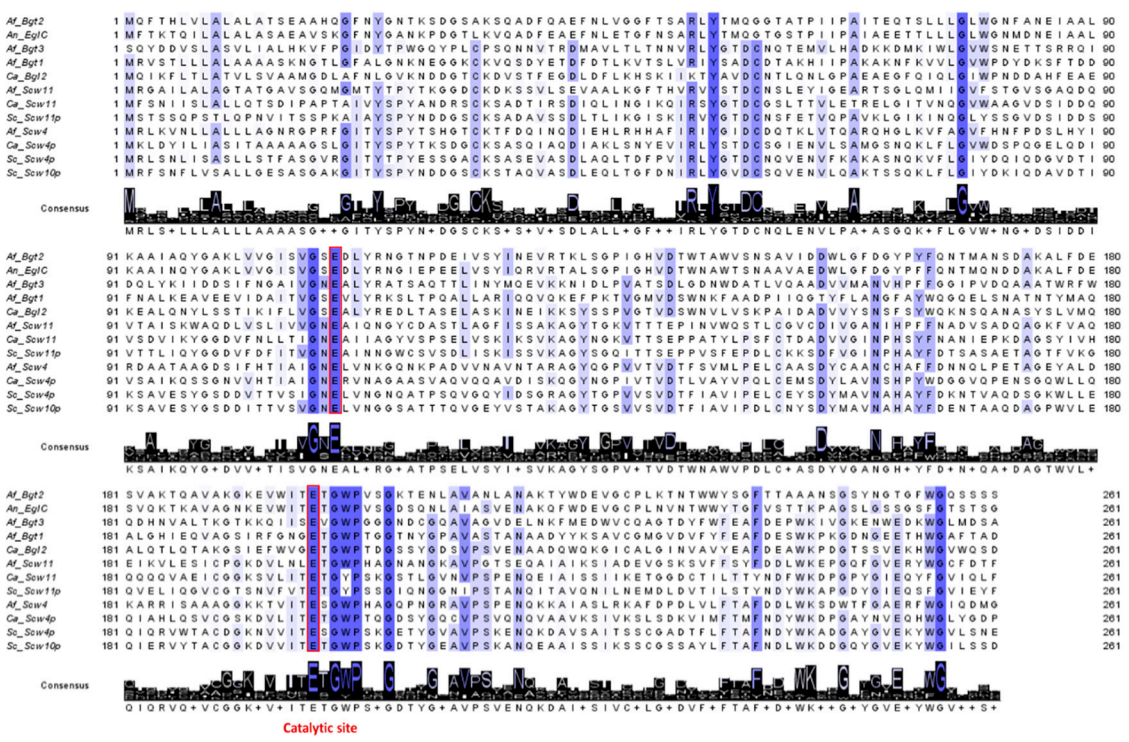


Figure S2. Protein alignment of the GH17 family of *A. fumigatus* (Af), *S. cerevisiae* (Sc), *C. albicans* (Ca), and *A. nidulans* (An). Conserved Amino acids between all proteins are highlighted in blue. Both glutamic acids, which are putative catalytic sites, are framed in red. After protein sequence alignment using MUSCLE v3.8.311, sequences were trimmed using TrimAl v3² to remove the spurious sequences or poorly aligned regions.

