Cross talk between the Cell Wall Integrity and Cyclic AMP/Protein Kinase A pathways in Cryptococcus neoformans

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Recommended Citation
Donlin, Maureen J.; Upadhya, Rajendra; Gerik, Kimberly J.; Lam, Woei; VanArendonk, Laura G.; Specht, Charles A.; Sharma, Neil K.; and Lodge, Jennifer K., "Cross talk between the Cell Wall Integrity and Cyclic AMP/Protein Kinase A pathways in Cryptococcus neoformans." mBio. 5,4. e01573-14. (2014).  
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2014. Cross Talk between the Cell Wall Integrity and Cyclic AMP/Protein Kinase A Pathways in *Cryptococcus neoformans*. mBio 5(4):. doi:10.1128/mBio.01573-14.

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Cross Talk between the Cell Wall Integrity and Cyclic AMP/Protein Kinase A Pathways in Cryptococcus neoformans

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ABSTRACT Cryptococcus neoformans is a fungal pathogen of immunocompromised people that causes fatal meningitis. The fungal cell wall is essential to viability and pathogenesis of C. neoformans, and biosynthesis and repair of the wall is primarily controlled by the cell wall integrity (CWI) signaling pathway. Previous work has shown that deletion of genes encoding the four major kinases in the CWI signaling pathway, namely, PKC1, BCK1, MKK2, and MPK1 results in severe cell wall phenotypes, sensitivity to a variety of cell wall stressors, and for Mpk1, reduced virulence in a mouse model. Here, we examined the global transcriptional responses to gene deletions of BCK1, MKK2, and MPK1 compared to wild-type cells. We found that over 1,000 genes were differentially expressed in one or more of the deletion strains, with 115 genes differentially expressed in all three strains, many of which have been identified as genes regulated by the cyclic AMP (cAMP)/protein kinase A (PKA) pathway. Biochemical measurements of cAMP levels in the kinase deletion strains revealed significantly less cAMP in all of the deletion strains compared to the wild-type strain. The deletion strains also produced significantly smaller capsules than the wild-type KN99 strain did under capsule-inducing conditions, although the levels of capsule they shed were similar to those shed by the wild type. Finally, addition of exogenous cAMP led to reduced sensitivity to cell wall stress and restored surface capsule to levels near those of wild type. Thus, we have direct evidence of cross talk between the CWI and cAMP/PKA pathways that may have important implications for regulation of cell wall and capsule homeostasis.

IMPORTANCE Cryptococcus neoformans is a fungal pathogen of immunocompromised people that causes fatal meningitis. The fungal cell wall is essential to viability and pathogenesis of C. neoformans, and biosynthesis and repair of the wall is primarily controlled by the cell wall integrity (CWI) signaling pathway. In this study, we demonstrate that deletion of any of three core kinases in the CWI pathway impacts not only the cell wall but also the amount of surface capsule. Deletion of any of the kinases results in significantly reduced cellular cyclic AMP (cAMP) levels, and addition of exogenous cAMP rescues the capsule defect and some cell wall defects, supporting a direct role for the CWI pathway in regulation of capsule in conjunction with the cAMP/protein kinase A pathway.

Cryptococcus neoformans is a fungal pathogen of immunocompromised people that causes an estimated 1 million infections each year among HIV-positive patients globally, resulting in 600,000 deaths annually (1). Much of the disease burden occurs in sub-Saharan Africa, where deaths from cryptococcal infections may exceed those from tuberculosis in some areas (1). Cryptococcal infections can be successfully treated with antifungal agents, but the mortality rate remains 15 to 30%, even in the context of antiviral treatments for HIV (2–4). The closely related species Cryptococcus gattii can infect immunocompetent people and animals. Although C. gattii is more common in Australia, it received global attention in 1999 when it emerged on Vancouver Island in Canada and has since spread into other areas of the Pacific Northwest (5–7).

Infection by C. neoformans occurs upon inhalation of spores or desiccated yeast cells, which can then disseminate to the brain and cause fatal meningitis (reviewed in references 8, 9, and 10). C. neoformans rapidly establishes an infection in lung alveoli, where low iron availability and increased carbon dioxide levels induce the formation of a polysaccharide capsule on the surface of the cryptococcal cell. The C. neoformans capsule has been shown to be protective against phagocytosis and oxidative stress as well as reducing the T-cell immune response (11, 12). The capsule is a key virulence factor, and strains with disruptions or deletions of capsule-related genes are usually avirulent or demonstrate attenuated virulence in murine models of infection (reviewed in reference 13).

C. neoformans is a soilborne pathogen found ubiquitously in...
the environment of temperate zones that can also infect and persist in mammalian hosts. Thus, *C. neoformans* must be able to grow under a wide range of pHs and temperatures and be able to cope with a variety of exogenous stresses secreted by other soil organisms or mammalian host cells. The ability to survive in such diverse environments requires that the cell be able to sense and process multiple signals from the environment that result in activation of various signaling cascades to allow adaption to and growth under different conditions (reviewed in reference 14).

