Supporting Information

Nützmann et al. 10.1073/pnas.1103523108

SI Results and Discussion

Microarray Analysis. To further analyze the global meaning of GcnE, the transcriptome present in the wild-type and the Δ*gcnE* mutant during standard cultivation and cocultivation was determined after 3 h by *A. nidulans* full-genome microarray analysis. Some of the data were verified by qRT-PCR analysis (Fig. S4 *A–C*). More than half of the differentially regulated genes ($P < 0.05$, absFC < 2) during cocultivation appear to be dependent on a functional Saga/Ada complex (Fig. S4*D*). The absolute fold change of differentially expressed fungal genes between wild type and Δ*gcnE* significantly increased upon contact with the bacterium when compared under noninducing conditions (Fig. S4*E*). A similar shift was observed for *S. cerevisiae* when the wild-type was compared with a *gcn5* mutant strain under osmotic stress (1). Our data suggest that GcnE is required for the fast fungal response to the bacteria that includes the activation of the *ors* cluster. We thus extend the importance of GcnE in response to abiotic alterations by a major function for biotic interactions.

SI Materials and Methods

Western Blot. For preparation of whole-cell extracts, mycelia was harvested and immediately frozen in liquid nitrogen. Mycelium was then ground under liquid nitrogen to a fine powder using mortar and pestle, resuspended in 1 mL phosphate buffer [50 mM KH_2PO_4, 150 mM NaCl (pH 7), 1 mM PMSF, and protease inhibitor (Sigma Aldrich)], placed on ice for 10 min, and centrifuged at 10,000 × *g* for 10 min. The supernatant was collected and the protein concentration determined using Coomassie Plus Protein Assay (Pierce). A total of 20 μg of protein was separated by SDS/PAGE and transferred to PVDF membrane. The membrane was incubated with the respective primary antibodies [goat polyclonal against S-tag (ab19321; Abcam), mouse monoclonal ANTI-FLAG M2 antibodies (Sigma; 1:2,000)] and detected with donkey anti-goat IgG-HRP (SC-2033) or goat anti-mouse IgG-HRP (sc-2005, 1:5,000; Santa Cruz Biotechnology) secondary antibodies and chemiluminescence detection kit for HRP (Applichem).

ChIP Coupled to qRT-PCR Analysis. ChIP was essentially performed as described previously (2). Antibodies used in this study are as follows: rabbit polyclonal against the C terminus of the human histone H3 (ab1791), rabbit polyclonal aniserum against histone H3 acetyl K9 (ab4441), rabbit polyclonal antiserum against histone H3 acetyl K14 (ab46984; Abcam), anti-acetyl K9-K14 histone H3 (06-599; Millipore), and mouse monoclonal ANTI-FLAG M2 antibodies (Sigma). A total of 2 μg of antibodies were used per reaction with 200 μg of total protein. The sonication buffer was prepared as described in Roze et al. (3), and for indirect sonication the Branson Sonifier 450 (G. Heinemann Ultraschall and Labortechnik) was used with the following settings: output control 10, duty cycle constant, 9× 75 s on/30 s off. For amplification and quantification of precipitated DNA by qRT-PCR, the iQ SYBR Green Supermix (BioRad) or the MyTaq HS Mix 2× (Bioline) in combination Evagreen (Biotium) were used with the MyiQ Thermal Cycler (BioRad) or the StepOnePlus Real-Time PCR System (Applied Biosystems) according to the manufacturers' instructions. ChIP oligonucleotides amplified 150- to 200-bp–long DNA products within a region of maximal 350 bp upstream of the translational start of the gene of interest. Each PCR was carried out twice. The relative amount of DNA was calculated by the ratio of precipitated DNA treated with antibodies targeted against acetylated H3 divided by the precipitated DNA treated with anti–C-terminus H3 antibody. For ChIP analysis with GcnE-3xFLAG, the relative amount of DNA was calculated by the ratio of immunoprecipitated DNA against input DNA. At least two biological replicates were analyzed, and SDs were calculated. Significance was determined using the Student *t* test.

