Developmental Growth Control Exerted via the Protein A Kinase Tpk2 in *Ashbya gossypii*

Lisa Wasserstrom,* Klaus Lengeler, Andrea Walther,* Jürgen Wendland

Carlsberg Laboratory, Yeast Genetics, Copenhagen, Denmark

Sporulation in *Ashbya gossypii* is induced by nutrient-limited conditions and leads to the formation of haploid spores. Using RNA-seq, we have determined a gene set induced upon sporulation, which bears considerable overlap with that of *Saccharomyces cerevisiae* but also contains *A. gossypii*-specific genes. Addition of cyclic AMP (cAMP) to nutrient-limited media blocks sporulation and represses the induction of sporulation specific genes. Deletion of the protein kinase A (PKA) catalytic subunits encoded by *TPK1* and *TPK2* showed reduced growth in *tpk1* but enhanced growth in the *tpk2* strain; however, both mutants sporulated well. Sporulation can be blocked by cAMP in *tpk1* but not in *tpk2* strains. Similarly, *TPK2* acts at a second developmental switch promoting the break in spore dormancy. In *S. cerevisiae*, PKA phosphorylates and inhibits Msn2/4. The transcript profiles of the *tpk1* and *msn2/4* mutants were very similar to that of the wild type under sporulation conditions. However, deletion of the single *A. gossypii Msn2*/*4* homolog generated a specific sporulation defect. We identified a set of genes involved in spor wall assembly that was downregulated in the *msn2/4* mutant, particularly *DIT2*, suggesting that poor spore viability may be due to lysis of spores. Our results reveal specific functional differences between the two catalytic PKA subunits in *A. gossypii* and identified Tpk2 as the key A kinase that transduces developmental decisions of growth. Our data also suggest that Msn2/4 is involved only at a late step of sporulation in *A. gossypii* and is not a major regulator of *IME1*.

Fungi have developed remarkably complex signaling networks composed of several central conserved parts to react to changing environmental stimuli. Of key importance is the regulation of growth in response to nutrient availability, mating in response to a mating partner, or sporulation under nutrient-limited conditions. Transmembrane proteins act as sensors for external environmental stimuli and signal through conserved signal transduction pathways, including mitogen-activated protein kinase (MAPK) modules, the calcium/calcineurin pathway, and the cyclic AMP (cAMP) pathway, and have been studied in a large variety of fungi (1). Often, these pathways harbor genes required for fungal pathogenicity of plant or animal pathogens (2, 3). *Saccharomyces cerevisiae* adapts to drastically changing environmental conditions by the activation of an environmental stress response (4). This shares features of the general stress response in which Msn2/4 activate transcription of genes that harbor STRE elements in their promoters (5–7). Another immediate response to various stresses is the repression of ribosomal proteins that are regulated by Rap1 (8). Nutrient starvation in *S. cerevisiae* leads to growth arrest, reduced gene expression, and increased stress resistance (9). Interestingly, starvation of yeast cells for either glucose, nitrogen, or phosphate was found to lead to similar cAMP-dependent transcriptional changes (10).

In yeast, the cAMP/protein kinase A (PKA) pathway governs all aspects of cell physiology, particularly morphogenesis, growth, and sporulation. Adenylyl cyclase is activated by either the Gpr1-Gpa2 glucose sensing pathway or by the Ras G-protein to produce cAMP. The heterotrimeric protein kinase A complex is composed of two regulatory subunits of Bcy1 and three catalytic subunits encoded in *S. cerevisiae* by *TPK1*, *TPK2*, or *TPK3*. Upon cAMP binding, Bcy1 releases the catalytic subunits. The Tpk kinases then phosphorylate downstream effectors, which results in altered transcriptional responses (4). Activation of PKA stimulates growth and, e.g., the Rap1-dependent expression of ribosomal genes, while PKA-dependent phosphorylation of Msn2/4 leads to a downregulation of stress responses (11, 12). The influence of the level of cAMP for entry into meiosis was identified by using temperature-sensitive alleles of *CYR1* resulting in low levels of cAMP and mutants in *BCY1*, leading to constitutively active PKA. While low levels of cAMP promoted entry into meiosis, *bcy1* mutants failed to sporulate (13). Mechanistically, PKA-dependent phosphorylation of Msn2/4 leads to cytoplasmic accumulation of these transcription factors that thus cannot induce the initiator of meiosis *IME1* through binding the upstream activating sequence element IREu (see Fig. 1) (14).

Msn2 and Msn4 were considered to play largely functionally redundant roles in stress responses (15). However, nonredundant and specific roles in stress-dependent gene expression were recently found using DNA microarrays (16). Similarly, the three catalytic PKA subunits redundantly promote growth and deletion of all three kinases results in lethality (17). However, Tpk2 was found to promote pseudohyphal and invasive growth via interaction with Sfl1, whereas Tpk3 was found to inhibit these processes (18, 19). Additional diversity was found in negative regulation of

Received 11 March 2015 Accepted 3 April 2015
Accepted manuscript posted online 10 April 2015

Citation Wasserstrom L, Lengeler K, Walther A, Wendland J. 2015. Developmental growth control exerted via the protein A kinase Tpk2 in *Ashbya gossypii*. Eukaryot Cell 14:593–601. doi:10.1128/EC.00045-15.

Address correspondence to Jürgen Wendland, juergen.wendland@carlsberglab.dk.
* Present address: Lisa Wasserstrom, Division of Applied Microbiology, Department of Chemistry, Lund University, Lund, Sweden; Andrea Walther, Novozymes A/S, Bagsvaerd, Denmark.

Supplemental material for this article may be found at http://dx.doi.org/10.1128/EC.00045-15.