The cryptococcal cell wall is vital for maintaining cell morphology and forms the scaffold for capsule attachment. Cell wall homeostasis is maintained by the cell wall integrity (CWI) pathway, which has 4 core kinases, protein kinase C (Pkc1), bypass of protein kinase C (Bck1), mitogen-activated kinase kinase (Mkk2), and mitogen-activated protein kinase (Mpk1), all of which are necessary for a fully functional cell wall. The primary kinase for this pathway is Pkc1, a diacylglycerol-activated protein kinase C essential for responding to a variety of cell wall stresses and whose deletion results in severe cell wall defects, reduced melanin, and disrupted capsule (15, 16). Strains with a deletion of the *BCK1* or *MKK2* gene show increased sensitivity to cell wall stressors and high temperature as well as delayed melanin formation (17). Deletion of the gene encoding the putative terminal kinase in the cell wall integrity pathway, *MPK1*, results in attenuated virulence (18) and has been shown to reduce virulence when deleted in *C. gattii* (19). Previous studies of the CWI pathway have used phosphorylation of the terminal kinase, Mpk1, as a marker for activation of the pathway (18). We have demonstrated that in response to nitrosative or oxidative stress, *PKC1* is required for phosphorylation of the terminal kinase, Mpk1 (16). However, in a *pck1Δ* strain, Mpk1 is still phosphorylated in response to heat shock, but not when the *BCK1* or *MKK2* gene is deleted (20), suggesting that inputs into this signaling cascade can bypass some of the core kinases and still result in activation of the pathway. We hypothesize that this pathway is likely to interact with other signaling cascades, such as the HOG1 and cyclic AMP (cAMP)/protein kinase A (PKA) pathways that respond to various exogenous stresses. To address this hypothesis, we used RNA sequencing to examine the genome-wide expression differences between the wild type and deletions in three of the core CWI kinases, *BCK1*, *MKK2*, and *MPK1*. We find strong evidence of cross talk between the cAMP/PKA and CWI pathways based on the genes differentially expressed in the kinase deletion strains. We demonstrate that deletion of any of the three kinases results in significantly decreased cAMP levels and reduced surface capsule and that exogenous cAMP can partially rescue the capsule- and cell wall-related defects of the *bck1Δ*, *mkk2Δ*, and *mpk1Δ* strains.

### RESULTS

**Impact of CWI kinases on the transcriptome.** The expression profiles of the three kinase deletion strains (*bck1Δ*, *mkk2Δ*, and *mpk1Δ* strains) were compared to wild-type *C. neoformans* KN99a MATa (KN99a) when grown at 30°C in yeast extract-peptone-dextrose (YPD) medium plus 1 M sorbitol to an optical density (OD) of 1.0. We initially included a deletion of the *PKC1* gene in the experiment, which necessitated the use of sorbitol to act as a stabilizer (16). The RNA expression data revealed that the *pck1Δ* strain was aneuploid, and thus, it was excluded from further analyses. Overall, 1,064 genes showed statistically significant differential expression with a corrected *P* value cutoff of <0.05 (Table 1; see Table S2 in the supplemental material) (21). More genes were differentially expressed in the *bck1Δ* strain (627 genes) than in the *mkk2Δ* (511 genes) and *mpk1Δ* (453 genes) strains. Of the 1,064 differentially expressed genes, 653 genes were found in only one of the three strains with a fairly even distribution: 244 genes were unique to the *bck1Δ* strain, 203 were unique to the *mkk2Δ* strain, and 206 were unique to the *mpk1Δ* strain (Fig. 1).

There were 116 transcripts differentially expressed in all three of the deletion strains, including genes involved in carbohydrate metabolism, cell wall biogenesis, transport, and signaling (see Table S3 in the supplemental material). Of the 116 genes, 115 were in concordance among the three mutant strains, with 71 upregulated genes and 44 downregulated genes compared to the wild type. The one gene that was not in concordance was a gene encoding a hypothetical protein of unknown function. We identified 10 of the

### TABLE 1 Number of differentially expressed genes

| Strain(s)                          | No. of genes | Up† | Down† | No. of unique genes | Total | Up  | Down |
|------------------------------------|--------------|-----|-------|---------------------|-------|-----|------|
| *bck1Δ* strain                     | 627          | 340 | 287   | 244                 | 171   | 73  |
| *mkk2Δ* strain                     | 511          | 121 | 390   | 203                 | 27    | 176 |
| *mpk1Δ* strain                     | 453          | 278 | 175   | 206                 | 127   | 79  |
| *bck1Δ* and *mkk2Δ* strains        | 164          | 39  | 123   |                     |       |     |
| *bck1Δ* and *mpk1Δ* strains        | 103          | 85  | 15    |                     |       |     |
| *mkk2Δ* and *mpk1Δ* strains        | 28           | 12  | 11    |                     |       |     |
| *bck1Δ*, *mkk2Δ*, and *mpk1Δ* strains | 116      | 44  | 71    |                     |       |     |

† For genes found in more than one strain, they were listed as upregulated (Up) or downregulated (Down) only if the direction of the expression difference was concordance.
115 genes as related to cell wall or capsule homeostasis, reflecting the importance of these kinases working in concert to maintain cell wall integrity (CWI).