Extraction, HPLC, and LC-MS Analysis of Secondary Metabolites. Fungal cultures were homogenized and exhaustively extracted with ethyl acetate. The resulting extracts were dried over sodium sulfate and concentrated under reduced pressure. For HPLC analysis, the extracts were dissolved in 2 mL of methanol. Analytical HPLC was performed on a Shimadzu LC-10Avp series HPLC system consisting of an autosampler, high-pressure pumps, column oven, and PDA. HPLC conditions: C18 column (Eurospher 100-5, 250 × 4.6 mm) and gradient elution [MeCN/0.1% (vol/vol) TFA (H_2O) 0.5/99.5 in 30 min to MeCN/0.1% (vol/vol) TFA 100/0, MeCN 100% for 10 min], flow rate, 1 mL·min^{-1}; injection volume, 20 μL. LC-MS measurements were performed using an Exactive Orbitrap High Performance Benchtop LC-MS Mass Spectrometer with an electrospray ion source (Thermo Fisher Scientific). HPLC conditions: C18 column (Betasil C18 3 μm, 150 × 2.1 mm) and gradient elution [MeCN/0.1% (vol/vol) HCOOH (H_2O) 5/95 for 1 min, going up to 98/2 in 15 min, then 98/2 for another 3 min], flow rate, 0.2 mL·min^{-1}; injection volume, 3 μL. Compounds were identified by UV and high-resolution electrospray ionization mass spectrometry (HRESI-MS) or by comparison with an authentic standard.

Generation of Transformation Cassettes. Transformation cassettes for gene deletion and gene replacement were constructed according to Szewczyk et al. (4). For gene deletion, ∼1,500-bp–long DNA fragments flanking the ORF of interest were amplified using genomic DNA of *A. nidulans* as a template and fused to the *argB* deletion cassette (5). The deletion primers marked with a Q (Table S3) were used for fusion PCR to assemble flanking regions and *argB* cassette. For *gcnE* replacement, transformation cassettes consisted of the *gcnE* coding sequence fused at the 3′ end with the codon-optimized 3xFLAG-tag or S-tag, the *pabaA*1 gene, and ∼1,500-bp–long DNA regions flanking *gcnE*. Southern blot analysis and DNA sequencing proved the correct fusion of GcnE with the tag and the integration of the encoding cassette into the *gcnE* locus.

Microarrays. Custom-made *A. nidulans* full-genome microarrays were applied [platform data available at the Gene Expression Omnibus (GEO) database, www.ncbi.nlm.nih.gov/geo (accession no. GPL11193)]. Cultivation of *A. nidulans*, RNA preparation, cDNA synthesis and labeling, hybridization, and microarray scanning was performed as described in Schroeckh et al. (5). Data were processed using robustspline and quantile normalization provided by the Linear Models for Microarray Data (LIMMA) packages (6) from Bioconductor (http://www.bioconductor.org/). *P* values were calculated with the empirical Bayes method and subsequently adjusted for multiple testing using the false discovery rate.

1. Xue-Franzén Y, et al. (2010) Genome-wide characterisation of the Gcn5 histone acetyltransferase in budding yeast during stress adaptation reveals evolutionarily conserved and diverged roles. *BMC Genomics* 11:200.
2. Bernreiter A, et al. (2007) Nuclear export of the transcription factor NirA is a regulatory checkpoint for nitrate induction in *Aspergillus nidulans*. *Mol Cell Biol* 27:791–802.
3. Roze LV, Arthur AE, Hong SY, Chanda A, Linz JE (2007) The initiation and pattern of spread of histone H4 acetylation parallel the order of transcriptional activation of genes in the aflatoxin cluster. *Mol Microbiol* 66:713–726.
4. Szewczyk E, et al. (2006) Fusion PCR and gene targeting in *Aspergillus nidulans*. *Nat Protoc* 1:3111–3120.
5. Schroeckh V, et al. (2009) Intimate bacterial-fungal interaction triggers biosynthesis of archetypal polyketides in *Aspergillus nidulans*. *Proc Natl Acad Sci USA* 106: 14558–14563.
6. Smyth GK (2005) Limma: Linear models for microarray data. *Bioinformatics and Computational Biology Solutions Using R and Bioconductor,* eds Gentleman R, Carey V, Dudoit S, Irizarry R, Huber W (Springer, New York), pp 397–420.

Fig. S1. Effect of *S. rapamycinicus* and selected sublethal concentrations of epigenetic modifiers on the *ors* gene cluster activation. *A. nidulans* was incubated in AMM as control (*a*), cocultivated with *S. rapamycinicus* (*b*), with *S. rapamycinicus* and anacardic acid (*c*), or with SAHA (*d*). (*A*) HPLC profiles of ethyl acetate extracts; 1, orsellinic acid; 2, lecanoric acid. (*B*) Structural formula of orsellinic acid (1) and lecanoric acid (2). (*C*) Northern blot analysis of *orsA*. Cocultivation with *S. rapamycinicus* (*b*) and addition of SAHA (*d*) induced formation of (*B*) 1 and 2, whereas anacardic acid (*c*) blocked the production despite the presence of the streptomycete.