Copyright © 2015, American Society for Microbiology. All Rights Reserved.
doi:10.1128/EC.00045-15
iron uptake by Tpk2, which also promotes trehalose degradation. Interestingly, tpk2 mutants grow better on ethanol-glycerol-containing media than do wild-type and tpk1 or tpk3 strains (20). The gene set upregulated during yeast sporulation has been determined using DNA microarrays. Temporal patterns were observed to classify early, middle, and late induction of gene expression under nutrient-limited conditions (21).

*Ashbya gossypii* is a distant relative of *S. cerevisiae* that solely grows in a hyphal form. Upon nutrient limitation, *A. gossypii* mycelia initiate developmental events leading to the formation of sporangia, hyphal fragmentation, sporulation, and riboflavin overproduction (22, 23). Previously, conserved roles of key *S. cerevisiae* genes regulating meiosis, e.g., IME1, IME2, IME4, and NDT80, for the sporulation in *A. gossypii* were identified (24). Similar to *bcy1* mutants in yeast, exogenous addition of cAMP to the growth medium promoting constitutive activation of PKA blocks sporulation in *A. gossypii* (25).

To elucidate the function of cAMP signaling in sporulation, we compared the transcriptional profiles of the wild type under nutrient-rich, nutrient-limited, and nutrient-limited/cAMP-supplemented conditions to identify the gene set upregulated under sporulation-inducing conditions. We found that a gene set comprising 560 genes is 5-fold upregulated under sporulation-inducing conditions, most of which were downregulated when cAMP was added to nutrient-limited medium. To identify functional differences between the catalytic PKA subunits, we analyzed *TPK1* and *TPK2* mutants. Strains with *TPK2* deleted grew faster than the wild type but were defective in cAMP-dependent repression of sporulation. In contrast, *tpk1* strains responded like the wild type to cAMP with repressed sporulation in nutrient-limited media. On the other hand, spor germination was severely reduced in *tpk2* strains. As a potential PKA target gene in sporulation, we analyzed *A. gossypii msn2/4*. The transcript profile of *msn2/4* was very similar to those of wild-type and *tpk1* strains. However, a small set of genes involved in spore wall formation, e.g., *DIT2*, was downregulated in *msn2/4* under nutrient-limited condition. A role for Msn2/4 in spore wall maturation is supported by a low level of viable spores in *msn2/4* strains.

**MATERIALS AND METHODS**

**Strains and media.** *A. gossypii* strains were grown in *Ashbya* full medium (AFM; 1% yeast extract, 1% peptone, 2% dextrose), and G418/Geneticin (200 μg/ml) was used for selection of antibiotic-resistant transformants. For sporulation, overnight cultures of *A. gossypii* adjusted to similar wet weights were further incubated in minimal medium (1.7 g/liter yeast nitrogen base [YNB] without ammonium sulfate and without amino acids, 0.79 g/liter Bio 101 complete synthetic mixture, 20 g/liter glucose, 2 g/liter asparagine, and 1 g/liter myo-inositol) for up to 3 days. Residual mycelia were digested with zymolyase, and spores were suspended in spore buffer (0.03% Triton-X-100). *A. gossypii* strains were grown at 30°C unless stated otherwise. *Escherichia coli* strain DH5α was used for plasmid propagation and grown at 37°C with ampicillin for the selection of antibiotic-resistant transformants.

**Generation of plasmids and gene fusions.** Disruption cassettes for *TPK1* and *TPK2* were obtained by cloning 5’ and 3’ homologous flanks to the GEN3 selectable marker. The 5’ flanking regions were amplified using the primer pair 1818/1819 for *TPK1* and the primer pair 1822/1823 for *TPK2*. SacI sites were included in primers 1818 and 1822, and BamHI sites were included in primers 1819 and 1823. The 3’ flanking regions were amplified by using the primer pair 1820/1821 for *TPK1* and the primer pair 1824/1825 for *TPK2*. BamHI sites were included in primers 1820 and 1824, and EcoRI sites were included in primers 1821 and 1825. The GEN3 marker was excised from pFA-GEN3 using BglII and cloned into the BamHI site of the BamHI site between the 5’ and 3’ flanking regions of each gene into pBluescript SK(+) (+). The GEN3 marker was inserted in the reverse orientation in the *TPK1* disruption cassette (pSK-tpk1::GEN3) and in the forward orientation in the *TPK2* disruption cassette (pSK-tpk2::GEN3). Oligonucleotides were obtained from Integrated DNA Technologies (Leuven, Belgium).

**Transformation of *A. gossypii*.** *A. gossypii* strains were transformed by electroporation using GEN3 as selectable marker, providing resistance to the antibiotic G418 as described previously (26). For each desired deletion mutant, two independent transformants were generated. The *A. gossypii msn2/4* deletion strains were generated by PCR-based gene targeting as described previously (26). The *A. gossypii tpk1* and *tpk2* deletion strains

![Diagram](https://example.com/diagram.png)
were generated by transformation with cloned disruption cassettes obtained by digesting pSK-tpk1::GEN3 and pSK-tpk2::GEN3 with SacI. Diagnostic PCR was used to verify the correct integration of a disruption cassette and the deletion of the target gene in two independent homokaryotic deletion strains as described previously (27).

**Microscopy.** Microscopy was carried out using a Zeiss Axioskop Imager M1 microscope (Zeiss, Jena, Germany) controlled by Metamorph 7 software (Molecular Devices Corp., Downingtown, PA). Images were acquired with a Photometrics CoolSNAP HQ camera (Princeton Instruments, Trenton, NJ). To monitor the germination of mutant spores, an Axiovert 200M microscope was used.