Differential expression of cell wall- and capsule-related genes. Among all of the differentially expressed transcripts, we identified 29 genes that are known or predicted to be involved in cell wall biogenesis, cell wall regulation, or capsule synthesis (Table 2). Six of the eight chitin synthase genes, CHS1, CHS4, CHS5, CHS6, CHS7, and CHS8, show altered expression in two or more of the kinase deletion strains (Table 2). The CHS1, CHS4, and CHS5 genes show altered expression in all three deletion strains, with CHS1 upregulated and CHS4 and CHS5 showing decreased expression. A deacetylase gene, FPD1, for which no function has yet been identified (22) was downregulated in all three deletion strains, suggesting a possible adaptive response to the cell wall stress induced by the deletions. The KRE6 gene, which is involved in β-1,6-glucan synthesis (23), was modestly upregulated in the bck1Δ strain, but KRE61, a homolog of KRE6 with no known function, was highly repressed in all three deletions, again suggesting a possible adaptive response or regulation of this gene by the CWI pathway. Of the nine capsule-related genes that are differentially expressed, seven are changed in the bck1Δ strain, but only one (CAP59) is found in all three deletion strains, precluding a significant role for the CWI pathway in transcriptional regulation of capsule biosynthesis. Although CAP59 has been associated mostly with capsule defects, it may have a role in general secretion, rather than a capsule-specific role (24).

Reduced chitin levels in the CWI kinase deletion strains. All of the deletion strains had significant cell wall phenotypes, which likely affect cellular chitin and chitosan levels. We determined the chitin and chitosan content of the cell walls, and all three had significantly more chitin and significantly less chitosan than did the wild-type KN99a strain (Fig. 2). The chitin synthase gene, CHS3, responsible for the majority of chitosan synthesis during vegetative growth was unchanged in these deletion strains, as were two of the three chitin deacetylase genes. Three chitin synthase genes, CHS1, CHS4, and CHS5, had altered expression in all three of these deletion strains (Table 2). Previous work on the CHS genes revealed no phenotypes when CHS1 was deleted, although CHS1 transcript could be detected in vegetatively growing cells (25). Strains with deletion of either CHS4 or CHS5 have reduced chitin and increased chitosan content, but otherwise had no other in vitro cell wall phenotypes (25). These data suggest a possible role for CHS1, CHS4, and/or CHS5 in maintaining cell wall morphology but one that is dependent on the CWI kinases. Previous work has demonstrated an important role for chitin oligomers in

### Table 2: Cell wall- or capsule-related genes

| Gene type and Broad ID | Annotation | Log2 fold changes | Reference(s) |
|------------------------|------------|------------------|--------------|
|                        |            | bck1Δ/WT         | mkk2Δ/WT     | mpk1Δ/WT     | |
| Cell wall-related genes |            | strains          | strains      | strains      | |
| CNAG_00261             | MPN10 putative mannoprotein | 0.43            |           |           | |
| CNAG_00546             | CHS4 chitin synthase activity | −1.22          | −1.33      | −1.01       | 25 |
| CNAG_00914             | KRE6 β-glucan synthase | 0.42            |           |           | 23 |
| CNAG_01230             | CDA2 chitin deacetylase | 0.61            | 0.61       |           | 22 |
| CNAG_01234             | SCO71 similar to S. cerevisiae spore wall assembly protein | −1.07          | 1.81       |           | |
| CNAG_01341             | MP11 putative mannose-6-phosphate isomerase | 0.87            |           |           | |
| CNAG_02071             | BNI4 scaffold protein | 0.67            |           |           | |
| CNAG_02217             | CHS7 chitin synthase | 1.19            | 1.15       | 1.15       | 25 |
| CNAG_02225             | EXG1 cellulase | 1.11            | 0.61       | 1.11       | 51 |
| CNAG_03099             | CHS1 chitin synthase | 0.66            | 0.87       | 1.22       | 25 |
| CNAG_03223             | MPN6 putative mannoprotein | −1.30          | −1.25      | −1.35       | |
| CNAG_03345             | SSD1 translational repressor | −0.63          |           |           | 17 |
| CNAG_03465             | LAC1 laccase melanin synthesis | 0.07            | −1.18      | −0.66       | 52 |
| CNAG_03782             | MPN11 putative mannoprotein | 0.68            |           |           | |
| CNAG_05663             | SCW1 similar to S. cerevisiae cell wall integrity protein | 0.37           | 0.55       |           | |
| CNAG_05818             | CHS5 chitin synthase | −1.46           | −1.31      | −1.34       | 25 |
| CNAG_06291             | FPD1 polysaccharide deacetylase | −0.68          | −1.19      | −0.66       | 22, 51 |
| CNAG_06487             | CHS6 chitin synthase | 0.51            | 0.50       | 0.50       | 25 |
| CNAG_06835             | KRE61 β-glucan synthase | −1.33           | −2.79      | −1.03       | 23 |
| CNAG_07499             | CHS8 chitin synthase | 0.59            |           | −0.56       | 25 |