Fig. S2. Generation of strains (*A*) Δ*gcnE* and *gcnE*^{c}, (*B*) Δ*adaB*, (*C*) Δ*laeA*, and (*D*) *gcnE*-3x*flag*. Schematic representation of genomic arrangements of wild-type and deletion strains. Arrows indicate genes, black boxes mark ∼1,500-bp–long regions serving for homologous recombination. The polygon in *D* indicates the FLAG tag. Restriction sites used for Southern blot analyses are indicated. As probes for Southern blot, the DNA regions marked by a black box with a star were used. (*Right*) Southern blot analyses show the expected restriction patterns for wild-type and deletion strains.

Fig. S3. Complementation of Δ*gcnE* restored the wild-type phenotype. (*A*) Northern blot analysis of *ors* cluster genes and HPLC profiles of wild type, Δ*gcnE*, and *gcnE*^{C} coincubated with *S. rapamycinicus*. mRNA of the analyzed *ors* cluster genes *orsA*, *orsB*, and *orsC* was present in the wild-type and complemented strain, but not in the deletion strain Δ*gcnE*. The *acn* gene used as a control was expressed to the same extent in all strains. HPLC profile indicates production of orsellinic acid (1) and lecanoric acid (2). (*B*) Northern blot analysis of selected sterigmatocystin and terrequinone cluster genes and HPLC profiles of wild type, Δ*gcnE*, and *gcnE*^{C} after 48 h and 72 h. Northern blot reveals expression of *aflR* and *tdiB* in both the wild-type and complemented strain *gcnE*^{C}. HPLC analysis proves the production of sterigmatocystin (5) and terrequinone A (6). 6* – wt HRESI -MS: *m/z* $[M\text{-}H]^{-}$ = 489.2182 (calculated for $C_{32}H_{29}N_2O_3$ 489.2184) – *gcnE*^{C} HRESI MS: *m/z* $[M\text{-}H]^{-}$ = 489.2185 (calculated for $C_{32}H_{29}N_2O_3$ 489.2184). (*C*) Percentage of produced penicillin of wild-type, Δ*gcnE*, and *gcnE*^{C} strains cultivated in fermentation medium for 72 h. The diagram shows the calculated penicillin titer with the wild-type set to 100%.