**Determining sporulation ability.** Sporulation efficiency was assayed in both homokaryons and heterokaryons for each mutant strain by isolating spores from the central part of mycelia grown for 10 days at 30°C on AFM plates supplemented with 1 g/liter myo-inositol. A circle of the central mycelia (15 mm in diameter) was cut out from the plate and suspended in 5 ml of Tris-EDTA buffer containing 200 µl of zymolase to degrade cell walls of vegetative mycelia and release the spores. After 3 h of incubation at 37°C (on a tilting rotor), the spores were counted centrifugation and washed twice in spore buffer (0.03% Triton X-100). For determination of the CFU, serial dilutions were performed in spore buffer, and 100 µl of appropriate dilutions was plated on AFM plates, followed by incubation at 30°C until colonies appeared. The data are presented as the percent CFU forming in the homokaryon compared to the heterokaryon of each deletion strain.

**Germination efficiency.** Spores were isolated from mycelia grown in sporulation media for 3 days. A total of 100 spores of the wild-type strain and the tpk2 deletion strain were micromanipulated using a Singer MSM 300 dissection microscope (Singer Instruments, Somerset, United Kingdom) and grown on AFM plates at 30°C up to for 3 days. Events scored (including by microscopy) were ungerminated spores, spores that only formed germ cells, spores that germinated but generated abortive mycelia, and spores that developed mycelia.

**RNA-seq.** Mycelia of two independent homokaryons for each deletion strain were grown in liquid AFM medium in baffled flasks for 16 h. Equal wet weights of mycelia were washed and grown either in AFM or under nutrient-limited conditions in minimal media for 16 h prior to total RNA isolation with a RiboPure-Yeast kit (Life Technologies). The RNA quality was assayed photometrically and by performing reverse transcription-PCR on selected target genes. To study the influence of CAMP on gene expression under nutrient-limited conditions, 5 mM cAMP was added to the minimal medium. The total RNA was used for Illumina HiSeq 2000 sequencing, and data were processed to remove linker DNA, rRNAs, and tRNA sequences. Short reads were discarded so that 16.5 to 28.0 million reads were obtained per strain. Reads were aligned, and read counts were generated for each annotated gene (using TopHat 2.0.4) based on the published A. gossypii genome. Differential expression based on the RNA-seq data was analyzed as described previously using edgR, DESeq, and cufflinks, and a false discovery rate of 0.05 was indicative of differential expression (24). RNA-seq was performed by LGC Genomics (Berlin, Germany).

GO-term analyses were carried out using the Generic Gene Ontology (GO) Term Finder (http://go.princeton.edu/cgi-bin/GOTermFinder) or the GO Term Finder at the Saccharomyces Genome Database (http://www.yeastgenome.org/cgi-bin/GO/goTermFinder.pl).

**RESULTS**

The *Ashbya gossypii* transcriptome under nutrient-limited conditions. *A. gossypii* produces abundant amounts of spores due to mycelial fragmentation and near quantitative conversion of hyphae into sporangia, which is much in contrast to its close relative, *Eremothecium cymbalariae* (28). *A. gossypii* spores are haploid and uninucleate, suggesting that the resulting mycelium formed by a single spore is homothallic since it is itself able to sporulate (29, 30). Previous RNA-seq analyses focused on a comparison of the transcriptomes of nonsporulating *A. gossypii* mutants, e.g., *ime1* and *ime2* strains, with the wild type (24).

In the present study, we sought to identify the set of *A. gossypii* genes that is differentially expressed under nutrient-limited conditions that result in sporulation. Wild-type mycelia were transferred from complete medium to either minimal or complete medium and incubated for 16 h. This is sufficient to induce sporulation in *A. gossypii*. Total RNA was isolated and used for RNA-seq transcript profiling. All experiments were conducted by pooling RNA of two independent transformants per assayed mutant. The complete data set is included as File SI in the supplemental material. We considered genes upregulated under these conditions as part of the transcriptional program of sporulation in *A. gossypii*. Using a cutoff 5-fold overexpression, we identified 559 unique genes that is differentially expressed under nutrient-limited conditions in *A. gossypii* and *S. cerevisiae* (based on reference 5). The number of genes indicated in the center are upregulated in both species, the number of genes to the left and right are regulated in a species-specific manner. (B) Based on GO term analyses specific GO IDs were identified as either up- or downregulated. The left part indicates processes regulated during sporulation in minimal medium, and the right part indicates processes regulated in minimal medium that was supplemented with 5 mM cAMP.
genes that included 454 genes with homologs in S. cerevisiae. This included some genes that are duplicated in A. gossypii. This gene set was compared to the set of genes upregulated during sporulation in yeast (21). A core set of 124 sporulation induced genes was found in both species (Fig. 2A and see File S1 in the supplemental material). Among these upregulated genes, for example, were the transcriptional regulators IME1 (upregulated 460-fold), IME2 (54-fold), and NDT80 (108-fold), the middle-sporulation specific MAPK SMK1 (1,500-fold), and the sporulation-specific septins SPR3 (1,950-fold) and SPR28 (120-fold). Genes for spore wall formation, such as DTR1 (806-fold), GAS2 (777-fold), GAS4 (666-fold), OSW1 (647-fold), DIT1 (496-fold), and DIT2 (306-fold), were also found to be highly upregulated. This provides an indication on the progress of the developmental process in A. gossypii mycelia within a 16-h period between a shift from complete to minimal medium. With just one sampling time point, we, of course, could not distinguish between an early, a middle, or a late phase of induction of these genes. Interestingly, a large set of homologous genes seems to be differentially upregulated in sporulation in A. gossypii or in S. cerevisiae. At the same time, ~100 genes were found to be upregulated during sporulation in each of the two species for which there was no homolog in the other species (Fig. 2A). Some of these genes (termed “NOHBY” since they

FIG 3 Role of components of the cAMP/PKA pathway for vegetative growth. (A) Comparison of radial growth rates of the wild-type strain and the tpk1, tpk2, and msn2/4 mutants at different temperatures. (B) Bar diagram comparing the radial growth of the mutants with the wild type after 7 days at 22, 30, and 37°C. Strains were grown on complete media plates, and the radial growth was measured after 7 days and is presented as the percent growth of the wild type. The bars represent duplicate experiments of the independent homokaryotic mutant strains for each gene.