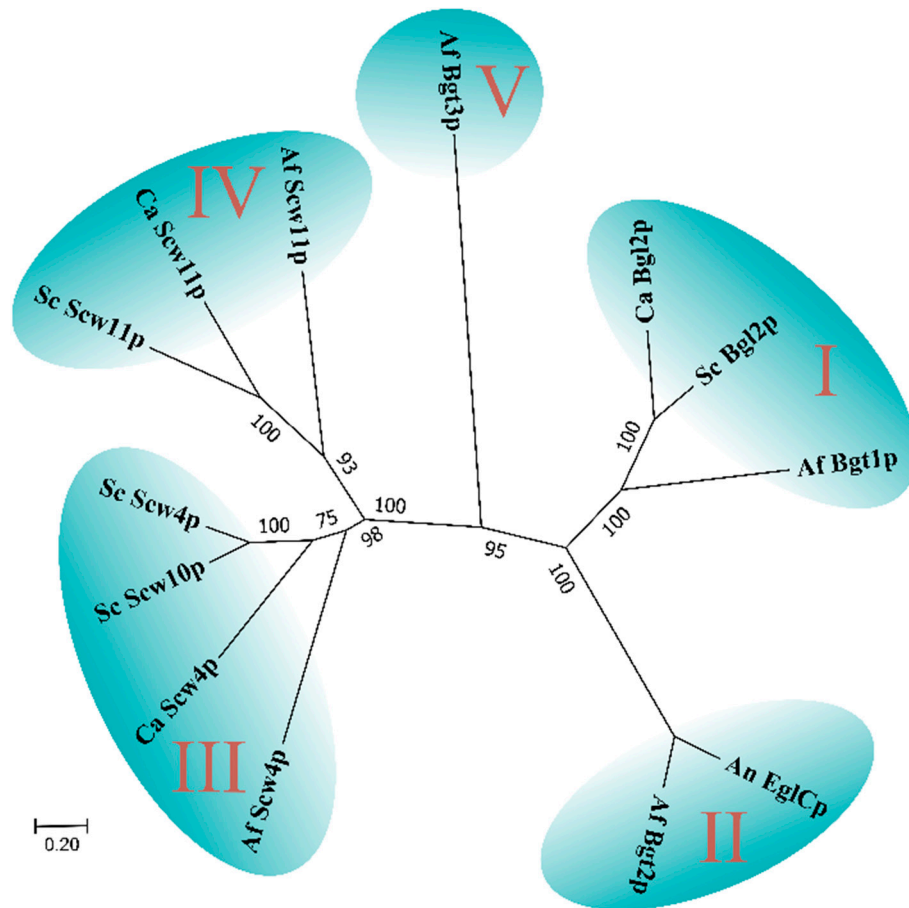


Figure S3. Non-rooted tree showing the maximum likelihood phylogenetic tree of the GH17 proteins of *A. fumigatus* (Af), *A. nidulans* (An), *S. cerevisiae* (Sc), and *C. albicans* (Ca). The protein sequences used have the following Pubmed accession numbers: For *A. fumigatus*: Bgt1p (AMO45773.1), Bgt2p (EAL86311.1), Bgt3p (Q4WUK5.1), Scw4p (XP_751116.1), and Scw11p (XP_747362.1); *A. nidulans*: (AAT90341.1); *S. cerevisiae*: Bgl2p (EGA58533), Scw10p (AJS99243.1), Scw4p (AJS06938.1), and Scw11p (AJS07159.1); *C. albicans*: Bgl2p (AOW28996.1), Scw11p (AOW29820.1), and Scw4p (AOW25936.1).

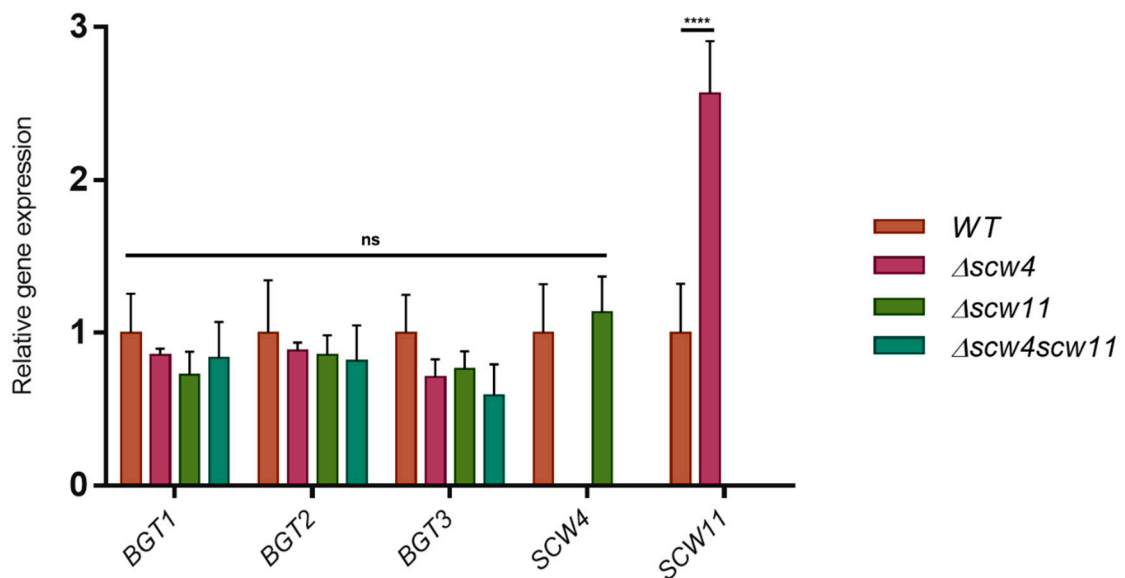


Figure S4. Gene expression of the five GH17 genes in the vegetative mycelium of the $\Delta scw4$, $\Delta scw11$, and $\Delta scw4scw11$ mutants and the parental strains after 16 h of growth in MM liquid medium (**** statistical significance between the parental and the mutant strain, $p < 0.0001$). Gene expression was determined by real-time RT-PCR.