Capsule-related genes

| Gene type and Broad ID | Annotation | Log2 fold changes | Reference(s) |
|------------------------|------------|------------------|--------------|
| CNAG_00600             | CAP60 capsule-associated protein | 0.81            |           |           | 53 |
| CNAG_00721             | CAP59 capsule-associated protein | 0.75            | 0.67       | 0.33       | 54 |
| CNAG_01172             | PBX1 parallel β-helix repeat protein | 0.35            | 0.35       | 0.35       | 55 |
| CNAG_01371             | CRC2 regulator of G-protein signaling | 0.46            |           |           | 56, 57 |
| CNAG_01654             | CAS34 capsule structure protein | 0.56            |           |           | 58 |
| CNAG_02581             | CAS33 capsule-associated protein | 0.39            |           |           | 59 |
| CNAG_03735             | CAP4 glycosyltransferase | 0.57            | 0.56       | 0.56       | 58 |
| CNAG_05081             | PDE1 phosphodiesterase | −1.07           | 0.49       | 0.49       | 60 |
| CNAG_07554             | CAP10 glycosyltransferase | 0.59            |           |           | 61 |

* Broad ID: Broad identification or locus tag.
* The log2 fold changes in the level of expression for the bck1Δ, mkk2Δ, and mpk1Δ deletion strains compared to that of the wild-type (WT) strain are shown.

Reference(s)
capsule attachment (26, 27). However, the source of the chitin for the oligomers has not been determined. It is plausible that CHS1, CHS4, and/or CHS5 may play a role in producing the chitin necessary for capsule attachment.

Overlap of differentially expressed genes with other stress-responsive signaling pathways. Because of the cell wall and stress phenotypes associated with the CWI kinase deletion strains, we compared our differentially expressed gene lists with those generated from deletions in genes that regulate the cAMP/PKA pathway (28), the Hog1 stress pathway (29), and capsule synthesis (30–32). There is a substantial overlap in genes identified as differentially expressed in all of these studies, which is expected given that these gene lists include several hundred to thousands of genes. We narrowed the search to examine the overlap of genes differentially expressed in all three of our deletion strains with these other data sets (see Table S3 in the supplemental material). We found the greatest overlap (34 and 56 genes, respectively) with genes dependent on HOG1, a mitogen-activated protein (MAP1)-type kinase involved in osmoregulation (33) and SSK1, a response receiver protein that modulates Hog1 activity (34). We found substantial overlap (38 genes) with RIM101-dependent genes (31), with genes dependent on NRG1 (31 genes) (32) and with genes dependent on SKN7 (27 genes), another response receiver protein that regulates sensitivity to Na\(^+\) ions (34). Out of the 115 genes differentially expressed in all three CWI kinase deletion strains were 10 genes that have a known or predicted role in cell wall or capsule biosynthesis or regulation. Of the 10 genes, 6 genes overlap with the genes of a skn7Δ strain, 5 overlap with those of a hog1Δ strain (29), and 5 overlap with those of a nrg1Δ strain (32) (Table S3). Although these high-throughput experiments were conducted under different conditions, the genes differentially expressed in various deletion strains suggest a central role for these genes in response to perturbation of the different signaling pathways and potential mechanisms of cross talk between the pathways.