FIG 4 Sporulation ability of the tpk1, tpk2, and msn2/4 mutants. (A and B) Sporulation ability of the indicated strains with or without the addition of 5 mM cAMP is shown by the presence of spore clumps or hyphae. Note the difference in spore shape and appearance of msn2/4 spores compared to spores of the other strains. (C) Chart showing the efficiency of colony formation from spores derived from the indicated strains. Wild type was set to 100%. For the mutant strains, the ratio was calculated based on a comparison of heterokaryotic and homokaryotic strains. The strains in panels A and B were grown for 3 days in liquid sporulation media. Then, spore suspensions were treated with zymolyase to digest the remaining cell walls from vegetative hyphae. Representative images derived from duplicate experiments of independent homokaryotic mutant strains for each gene are shown. Scale bar, 10 μm.
have “NO Homolog in Baker’s Yeast” [30]) were actually upregulated to a high level and will make interesting candidates for future studies. We used the set of 454 A. gossypii genes upregulated under nutrient-limited conditions that share a S. cerevisiae homolog and queried the GO database (http://go.princeton.edu/cgi-bin/GOTermFinder) in order to find genes belonging to the same process (Fig. 2B). As expected, the upregulated genes belong to processes of meiosis, sporulation, and spore wall formation. Among the downregulated genes, translation and gene expression were the most abundant (see Table S1 in the supplemental material).

**cAMP blocks sporulation specific gene expression in A. gossypii.** In A. gossypii, the exogenous addition of cAMP blocks sporulation and riboflavin overproduction (25). We thus added cAMP to a nutrient-limited culture to identify the cAMP-repressed gene set (Fig. 2B). We identified 479 genes that were >2.5-fold downregulated, and the GO terms were exactly those that were upregulated under nutrient-limited conditions, i.e., genes involved in sporulation. Specifically, the expression levels of IME1, IME2, IME4, and NDT80 were strongly reduced by the addition of cAMP. This indicates that the cAMP/PKA pathway controls all developmental events leading to sporangium formation and sporulation. However, we did not find a cAMP repression of any of the riboflavin biosynthesis genes under nutrient-limited conditions. Only a small set of genes was found to be upregulated under these conditions, including CWP1 and AEL111C (YKL164C) involved in cell wall stability or genes involved in amino acid biosynthesis (Fig. 2B).

**Specific signaling functions of TPK1 and TPK2 during growth and sporulation.** Due to the central role of PKA for development in A. gossypii, we wanted to determine whether the catalytic subunits encoded in A. gossypii by TPK1 and TPK2 are redundantly regulating sporulation or harbor specific functions. The tpk1 and tpk2 mutant strains were assayed for radial growth speed on complete medium at different temperatures (Fig. 3A). Strains with TPK1 deleted showed ca. 25% reduced growth at 30 and 37°C, while tpk2 strains grew faster than the wild type at these temperatures (Fig. 3B). This suggests specific roles for Tpk1 and Tpk2 in hyphal growth (see Discussion).

Both tpk1 and tpk2 strains were able to sporulate and, in fact, produced a large amount of spores (Fig. 4A). Since the addition of cAMP blocks sporulation in the A. gossypii wild type under nutrient-limited conditions, we tested whether this development is also repressed by cAMP in tpk1 and tpk2 strains. We found that, as in the wild type, sporulation was repressed by the addition of cAMP in tpk1 mutant strains. Surprisingly, however, tpk2 strains were unresponsive to cAMP addition and sporulated abundantly (Fig. 4B). This indicates that Tpk2 acts as a gate keeper to control development and initiate sporulation by transducing nutrient signals to downstream effectors.

**Spores of tpk2 strains exhibit a severe germination defect.** To determine the viability of the tpk1 and tpk2 spores, we purified spores by digesting mycelial fragments with zymolyase and plating them on complete media to determine the number of CFU (Fig. 4C). With the wild type set to 100%, we compared the CFU of tpk1 and tpk2 homokaryotic versus heterokaryotic strains. The heterokaryotic TPK/tpk strains served as a control for assessing the recessive sporulation defect. We found that the deletion of TPK1 reduced the ability of spores to form colonies by half since 43.3% of the homokaryotic spores formed CFU compared to the heterokaryon—only 2.1% CFU in the homokaryon versus the heterokaryon—even though spores

---

**FIG 5 Germination defect of tpk2 spores in liquid medium.** Microscopic images of spores of the wild-type and tpk2 strains that were germinated in complete liquid medium overnight at room temperature without (A) or with (B) the addition of 5 mM cAMP to the growth medium are shown.
appeared to be wild type-like. We here discovered a key role of Tpk2 to govern the developmental switch between growth and sporulation. The poor ability to generate mycelia from spores led us to investigate a second developmental switch: that of breaking the dormancy in a spore to promote germination and hyphal growth.