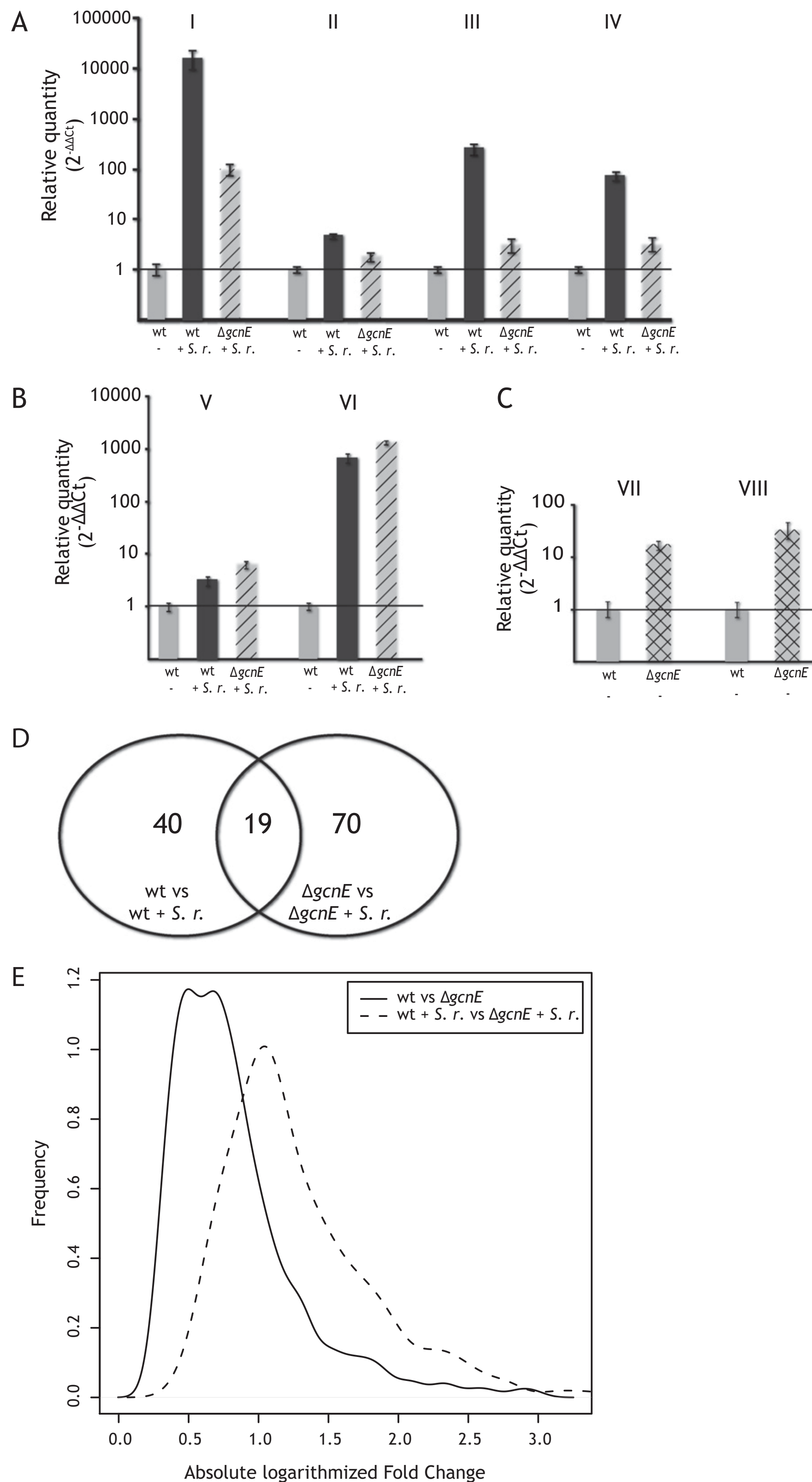

Fig. S4. Full-genome microarray analysis of wild type and Δ*gcnE* during standard cultivation and cocultivation with *S. rapamycinicus*. (*A*) Quantification of GcnE-dependent gene expression in *A. nidulans*. Relative transcript levels of AN9315 (I), AN2846 (II), AN5831 (III), and AN4905 (IV) increased in a GcnE-dependent manner when *A. nidulans* was cocultivated with *S. rapamycinicus*. The investigated genes were found to be differentially regulated in full genome microarray. Relative quantities of mRNA steady-state levels were determined by qRT-PCR. Relative quantities are given as log2 of −ΔΔCt. (*B*) Quantification of GcnE-independent gene expression in *A. nidulans*. The enhanced expression of genes AN3974 (V) and AN9397 (VI) in cocultivation is independent of GcnE. The investigated genes were found to be differentially regulated in full genome microarray. Relative quantities of mRNA steady-state levels were determined by

Legend continued on following page

qRT-PCR. Relative quantities are given as log2 of −ΔΔCt. (*C*) Quantification of GcnE-dependent gene expression in *A. nidulans*. The transcription of AN6669 (VII) and AN2839 (VIII) shows a GcnE-dependent regulation independent of *S. rapamycinicus*. The investigated genes were found to be differentially regulated in full genome microarray. Relative quantities of mRNA steady-state levels were determined by qRT-PCR. Relative quantities are given as log2 of −ΔΔCt. (*D*) The influence of *S. rapamycinicus* on the gene expression of the *A. nidulans* wild-type and the *gcnE* deletion strain is shown. Only genes whose fold changes (absolute values) are >2 while having adjusted *P* values (FDR correction) <0.05 are included. (*E*) Impact of *S. rapamycinicus* on absolute logarithmized fold changes (logFC) density distribution in wild-type vs. Δ*gcnE* strain analyzed by full genome microarray. The graph illustrates the frequency distribution of the absolute logFC of all differentially regulated genes for the comparisons of wild type and Δ*gcnE* with and without interaction of *S. rapamycinicus*. Only genes with statistically significant logFC (FDR-corrected *P* value ≤ 0.05) are included. Low logarithmized fold changes are excluded because small disturbances of the signal have a high effect on the logFC. The mean of the density distribution of the samples with *S. rapamycinicus* interaction is significantly higher (Wilcoxon rank sum test: *P* value < 2.2e-16, difference = 0.487), demonstrating the strong influence of *gcnE* on the fold changes of differentially expressed genes when *S. rapamycinicus* is present.