Reduced intracellular cAMP in CWI kinase deletion strains. Recent work has demonstrated the importance of the RIM101 transcription factor in the cAMP/PKA-dependent regulation of capsule production, defining a novel interaction between the Rim and PKA signaling pathways in C. neoformans (30). PKA1 activates the transcription factor NRG1, leading to the transcriptional activation of genes directly involved in capsule assembly (35). The Hog1 kinase is known to be a negative regulator of capsule synthesis in serotype A (33), a process that requires CAMP. In addition, the gene encoding Smg1, identified as a suppressor of Gpa1, the G alpha subunit that functions in CAMP signaling (36), was significantly repressed in all three CWI kinase deletion strains. The overlap between genes differentially expressed in the kinase deletion strains and those differentially expressed in gene deletion strains related to the PKA/cAMP pathway led us to ask if loss of the CWI kinases might negatively impact cellular cAMP levels. We measured CAMP levels in the three deletion strains and wild-type KN99a during log-phase growth in YPD medium. These experiments were done on two separate days, with three replicates for each strain. Since we observed the differential gene expression under log growth in nutrient-rich conditions and not in response to stress, we wanted to measure the CAMP levels under similar conditions. The kinase deletion strains, bck1Δ, mkk2Δ, and mpk1Δ strains, all showed significantly less CAMP compared to the KN99a wild-type strain (Fig. 3A). The experiments do not address the effect of cAMP in response to stress; however, the significant decrease in cAMP levels among all three deletion strains provides strong evidence for an impact on basal CAMP activity.

We tested whether the addition of exogenous cAMP could mitigate the sensitivity of the deletions to SDS, calcofluor white, and Congo red. Exogenous CAMP almost completely rescues the sensitivity to SDS for bck1Δ, mkk2Δ, and mpk1Δ strains after 5 days (Fig. 3B), but it has a lower effect on sensitivity to calcofluor white and does not rescue sensitivity to Congo red (data not shown). It is possible that the different stresses activate the CWI and cAMP/PKA pathways by different mechanisms, with various degrees of overlap between the activating mechanisms. An alternative explanation may be that cell membranes are more permeable in the presence of SDS. CAMP does not readily cross cell membranes, and the fact that we saw an effect with SDS but not with Congo red may reflect increased permeability in the presence of SDS, which does not happen with Congo red treatment.

Capsule defect in the CWI kinase deletion strains. To further investigate the cross talk between the CAMP/PKA and CWI pathways, we examined phenotypes associated with disrupted CAMP levels, specifically, capsule formation when grown in capsule-inducing low-iron medium (LIM) (37). When the deletion strains were grown in LIM, all three had visibly reduced capsule com-
pared to wild-type KN99a (Fig. 4A and C), and measurement of the capsule diameters showed significantly reduced capsule diameters for bck1∆, mkk2∆, and mpk1∆ strains compared to the wild-type KN99a strain (Fig. 4B and C and Table 3). The addition of 10 mM cAMP to the medium increased the size of the capsule in all three deletion strains to wild-type levels while having essentially no effect on the KN99a strain (Fig. 4B and C and Table 3). These data point to an important, and previously unknown, role for the CWI kinases in regulation of cAMP levels. It suggests that production of cAMP is dependent on a functioning CWI pathway, as disruption of the pathway leads to decreased cAMP levels and causes impairment of capsule induction in LIM.

**Analysis of shed capsule in the CWI kinase deletion strains.**

The defect in the increase of capsular polysaccharide in the mutant strains under capsule-inducing conditions suggests that the disruption of the CWI pathway affects the biosynthesis of the capsule, secretion of the capsule material, or attachment of the secreted capsule to the fungal cell wall. To differentiate between these possible explanations, we collected the shed capsular material from the wild-type and mutant strains. Secreted capsular material corresponding to an equal number of yeast cells was resolved on an agarose gel, transferred to a nylon membrane, and probed to determine the amount and relative size of the capsular material, including 29 cell wall- or capsule-related genes (Table 2) and 115 genes with concordant differential expression in all three strains (Table S3). These data are consistent with a significant adaptive response of the cell to the loss of the CWI kinases.

We hypothesized that disruption of three core kinases in the CWI pathway affects signaling in other pathways that impact cell wall and capsule homeostasis and looked for overlap between the 115 genes showing differential expression in all three kinase deletion strains (see Table S3 in the supplemental material), including 29 cell wall- or capsule-related genes (Table 2) and 115 genes with concordant differential expression in all three strains (Table S3). These data are consistent with a significant adaptive response of the cell to the loss of the CWI kinases.

**DISCUSSION**

Eukaryotic cellular signaling cascades receive inputs from several proteins simultaneously and then balance the signals to generate an appropriate response. One of the kinases in the CWI pathway, PKCI, plays a central role in the response to various cell wall-perturbing agents and production of virulence factors, capsule, and melanin (15, 16). However, the CWI pathway can be induced by some stresses, such as heat shock, in a PKCI-independent manner (20). To explore possible alternative pathway connections or cross talk, we determined the global transcription response to the loss of three other CWI kinases, BCK1, MKK2, and MPK1. We found that over 1,000 genes were differentially expressed in one or more of the deletion strains (see Table S2 in the supplemental material), including 29 cell wall- or capsule-related genes (Table 2) and 115 genes with concordant differential expression in all three strains (Table S3). These genes are consistent with a significant adaptive response of the cell to the loss of the CWI kinases.