To assess whether the inability to form colonies was due to a germination defect or, e.g., postgermination lysis of mycelia, we inoculated spores of the wild-type and tpk2 mutant strains into liquid complete medium. Wild-type spores readily germinated and formed juvenile mycelia by 16 h after inoculation. In contrast, tpk2 spores remained largely ungerminated, and only a few mycelia developed (Fig. 5A). The germination efficiency of the tpk2 spores was quantified by micromanipulation of 100 spores each from the wild-type and tpk2 strains on full medium plates. Only ca. 10% of tpk2 spores germinated and formed mycelia, whereas almost 80% of wild-type spores germinated, even though 20% of the spores did not mature into mycelia (Table 1). We also observed a large germination delay in tpk2 spores in comparison to the wild type (not shown).

To investigate whether the block in germination could be suppressed by additional supplementation with cAMP to promote breaking the dormancy of tpk2 spores, e.g., by overactivating Tpk1, wild-type and tpk2 spores were germinated in liquid and solid complete media supplemented with cAMP (Fig. 5B and 6). However, CAMP-addition did not improve the germination rate of tpk2 spores and also had no effect on wild-type or tpk1 spores (data not shown).

Deletion of MSN2 results in low spore viability and downregulation of spore wall biosynthetic genes. Two of the key downstream effectors of PKA in S. cerevisiae are Msn2 and Msn4 (31, 32). A. gossypii has one homolog denoted MSN2/4. Deletion of MSN2/4 does not result in a growth defect (Fig. 3A). Deletion mutants of MSN2/4 are able to sporulate, and this development can be suppressed by the addition of cAMP to nutrient-limited medium (Fig. 4A and B). However, we observed a low rate of colony formation from msn2/4 spore preparations (Fig. 4C). Microscopic inspection of the spores showed that spores were often broken and were of granulated appearance (“ghost-like”, Fig. 4A). The RNA-seq transcript profile of msn2/4 strains under sporulation conditions was mostly congruent with those of the wild-type and tpk1 mutant strains (see File S1 in the supplemental material). However, we observed a specific downregulation of genes involved in spore wall formation when comparing the msn2/4 strain to the wild type under sporulation conditions, particularly that of DIT2 (Table 2). Even though the genes listed in Table 2 demonstrated an upregulation compared to wild type grown in full medium, they nevertheless were induced to a far lesser level (only one-third) compared to the wild type in nutrient-limited medium. This suggests that poor cell wall formation reduces spore viability, which may be exacerbated when these spores are treated with zymolyase during preparation.

**DISCUSSION**

Key decisions on cell fate in fungi are gated to control metabolism, stress response, pathogenicity, growth, and developmental switches for entering quiescence, sporulation, or breaking the dormancy of spores (2, 33, 34). Signal transduction cascades play an essential role to parse environmental information and result in appropriate cellular responses (1). Nutrient availability is signaled through the cAMP/PKA pathway to promote growth and developmental decisions (35). Changes in metabolism often require large-scale transcriptional changes affecting hundreds of genes. In S. cerevisiae such large-scale changes were identified under various stress conditions, nutrient limitation, and sporulation (4, 10, 21, 36, 37).

We have shown that in A. gossypii sporulation leads to differential expression of ~900 genes, including the upregulation of conserved genes involved in sporulation, meiosis, and spore wall assembly and the downregulation of genes involved in translation and gene expression. Although there is considerable overlap with the transcriptional program of S. cerevisiae sporulation, there are several hundred genes specifically upregulated in A. gossypii, including 100 genes that do not share a homolog with yeast. These genes, particularly the most highly upregulated ones, could be informative to elucidate differences of spore shapes in A. gossypii (needled-shaped) versus S. cerevisiae (round spores).

**TABLE 1 Reduced germination efficiency of tpk2 spores**

| Spore type          | Germination efficiency (no. of spores) |
|---------------------|---------------------------------------|
|                     | Wild type | tpk2 mutant |
| Mycelia             | 58        | 11          |
| Ungerminated        | 22        | 89          |
| Germ cell           | 8         | 0           |
| Abortive mycelia    | 12        | 0           |
| Total               | 100       | 100         |

**FIG 6 Germination defect of tpk2 spores on solid medium.** The germination defect of tpk2 spores cannot be suppressed by growth on solid medium. Microscopic images of spores of the wild-type and the tpk1 and tpk2 strains that were plated on complete medium and grown overnight are shown.
The addition of cAMP to nutrient-limited conditions resulted in the downregulation of genes involved in translation comparable to the wild type without the addition of cAMP, and yet it specifically inhibited the expression of sporulation-specific genes and effectively blocked the sporulation in *A. gossypii*. Overactivation of cAMP signaling, e.g., by deletion of the regulatory subunit of PKA or by overexpression of the catalytic unit, was shown to result in reduced conidiation in *Aspergillus fumigatus* and *Alternaria alternate* (38–40). Similarly, deletion of genes encoding phosphodiesterases, which hydrolyze cAMP, resulted in drastically reduced conidiation in *Botrytis cinerea* and *Magnaporthe oryzae* (41, 42).