(A)
wt Δ laeA
+ S. r.
orsA
orsB
orsC
acn
rRNA

(B)
wt Δ gcnE
- + - +
laeA
rRNA

(C)
wt Δ gcnE
laeA
rRNA

Fig. S5. Expression of *ors* cluster genes in the Δ*laeA* mutant strain, expression of the *laeA* gene in the Δ*gcnE* strain, and during cocultivation. (*A*) Northern blot analysis of *ors* cluster genes in response to *S. rapamycinicus* in Δ*laeA* and wild type. (*B*) Northern blot analysis of *laeA* gene in wild-type and Δ*gcnE* strains incubated without (–) or with (+) *S. rapamycinicus*. (*C*) Northern blot analysis of *laeA* after 48 h of cultivation.

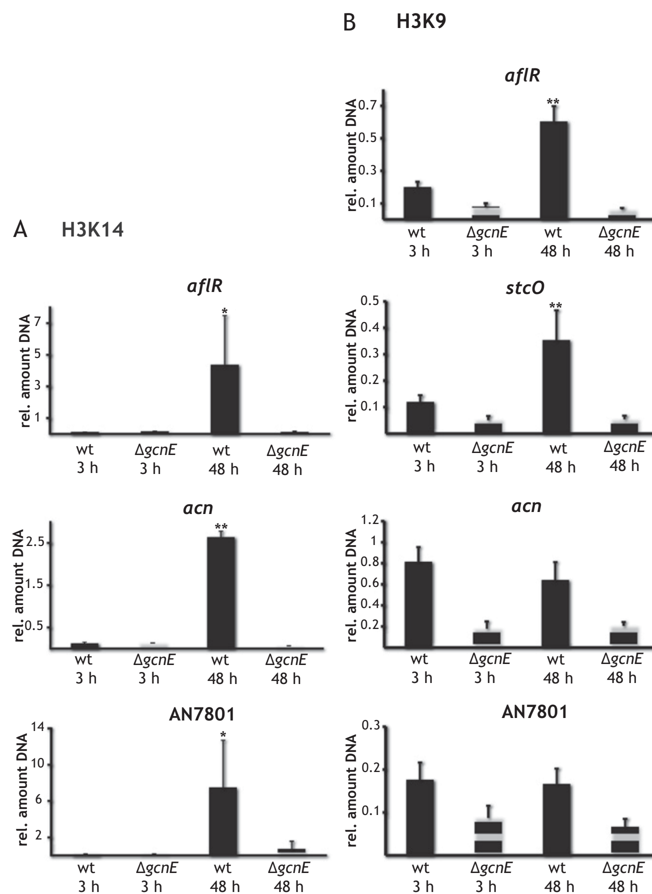

Fig. S6. H3K9 and H3K14 acetylation of sterigmatocystin cluster genes. ChIP experiment of wild-type and Δ*gcnE* deletion strains incubated under sterigmatocystin nonproducing (3-h incubation) and producing (48-h incubation) conditions. Promoter regions of *aflR*, *stcO*, AN7801, and *acn* were analyzed by qRT-PCR. SDs of the mean of two (K14) and three (K9) biological replicates are shown. Data are given as the relative amount of DNA obtained from acetylated H3 protein relative to the total amount of H3 protein. The low DNA amounts in the Δ*gcnE* samples under producing conditions represent the involvement of Saga/Ada in H3K9 and H3K14 acetylation of these secondary metabolite cluster genes. Statistical significance of data obtained for *aflR*, *stcO*, AN7801, and *acn* promoters of wild type incubated under nonproducing or producing conditions is given by the *P* value (**P* < 0.05; ***P* < 0.01). (*A*) Acetylation of H3K14. (*B*) Acetylation of H3K9.