We observed a loss of surface capsule with deletion of the CWI kinases and restoration of the surface capsule in those strains with addition of exogenous cAMP (Fig. 4). This is the first experimental evidence of a direct connection between the CWI pathway and...
capsule regulation in *C. neoformans*. The reduced capsule does not appear to be due to a defect in synthesis or secretion but is more likely due to a defect in attachment to the cell wall, as we did not observe a significant difference in the amount of shed capsule between the wild-type and kinase deletion strains (Fig. 5). The nature of this defect is not clear, but it is known that α-glucan and chitin oligomers or chitin-like structures are required for capsule attachment (26, 27, 38). The CWI kinase deletion strains have reduced chitin/chitosan ratio compared to wild-type cells (Fig. 2), and a similarly reduced chitin/chitosan ratio was also observed in *chs4Δ* and *chs5Δ* strains (25). Expression of both *CHS4* and *CHS5* was downregulated in all three kinase deletion strains (Table 2); however, neither the *chs4Δ* nor *chs5Δ* strain had a measurable capsule defect when grown in LIM (data not shown). A third chitin synthase gene, *CHS1*, was upregulated in all three deletion strains (Table 2), but deletion of *CHS1* has no discernible cell
three genes, only one, CNAG_05290 which encodes SPt3, a sub-

CNAG_07775 (see Table S3 in the supplemental material). Of the
three genes were CNAG_01103, CNAG_05290, and

were differentially expressed in all three CWI deletion strains; the
CWI kinases may play antagonistic roles in the regulation of cell

deletion strains. This raises the possibility that

/H9004

1.18

mpk1

ratio, and two chitin synthase genes,

/H9004

1.19

mkk2

interestingly, the

NaCl but insensitive to SDS, calcofluor white, or Congo red. More
kinase deletion strains. The

significantly different phenotypic characteristics compared to the CWI

strains. The

C. neoformans

encodes SPt3, a sub-
unit of the SAGA transcriptional regulatory complex seems likely
to have a role in cell wall or capsule regulation (32, 39). The
CNAG_05290 transcript for the putative transcription factor,
SPt3, is upregulated in an ada2Δ strain at 37°C with CO2,

compared to the wild type (32), but no further characterization of
this putative transcription factor has been published.

The regulation of capsule production in

C. neoformans

is very complex. Capsule synthesis is responsive to iron and CO2
levels via the cAMP/PKA signaling pathway (reviewed in reference 13),
and the downstream changes in capsule biosynthetic and trafficking
gene expression are controlled by at least five different transcription
factors, which are also responsive to a number of other proteins (30, 32, 35, 40–42). Therefore, the hypothesis that the
CWI pathway might have a role in the regulation of capsule pro-
duction is plausible. One possible mechanism of capsule regulation
is that the CWI kinases and some subset of chitin synthases
interact to regulate the synthesis of the chitin oligomers that are
necessary for capsule attachment (26, 27). However, experimentally
discerning the mechanism of that regulation is beyond the
scope of this study.

In previous studies, deletions of

C. neoformans

genes with homology to regulators of the

Saccharomyces cerevisiae

CWI pathway,

ROM2, LRG1, and

SIT4

(reviewed in reference 43) resulted in
moderate to severe cell wall-related phenotypes and increased
sensitivity to cell wall stressors (17). However, we saw no differential
expression of these genes in any of the CWI kinase deletion
strains, nor did we observe differential expression of the regulators of
the HOG pathway, SKN7, SSK1, and TCO1 or TCO2 (33, 34) in
the kinase deletion strains. However, we did observe considerable
overlap between genes differentially expressed in the CWI kinase
deletion strains with genes that are differentially expressed in
response to the deletion of the stress-responsive genes

HOG1, SSK1,

and

SKN7

(29, 33, 34). The lack of differences in expression of genes previously identified as critical for stress response may reflect the fact that regulation of their activity occurs primarily via
protein modifications, not by transcriptional changes. We also
conducted our expression analysis of the CWI kinase deletion
strains under nutrient-rich conditions in the absence of exoge-
"nous stress. It is possible that if the CWI kinase deletion strains
were exposed to an external stress, we would observe transcriptional changes in some of these other pathway regulators.

In summary, we have demonstrated a direct connection be-
tween the CWI and cAMP/PKA pathways in the regulation of
intracellular cAMP levels. These data support a role for the CWI
pathway in the regulation of surface capsule. The mechanisms and
transcription factors, which mediate the cAMP and capsule re-
response to the CWI pathway, remain to be elucidated.