Of great interest has been the regulation of pseudohyphal growth in *S. cerevisiae* upon starvation for nitrogen (18, 43). Particularly, diverged and specific functions in yeast pseudohyphal growth were discovered with Tpk2 promoting it, whereas Tpk3 particularly, diverged and specific functions in yeast pseudohyphal growth. Tpk2 regulates dimorphism, and Tpk3 has decisively distinct functions in transducing the cAMP signal and morphogenesis and pathogenicity in *Aspergillus fumigatus* (24, 38). In *Candida albicans*, Tpk2 regulates dimorphism, and Tpk2 strains are crippled in their ability to invade tissues and thus reduced in virulence (44). Contact-induced appressorium formation and host penetration in *M. oryzae* and morphogenesis and pathogenicity in *Usatalgo maydis* require signaling via the cAMP/PKA pathway (45). We have shown that the catalytic PKA subunits of *A. gossypii* have decisively distinct functions in transducing the cAMP signal to affect developmental decisions. TPK1 deletion affects vegetative growth but not developmental decisions in *A. gossypii*. In contrast, Tpk2 is required at key developmental transitions. On the one hand, Tpk2 is essential for blocking sporulation when cAMP levels are high, which signals abundant nutrient supply. TPK2 deletion mutants are completely defective in blocking this developmental step and simply override this block. On the other hand, Tpk2 is needed for the initiation of germination to break the dormancy of spores. TPK2 mutants show a severe reduction in germination efficiency. At both of these stages, signals of favorable growth conditions and abundant nutrient supply are not relayed in tpk2 to promote growth, identifying Tpk2 as a key gatekeeper of developmental decisions in *A. gossypii*. Interestingly, when Tpk2 is the sole A kinase, i.e., in the tpk1 mutant strain, radial growth rate is reduced. This suggests an inhibitory function of Tpk2, resulting in submaximal radial growth rate. Conversely, deletion of TPK2 leads to increased growth rates. This, therefore, indicates a third specific function for Tpk2, distinguishing it further from Tpk1.

Sensitivity of germination to cAMP signaling has also been reported in *Aspergillus nidulans*. Here, carbon source signaling is relayed via the heterotrimeric G protein GanB(α)-SfaD(β)-Gpaα(γ) to PKA. The deletion of GanB results in a severe germination defect (46). Similarly, deletion of the catalytic PKA subunits pkaC1 and pkaC2 in *A. fumigatus* resulted in delayed germination (47).

One of the functions of PKA is to regulate stress responses via Msn2/4 (32). We have previously studied regulation of sporulation in *A. gossypii* and described a sporulation defect of *ime1* and *ime2* mutants (24). To address whether Msn2/4 could establish a link between PKA signaling and IME1 expression, we generated Msn2/4 deletion strains. These strains, however, showed transcript profiles similar to that of the wild type under nutrient-limited conditions and produced spores. Nevertheless, spore viability was drastically reduced in *Amsn2/4* strains. We have provided evidence that this may be due to the downregulation of genes involved in spore wall formation, e.g., *DIT2*. A spore wall defect of *msn2/4* mutants was recently also described for *S. cerevisiae* (48). Thus, our current research aims at identifying other more potent links connecting the cAMP/PKA pathway with, e.g., IME1 and induction of the transcriptional program of sporulation in *A. gossypii*.

### Table 2: Genes involved in spore wall formation, which are downregulated in the msn2/4 strain versus the wild type under sporulation conditions

| *A. gossypii* gene | *S. cerevisiae* homolog | Gene | No. of reads* | Fold downregulation |
|-------------------|-------------------------|------|---------------|---------------------|
|                   |                         |      | leu2/spo      | leu2/AFM msn2/4spo  |
| AFR400C           | YDR402C                 | DIT2 | 2,455         | 8                   | 372                  | –6.60               |
| AFR401W           | YDR403W                 | DIT1 | 31,248        | 63                  | 7,103                | –4.40               |
| ACL102W           | YIR026C                 | YVH1 | 190           | 293                 | 51                   | –3.73               |
| AGR195W           | YBR180W                 | DTR1 | 105,271       | 129                 | 32,183               | –3.27               |
| ACR135C           | YOR242C                 | SSP2 | 88,026        | 69                  | 27,567               | –3.19               |
| ADL315C           | YPR054W                 | SMK1 | 48,690        | 32                  | 15,460               | –3.15               |
| AFR517C           | YLR054C                 | OSW2 | 53,481        | 38                  | 17,029               | –3.14               |
| ACL182C           | YLR343W                 | GAS2 | 30,309        | 39                  | 9,709                | –3.12               |
| AFR725C           | YCL048W                 | SPS2 | 56,780        | 42                  | 18,572               | –3.06               |
| AAL105C           | YOR255W                 | OSW1 | 11,005        | 17                  | 3,793                | –2.90               |
| AGR105C           | YDR104C                 | SPO71| 65,188        | 627                 | 22,777               | –2.86               |
| AFR724C           | YDR523C                 | SPS1 | 30,126        | 33                  | 10,547               | –2.86               |
| ABL089W           | YBR045C                 | GIP1 | 32,406        | 38                  | 11,463               | –2.83               |
| AGR274C           | YOR177C                 | MPC54| 4,862         | 4                   | 1,722                | –2.82               |
| ADL105C           | YER046W                 | SPO73| 2,640         | 62                  | 944                  | –2.80               |
| ACL179C           | YLR341W                 | SPO77| 24,172        | 83                  | 8,714                | –2.77               |
| ADL135C           | YGR225W                 | AMA1 | 20,387        | 589                 | 7,562                | –2.70               |
| AFR524W           | YOR298W                 | MUM3 | 2,632         | 51                  | 983                  | –2.68               |
| AFR604C           | YOL091W                 | SPO21| 30,580        | 611                 | 11,602               | –2.64               |
| AAR069W           | YCR045C                 | RRT12| 20,571        | 544                 | 8,103                | –2.54               |

*The total numbers of reads obtained by RNA-seq expression profiling of the parental strain under sporulation conditions (leu2/spo strain), the parental strain in complete AFM medium (leu2/AFM), and the msn2/4 strain under sporulation conditions (msn2/spo) are shown.*
REFERENCES

1. Rispail N, Soanes DM, Ant C, Czajkowski R, Gruner A, Huguet R, Perez-Nadalea E, Poli A, Sartorel E, Valiante V, Yang M, Beffa R, Brakhage AA, Gow NA, Kahmann R, Lefrun MH, Lenasi H, Perez-Martín J, Talbot NJ, Wendland J, Di Pietro A. 2009. Comparative genomics of MAP kinase and calcium-calmodulin signaling components in plant and human pathogenic fungi. Fungal Genet Biol 46:287–299. http://dx.doi.org/10.1016/j.fgb.2009.01.002.