Table S1. Deletion of genes encoding putative acetyltransferases

Gene number	Name	Homologous proteins human*	Homologous proteins yeast*	Deletion	Phenotype under conditions tested
Putative GNAT-type acetyltransferases					
AN2161.4	*ngn1*			Yes	—
AN2102.4	*ngn2*			Yes	—
AN2294.4	*elp3*	Elp3 (hKat9)	Elp3 (yKat9)	Yes	Slight differences[†]
AN3621.4	*gcnE*		Gcn5 (yKat2)	Yes	Major differences[‡]
AN3879.4	*spt10*		Spt10	No	
AN1328.4	*nnaA*	Naa10	Ard1	No	
AN4993.4	*nnaC*	Naa30	Mak3	Yes	Slight differences[†]
AN7944.4	*ngn3*			Yes	—
AN3162.4	*ngn4*			Yes	—
AN7374.4	*ngn5*			Yes	—
AN9204.4	*ngn6*			Yes	—
AN0743.4	*ngn7*			Yes	—
AN2745.4	*nnaB*	Naa20	Nat3	Yes	Major differences[‡]
AN1621.4	*ngn8*			Yes	—
AN8005.4	*ngn9*			Yes	—
AN10234.4	*ngn10*			Yes	—
AN8373.4	*ngn11*			Yes	—
AN9493.3	*ngn12*			Yes	—
AN8706.4	*gna1*			Yes	Major differences[‡]
AN7171.4	*ngn13*			Yes	—
AN11810.4	*ngn14*			Yes	—
AN2870.4	*ngn15*			Yes	—
AN2479.4	*ngn16*			Yes	—
AN0969.4	*ngn17*			Yes	—
AN11841.4	*ngn18*			Yes	Slight differences[†]
AN1360.4	*ngn19*			Yes	—
AN5866.4	*ngn20*			Yes	—
AN10238.4	*ngn21*			Yes	—
AN0626.4	*ngn22*			Yes	—
AN8604.4	*ngn23*			Yes	—
AN8684.4	*ngn24*			Yes	Major differences[‡]
AN3825.4	*ngn25*			Yes	—
AN8539.4	*ngn26*			Yes	—
AN3344.4	*ngn27*			Yes	—
AN6411.4	*ngn28*			Yes	—
Putative MYST-type acetyltransferases					
AN10956.4	*esa1*	Tip60/PLIP (hKat5)	Esa1 (yKat5)	No	
AN5640.4	*nmy1*	HBO1/MYST2 (hKat7)	Sas3 (yKat6)	No	
AN3071.4	*nmy2*	HMOF/MYST1 (hKat7)	Sas3 (yKat6)	Yes	Slight differences[†]
Putative Rtt109-type acetyltransferase					
AN8807.4	*rtt109*			Yes	Major differences[‡]
Putative Hat1 acetyltransferase					
AN6214.4	*nha1*	HAT1 (hKat1)	Hat1	Yes	Slight differences[†]
No putative p300/CBP-type acetyltransferase					

Targets for gene deletion were chosen according to the Broad Institute *Aspergillus* Comparative Database feature search for the following gene families: GNAT, MYST, p300/CBP, and Rtt109. Targets represent the major families of acetyltransferases (1). The deletion strains were obtained by homologous recombination using *argB* as a selectable marker. Correct integration of the deletion cassette was verified by Southern blot as shown for Δ*gcnE* and Δ*adaB* in Fig. S1. All deletion strains were phenotypically tested on different media and exposed to stress conditions. Strains showing a phenotype different from the wild type are indicated.

*NCBI blast score >130.

[†]In at least two conditions, minor changes in color or growth compared with the wild type.

[‡]Deletion strain phenotype strongly differs from wild-type strain.

1. Sterner DE, Berger SL (2000) Acetylation of histones and transcription-related factors. *Microbiol Mol Biol Rev* 64:435–459.

Table S2. Bacterial and fungal strains

Strain	Genotype	Ref.
Streptomyces rapamycinicus		(1)
Aspergillus nidulans		
A1153	*yA*1, *pabaA*1; *argB*2; *pyroA*4, *nkuA::bar*	(2)
A1153Δ*gcnE*	*yA*1, *pabaA*1; *gcnE*::*argB*2; *pyroA*4, *nkuA::bar*	This study
A1153Δ*adaB*	*adaB*::*argB*2, *yA*1, *pabaA*1; *pyroA*4, *nkuA::bar*	This study
A1153Δ*laeA*	*yA*1, *pabaA*1; *pyroA*4, *nkuA::bar*; *laeA*::*argB*2	This study
A1153*gcnE*^{C}	*yA*1, *pabaA*1; (*gcnE*::*argB*2)::*gcnEp-gcnE-pabaA*1; *pyroA*4, *nkuA::bar*	This study
A1153*gcnE-3xflag*	*yA*1, *pabaA*1; *gcnE*::*gcnEp-gcnE-3x-flag-pabaA*1; *pyroA*4, *nkuA::bar*	This study
A1153*gcnE-S-tag*	*yA*1, *pabaA*1; *gcnE*::*gcnEp-gcnE-S-tag-pabaA*1; *pyroA*4, *nkuA::bar*	This study

1. Kumar Y, Goodfellow M (2008) Five new members of the *Streptomyces violaceusniger* 16S rRNA gene clade: *Streptomyces castelarensis sp. nov.*, *comb. nov.*, *Streptomyces himastatinicus sp. nov.*, *Streptomyces mordarskii sp. nov.*, *Streptomyces rapamycinicus sp. nov.* and *Streptomyces ruanii sp. nov. Int J Syst Evol Microbiol* 58:1369–1378.
2. Nayak T, et al. (2006) A versatile and efficient gene-targeting system for *Aspergillus nidulans*. *Genetics* 172:1557–1566.