### TABLE 3 Average induced capsule and cell diameters

| Strain or genotype | Capsule diam | P value | Capsule diam | P value | Cell diam | Cell diam |
|--------------------|--------------|---------|--------------|---------|-----------|-----------|
| KN99a              | 2.05 ± 0.61  | <0.001  | 2.83 ± 0.79  | 1.00    | 6.01 ± 1.10| 6.16 ± 1.77| 0.45 |
| bck1Δ              | 1.19 ± 0.31  | <0.001  | 2.28 ± 0.39  | 1.00    | 4.92 ± 0.61| 5.58 ± 0.87| <0.001 |
| mkk2Δ              | 1.24 ± 0.24  | <0.001  | 1.83 ± 0.51  | 0.78    | 4.56 ± 0.72| 5.22 ± 0.74| <0.001 |
| mpk1Δ              | 1.18 ± 0.31  | <0.001  | 1.48 ± 0.53  | 1.00    | 4.36 ± 0.69| 5.39 ± 1.2 | <0.001 |

* a: Capsule and cell diameters of cells grown in LIM alone or in LIM plus cAMP are reported as averages ± standard deviations of at least 100 measurements.
 b: P value comparing the capsule diameters of deletion strains to that of the WT strain (KN99a) in low-iron medium (LIM) only.
 c: P value comparing the capsule diameters between deletion strains and WT in LIM plus cAMP.
 d: P value comparing the cell diameters for each strain with and without cAMP in the medium.

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**FIG 5** The levels of capsule shed by the bck1Δ, mkk2Δ, and mpk1Δ strains were similar to the level shed by the wild-type KN99a strain. The wild-type, bck1Δ, mkk2Δ, mpk1Δ, and cap59Δ strains were grown in YPD medium for 5 days, and the number of cells was determined by absorption at 650 nm. The supernatants were collected, and the cell counts were normalized before loading. The gel was transferred to a blot and probed with the SC2 anti-GXM monoclonal antibody.
Chitin and chitosan levels. Strains and media. Wild-type (WT) C. neoformans var. grubii strain KN99 (serotype A, MATa) was used in this study (see Table S1 in the supplemental material). Strains containing deletions in BCK1 or MKK2 in the KN99 MATa (KN99a) background were generated by overlap PCR (44) using the primers listed in Table S1. A strain deleted for MPK7 in the KN99 MATa background was generated by amplification of the mpk7Δ cassette (pNAT-STMI50) from strain K3, containing mpk7Δ in the H99 MATa background (generously provided by Joseph Heitman, Duke University) (45). Each fragment was biolistically transformed into strain KN99a (46), and isolates were selected and verified by PCR screening as described previously (17) utilizing the primers listed in Table S1. Southern blotting was performed, using the selectable marker as a probe to rule out ectopic integrations.

RNA preparation and sequencing. The KN99a, bck1Δ, mkk2Δ, and mpk7Δ cells were grown for 3 days on plates containing yeast extract-peptone-dextrose (YPD) medium supplemented with 1 M sorbitol. A 50-ml flask of YPD medium supplemented with 1 M sorbitol was inoculated and grown overnight at 30°C with shaking (300 rpm). Cells were diluted to an optical density at 650 nm (OD650) of 0.004 and grown over-night to an OD650 of 0.75 to 1.0. A strain with a deletion in the PKC1 gene, which required sorbitol to grow, was originally part of this study, but it was later determined to have an aneuploid chromosome. It was excluded from further analyses (data not shown). RNA was prepared from three biological replicates using the Qiagen RNeasy plant minikit (Qiagen, Valencia, CA) with minor modifications (details of methods available upon request). RNA quality was assessed on a formaldehyde agarose gel, and the ratio of 25S/18S rRNA was quantified using ImageQuant software (GE Healthcare Biosciences, Pittsburgh, PA). Total RNA (10 μg) from each sample was used as starting material to prepare sequencing libraries with the Illumina mRNA sequencing sample preparation kit (Illumina, San Diego, CA) following the manufacturer’s instructions. Samples were bar-coded and sequenced on a single lane of an Illumina HiSeq sequencing system to generate nondirectional, single-ended 50-bp reads. The library preparation and RNA sequencing were performed by the Genome Technology Access Center at Washington University (http://gtac.wustl.edu). The bar code sequences were trimmed to 42 bp, and quality-filtered reads were mapped to the H99 reference genome sequence prepared by the Broad Institute (http://www.broadinstitute.org/annotation/genome/cryptococcus_neoformans/MultiHome.html) using Bow tie 2.1.0 as implemented in the TopHat-Cufflinks suite (21, 47).

Differential gene expression. The C. neoformans H99 transcript file prepared by the Broad Institute was used as the reference. Transcript files for each biological replicate were generated from each alignment file using Cufflinks, merged into a single transcript file using Cuffmerge, and differentially expressed transcripts were identified using Cuffdiff (21). Genes were considered differentially expressed if P values were <0.05 after Benjamini-Hochberg correction for multiple testing.