2. Fuller KK, Rhodes JC. 2012. Protein kinase A and viral virulence: a sinister side to a conserved nutrient sensing pathway. Virulence 3:109–121. http://dx.doi.org/10.4161/viru.19396.

3. Lenger KB, Davidson RG, D’Souza C, Harashima T, Shen WC, Wang P, Pan X, Waugh M, Heitman J. 2000. Signal transduction cascades regulating fungal development and virulence. Microbiol Mol Biol Rev 64:746–785. http://dx.doi.org/10.1128/MMBR.64.4.746-785.2000.

4. Gasch AP, Spellman PT, Kao CM, Carmel-Harel O, Eisen MB, Storz G, Fuller KK, Rhodes JC. 2004. Identification of cis- and trans-components of a novel heat shock stress regulatory pathway in Saccharomyces cerevisiae. Mol Cell Biol 13:248–256.

5. Marchler G, Schuller C, Adam G, Ruis H. 1993. A Saccharomyces cerevisiae UAS element controlled by protein kinase A activates transcription in response to a variety of stress conditions. EMBO J 12:1997–2003.

6. Martinez-Pastor MT, Marchler G, Schuller C, Marchler-Bauer A, Ruis H, Estruch F. 1996. The Saccharomyces cerevisiae zinc finger proteins Msn2p and Msn4p are required for transcriptional induction during the stress response element (STRE). EMBO J 15:2227–2235.

7. Moech ML, Hinnenbosch AG. 1991. Association of RAPI binding sites with stringent control of ribosomal protein gene transcription in Saccharomyces cerevisiae. Mol Cell Biol 11:2723–2735.

8. Gray JV, Petsko GA, Johnston GC, Ringe D, Singer RA, Werner-Washburne M. 2004. “Sleeping beauty”: quiescence in Saccharomyces cerevisiae. Microbiol Mol Biol Rev 68:187–206. http://dx.doi.org/10.1128/MMBR.68.2.187-206.2004.

9. Conway MK, Grunwald D, Heideman W. 2012. Glucose, nitrogen, and phosphate repletion in Saccharomyces cerevisae: common transcriptional responses to different nutrient signals. G3 (Bethesda) 2:1003–1017. http://dx.doi.org/10.1534/g3.112.1002808.

10. Gevim J, Bergstrom S. 2009. Genome reprogramming during sporulation. Int J Dev Biol 53:425–432. http://dx.doi.org/10.1387/ijdb.082687fg.

11. Santangelo GM. 2006. Glucose signaling in Saccharomyces cerevisiae. Microbiol Mol Biol Rev 70:253–282. http://dx.doi.org/10.1128/MMBR.70.1.253-282.2006.

12. Matsamoto K, Uno I, Ishikawa T. 1983. Initiation of meiosis in yeast mutants defective in adenylate cyclase and cyclic AMP-dependent protein kinase. Cell 32:417–423. http://dx.doi.org/10.1016/0092-8674(83)90461-0.

13. Sagee S, Sherman A, Shenhar G, Robzyk K, Ben-Doy N, Simchen G, Kassir Y. 1998. Multiple and distinct activation and repression sequences mediate the regulated transcription of IME1, a transcriptional activator of meiosis-specific genes in Saccharomyces cerevisiae. Mol Cell Biol 18:1985–1995.

14. Tregter JM, Schmitt AP, Simon JR, McEntee K. 1998. Transcriptional factor mutations reveal regulatory complexities of heat shock and newly identified stress genes in Saccharomyces cerevisiae. J Biol Chem 273:26875–26879. http://dx.doi.org/10.1074/jbc.273.26.26875.

15. Berry DB, Gasch AP. 2008. Stress-activated genic expression changes serve a preparative role for impending stress in yeast. Mol Cell Biol 19: 4580–4587. http://dx.doi.org/10.1128/mcb.00707-0680.

16. Toda T, Cameron S, Sass P, Zoller M, Wigler M. 1987. Three different genes in Saccharomyces cerevisiae encode the catalytic subunits of the cAMP-dependent protein kinase. Cell 56:277–287. http://dx.doi.org/10.1016/0092-8674(87)90223-6.

17. Pan X, Heitman J. 1999. Cyclic AMP-dependent protein kinase regulates pseudohyphal differentiation in Saccharomyces cerevisiae. Mol Cell Biol 19:4874–4887.

18. Robertson LS, Fink GR. 1998. The three yeast A kinases have specific signaling functions in pseudohyphal growth. Proc Natl Acad Sci U S A 95:13783–13787. http://dx.doi.org/10.1073/pnas.95.23.13783.

19. Wasserstrom L, Lengeler KB, Walther A, Wendland J. 2013. Molecular determinants of sporulation in Ashbya gossypii. Genetics 195:87–99. http://dx.doi.org/10.1534/genetics.113.151019.

20. Stahlmann KP, Arnt HN, Jr, Althofer H, Revuelta JL, Monschau N, Schlupen C, Gatsens C, Wiesenburg A, Schlosser T. 2001. Ribolivarin, overproduced during sporulation of Ashbya gossypii, protects its hyaline spores against ultraviolet light. Environ Microbiol 3:545–550. http://dx.doi.org/10.1042/0966-842X(00)00225.x.