Table S3. Oligonucleotides used to create probes for Northern blots, gene knockout cassettes, ChIP experiments, and qRT-PCR

Oligonucleotide	Sequence
Oligonucleotides used to generate transformation cassettes	
gcnE	
3621lbfor	GAGAGGGTAAAGTATGGTTCC
3621lbforQ	GATTGCATTGTGCAGCCAGG
3621lbrev	GCAAACAGAACTTTGACTCCC ATTGTAAGCTTGTTGCTATGCGAG
3621rbfor	ATTGACATGTTCTCTCGCTTCCCCCTTGCATCGCGTGGC
3621rbrev	CTGCTCATTCGACATTGTCCG
3621rbrevQ	GAGGAAAGCTGACAGTCTCTG
AdaB	
10763lbfor	CGAGACACATCAAACTTGAATGC
10763lbforQ	CGTACGGAAGGTACTTGGTTG
10763lbrev	GCAAACAGAACTTTGACTCCCAT TGCTTGATGTCTCCGCAGC
10763rbfor	ATTGACATGTTCTCTCGCTTCC TTACAAGTTTTATCAAATATCATTTCAGTC
10763rbrev	GAACTCGCTAAGATTCTCAAGG
10763rbrevQ	GAGAACTGTTCAACAAGAGTCC
argBcassfor	ATGGGAGTCAAAGTTCTGTTTGCC
argBcassrev	GGAAGCGAGAGAACATGTCAATTAG
gcnE^{C}	
3621komplbrev	GACCTTTCTACAGATCTGGCAGTAGTAGACTGGATC CAAAGG
3621komprbfor	CTCCGTCGCATGTCCAGATTATAGTTGGCTGGTGGT GGAG
3621komprbrevQ	GACGTGCCATTATCGATAAGG
3621komprbrev	CCAGCAACGAATGTTTCTTGG
gcnE-3xflag, gcnE-S-tag	
3621stagntermlbrev	GCGGCGGCGGTCTCCTTCATTGTAAG CTTGTTGCTATGCGAG
3621stagntermorffor	ATGAAGGAGACCGCCGCCGCCAAGTTCG AGCGCCAGCACATGGACTCCACCGGAACCACCGGAAC CACTGAAAGTGGGTTGCAGGC
3621stagctermorfrev	GGAGTCCATGTGCTGGCGCTCGA ACTTGGCGGCGGCGGTCTCCTTGGTTCC GGTGGTTCCGGTAATTGTACTTACCGACCACTCG
3621stagctermdsfor	AGCGCCAGCACATGGACTCCTGACCCTTGC ATCGCGTGGC
36213flagtagntermlbrev	CCGTCGTGGTCCTTGTAGTCCATTGT AAGCTTGTTGCTATGC
36213flagtagntermorffor	ATGGACTACAAGGACCACGACGGTGACTACAAG GACCACGACATCGACTACAAGGACGACGACGACAAGA CCGGAACCACCGGAACCACTGAAAGTGGGTTGCAGGC
36213flagtagctermorfrev	GGTTCCGGTGGTTCCGGTCTTGTCGTCGTCGTCCTTGT AGTCGATGTCGTGGTCCTTGTAGTCACCGTCGTGGTCC TTGTAGTCGGTTCCGGTGGTTCCGGTAATTGTACTTAC CGACCA
36213flagtagctermdsfor	AGACCGGAACCACCGGAACCTGACCCTTGCATCG CGTGGC
Oligonucleotides for probes used in Northern blots	
aatbfor	GTTAACCTAATCCAGCTCACC
aatbrev	CAATGTCGCTAGATCGCTTCC
aflRfor	GAGAGTTGCATCTCGTGCTC
aflRrev	GAGAGTGACCACGTACTCATC
stcOfor	CCAGTGACCTCACAGTGAATG
stcOrev	CCTTGTCCATGCAGCTCATC
7801for	CATCGACCAAGTGAGACAGG
7801rev	CACTCCCATGATCTTCATCAAG
7826for	CTGATATGCGTGACAAGCAGG
7826rev	GAAGTCAGTGTGCGAACCTG
tdiAfor	GTATACCACCCAAACAGCATC
tdiArev	GGTGTCTGCTTATCAGGTTAAG

Table S3. Cont.