Capsule measurements. Strains were grown in low-iron medium [LIM plus ethylenediamine-N,N′-bis(2-hydroxyphenylacetic acid) (EDDA)] (37) with and without exogenous 10 mM CAMP for 4 days at 30°C. All mutant strains were compared to the wild-type KN99a strain. Capsule-induced strains were suspended in a 1:4 India ink-H2O solution and photographed on an Olympus BX61 microscope at a magnification of ×60. Cell diameters (one including the capsule and one excluding it) were measured for a minimum of 100 cells per strain using SlideBook, version 5.0. Capsule length was calculated as the difference between the radii obtained from the diameters. All values were averaged, and comparisons were considered significant if the P value was <0.05 using a one-way analysis of variance (ANOVA) with a Dunnett’s posthoc test (one-tailed comparison; < control).

Chitin and chitosan assays. The cellular chitin and chitosan levels were determined as previously described (22). Samples were divided into two aliquots. One aliquot was treated with acetic anhydride to measure chitin plus chitosan. The other aliquot was left untreated to measure total chitin. Chitosan was estimated from the difference between the two measurements.

Measurement of cAMP. Overnight cultures of the WT and the deletion strains were diluted in 50 ml YPD medium to an OD650 of 0.05 and grown for 20 h at 30°C with shaking (300 rpm). Cells were harvested, washed, and resuspended in MES-EDTA buffer (10 mM morpholineethanesulfonic acid [MES], 0.1 mM EDTA, pH 6.0). Cells were counted using a hemocytometer, centrifuged, and resuspended at a concentration of 3 × 10⁷ cells/ml. Cells (0.5 ml) were lysed by bead beating in 2.5% trichloroacetic acid at 4°C with 0.5-mm glass beads for 1 min, followed by a 2-min rest, for a total of 4 cycles. Crude lysates were centrifuged at 20,800 × g for 15 min. Lysates were extracted four times with water-saturated diethyl ether and centrifuged for 20,800 × g at 4°C for 2 min between extractions, frozen in liquid nitrogen, and lyophilized overnight. The lyophilized samples were suspended in 0.5 ml of 0.1 M HCl, and cAMP assays were performed according to Sigma cAMP enzyme immunoassay kit (catalog no. CA200; Sigma, St. Louis, MO). Assays were performed twice with three technical replicates. CAMP concentrations were calculated for individual samples, and statistical significance was determined using a one-way ANOVA with Dunnet’s posthoc test (two-tailed test) using IBM SPSS Statistics (version 20).

SDS viability assays. Overnight cultures of wild-type strain KN99a and bck1Δ, mkk2Δ, and mpk7Δ strains in YPD medium were diluted to an OD650 of 1.0 with phosphate-buffered saline (PBS). Tenfold serial dilutions were plated on YPD medium plus 0.01% SDS and YPD medium plus 0.01% SDS and 10 mM CAMP. The plates were incubated at 30°C for up to 5 days and photographed. The CAMP concentration used was based on levels determined to be deleterious, but not lethal, to the mutant strains.

Immunoblotting of the secreted capsule. Immunoblotting of the shed capsular material was performed as described previously (48). Briefly, conditioned medium for each strain corresponding to an equal number of yeast cells grown in YPD medium was passed through a 0.22-μm filter, mixed with DNA loading dye, and separated on a 6% agarose gel using Tris-acetic acid-EDTA buffer (pH 8.0). The gel was transferred onto a positively charged nylon membrane by capillary transfer and immunoblotted with 1 μg/ml of antigulactosylxylosylolaminan (anti-GXM) 3C2 antibody (generously provided by Thomas Kozel, University of Nevada) (49).

Microarray data accession number. RNA sequences/microarray data were deposited in the NCBI GEO database and assigned accession number GSE57217.

SUPPLEMENTAL MATERIAL
Supplemental material for this article may be found at http://mbio.asm.orglookup/suppl/doi:10.1128/mBio.01573-14/-/DCSupplemental.

Table S1, DOCX file, 0.1 MB.
Table S2, PDF file, 0.3 MB.
Table S3, PDF file, 0.1 MB.

ACKNOWLEDGMENTS
We thank Ping Wang for technical assistance with cAMP assays. David Gohara for technical assistance with analysis of the RNA sequence data, and Nicole Gilbert for helpful discussions and manuscript review. We thank the Genome Technology Access Center in the Department of Genetics at Washington University School of Medicine for help with genomic analysis.

This work was supported by the National Institutes of Health grant R01 AI50184 to J.K.L. The Genome Technology Access Center is partially supported by NCI Cancer Center support grant P30 CA91842 to the Site- man Cancer Center and by ICTS/CTS grant UL1TR000448 from the National Center for Research Resources (NCRR), a component of the National Institutes of Health (NIH) and NIH Roadmap for Medical Research.

This publication is solely the responsibility of the authors and does not necessarily represent the official view of NCRR or NIH.
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