21. Wendland J, Ayad-Durieux Y, Knechtle P, Rebischung C, Philipsen P. 2000. PCR-based gene targeting in the filamentous fungus Ashbya gossypii. Gene 242:381–391. http://dx.doi.org/10.1016/S0378-1119(99)00509-0.

22. Walther J, Wendland J. 2008. PCR-based gene targeting in Candida albicans. Nat Protoc 3:1414–1421. http://dx.doi.org/10.1038/nprot.2008.137.

23. Wendland J, Walther A. 2011. Genomic evolution in the Eremothecium clade of the Saccharomyces complex revealed by comparative genomics. G3 (Bethesda) 1:539–548. http://dx.doi.org/10.1534/g3.111.001032.

24. Wendland J, Dunkler A, Walther A. 2011. Characterization of alpha-factor pheromone and pheromone receptor genes of Ashbya gossypii. FEMS Yeast Res 11:418–429. http://dx.doi.org/10.1111/j.1567-1364.2011.00732.x.

25. Klein C, Struhl K. 1994. Protein kinase A mediates growth-regulated expression of yeast ribosomal protein genes by modulating RAPI transcriptional activity. Mol Cell Biol 14:1920–1928.

26. Smith A, Ward MP, Garrett S. 1998. Yeast PKA represses Msn2p/Msn4p-dependent gene expression to regulate growth, stress response and glycerol accumulation. EMBO J 17:3536–3546. http://dx.doi.org/10.1093/emboj/17.13.3536.

27. Borges-Walmsley M, Walmsley AR. 2000. cAMP signalling in pathogenic fungi: control of dimorphic switching and pathogenicity. Trends Microbiol 8:133–141. http://dx.doi.org/10.1016/S0966-842X(00)01698-X.

28. Madhani HD, Fink GR. 1998. The control of filamentous differentiation and virulence in fungi. Trends Cell Biol 8:348–353. http://dx.doi.org/10.1016/S0962-8924(98)01298-7.

29. Coccetti P, Alberghina L, Vanoni M. 2010. Glucose signaling-mediated coordination of cell growth and cell cycle in Saccharomyces cerevisiae. Sensors (Basel) 10:6195–6240. http://dx.doi.org/10.3390/s10066195.
kinase A negatively regulates conidia formation by the tangerine pathotype of Alternaria alternata. World J Microbiol Biotechnol 29:289–300. http://dx.doi.org/10.1007/s11274-012-1182-3.

40. Zhao W, Panepinto JC, Fortwendel JR, Fox L, Oliver BG, Askew DS, Rhodes JC. 2006. Deletion of the regulatory subunit of protein kinase A in Aspergillus fumigatus alters morphology, sensitivity to oxidative damage, and virulence. Infect Immun 74:4865–4874. http://dx.doi.org/10.1128/IAI.00565-06.

41. Harren K, Brandhoff B, Knodler M, Tudzynski B. 2013. The high-affinity phosphodiesterase BcPde2 has impact on growth, differentiation and virulence of the phytopathogenic ascomycete Botrytis cinerea. PLoS One 8:e78525. http://dx.doi.org/10.1371/journal.pone.0078525.

42. Ramanujam R, Naqvi NI. 2010. PdeH, a high-affinity cAMP phosphodiesterase, is a key regulator of asexual and pathogenic differentiation in Magnaporthe oryzae. PLoS Pathog 6:e1000897. http://dx.doi.org/10.1371/journal.ppat.1000897.

43. Song Q, Johnson C, Wilson TE, Kumar A. 2014. Pooled segregant sequencing reveals genetic determinants of yeast pseudohyphal growth. PLoS Genet 10:e1004570. http://dx.doi.org/10.1371/journal.pgen.1004570.

44. Sonneborn A, Bockmuhl DP, Gerads M, Kurpanek K, Sanglard D, Ernst JF. 2000. Protein kinase A encoded by TPK2 regulates dimorphism of Candida albicans. Mol Microbiol 35:386–396. http://dx.doi.org/10.1046/j.1365-2958.2000.01705.x.

45. Lee N, D’Souza CA, Kronstad JW. 2003. Of smuts, blasts, mildews, and blights: cAMP signaling in phytopathogenic fungi. Annu Rev Phytopathol 41:399–427. http://dx.doi.org/10.1146/annurev.phyto.41.052002.095728.

46. Lafon A, Seo JA, Han KH, Yu JH, d’Enfert C. 2005. The heterotrimeric G-protein Gsn(B(a)-SfaD(b)-GpgA(c)) is a carbon source sensor involved in early cAMP-dependent germination in Aspergillus nidulans. Genetics 171:71–80. http://dx.doi.org/10.1534/genetics.105.040584.

47. Fuller KK, Richie DL, Feng X, Krishnan K, Stephens TJ, Wikenheiser-Brokamp KA, Askew DS, Rhodes JC. 2011. Divergent protein kinase A isoforms coordinately regulate conidial germination, carbohydrate metabolism and virulence in Aspergillus fumigatus. Mol Microbiol 79:1045–1062. http://dx.doi.org/10.1111/j.1365-2958.2010.07509.x.

48. Sarkar S, Dalgaard JZ, Millar JB, Arumugam P. 2014. The Rim15-endosulfine-PP2Acdc55 signaling module regulates entry into gametogenesis and quiescence via distinct mechanisms in budding yeast. PLoS Genet 10:e1004456. http://dx.doi.org/10.1371/journal.pgen.1004456.