Oligonucleotide	Sequence
tdiBfor	CTACAGAATACTGGTCCCGTC
tdiBrev	CATGAGTTCGGACACATCCTG
laeAfor	GTATCGGAGAGTCTGATCTAC
laeArev	CCTAGCCTGGTATATGTGCAG
aatAfor	GATTACAGAAGCTGGTATCATTGG
aatArev	GCTAAAGGTCATGACAAAGGTC
acvAfor	ACATTCCCGAGAGCCAATTTGCG
acvArev	GTCGTGCGGAATCATGTATCGG
orsAfor	CAGCGATCTTATCCGGACATGCAGG
orsArev	CATCGACATTGAACCGGCTCTCGG
orsBfor	TGGACCCAGTGCCGAAGCCTGC
orsBrev	CGTTGATTATGTCCCATTCGACAGTGC
orsDfor	TTGCACGACAAGATGCCCCCAGTGAG
orsDrev	TCGCAGACCCTCACCAGATGTGTCGGC
AN7915for	TTAACGAGCAGGAGACCAACCGGACCG
AN7915rev	AACCCTCGACACTGAACTGCATGTTAG G
AN7918for	GACCACAGCGCGGAAGCACGTC
AN7918rev	CTTCCGCCATATCCACCAGACTATCTGC
actfor	ATCGGTATGGGTCAGAAGGACTC
actrev	AGTGGTGACGTGGATACCACCGC
Oligonucleotides used for ChIP experiments	
7909pchipfor	CAGCTTCCAGCCATGATTAAG
7909pchiprev	GCACTGCTGTTCTATTGCC
7913pchipfor	GTGAGTCCAGAGTATCCCAG
7913pchiprev	AATGAGAAGAATGCCAAGCC
7915pchipfor	CGGTAGACCCTAAACTAAATGG
7915pchiprev	GCGGTAAAAGGAACGGAAG
7918pchipfor	AGAATGAAGACGAGACGGAC
7918pchiprev	ATTTGGCTGTGGAAGGGTG
stcOpFchip	CCTGATGTAGGATTAGGATAGAATG
stcOpRchip	AAGGCTGGGCTGAAGATTATCGAG
AN7801pFchip	TGTACCCAATAGCGTCCCATCATAAG
AN7801pRchip	CACACTTCAACTCTGTAATCCAAGG
aflRpromfwdchip	GTACAGCAAAGACAAAGATATGCG
aflRpromrevchip	GTACTGTGTAAGCTGTACTTGGG
acnchipfor	CTGGGCTGAACCATCATTAC
acnchiprev	ACTACACAAAGACTGCTACG
tdiAchipfor	CGTCAGCGTGTAATATGAAC
tdiAchiprev	CAGAAGGGTCTCAATGAGTG
tdiBchipfor	GTAAGTCCAAATCAGGCCCG
tdiBchiprev	ACTGTCATCATATATACGCCCC
Oligonucleotides used for qRT-PCR	
9315qrtfor3	GGAGCAAGTTACGGCAAAG
9315qrtrev3	TAAGGAACCGTCGAGGAAG
5831qrtfor	TTGGGGAGCATATCACGGAG
5831qrtrev	GGTAGTCGTGTCGGATCATC
4905qrtfor	ATGTGCCTAGTCCGCATAC
4905qrtrev	GCATCATTCTTCATCCCCTC
2846qrtfor	TCAACGGAGATAATGCGAAC
2846qrtrev	CTTTATCCTCTTCAACCCCAAC
9397qrtfor	GCGACGAAGAAGAACCTTG
9397qrtrev	GTTGAACTCCGTGAACTCC
3974qrtfor	GACGAAGAACATCTGAATCCC
3974qrtrev	TCAGCCTCTACAGCAATCC
6669qrtfor	GCATCATTGCTGTCATCACC
6669qrtrev	AGCCCCAGATGAAGAACACC
2839qrtfor	TCCTCAATGCCGCAGAAAC
2839qrtrev	ACCAGAAAGAACCCATCTCC