The SrkA Kinase Is Part of the SakA Mitogen-Activated Protein Kinase Interactome and Regulates Stress Responses and Development in Aspergillus nidulans

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Fungi and many other eukaryotes use specialized mitogen-activated protein kinases (MAPK) of the Hog1/p38 family to transduce environmental stress signals. In Aspergillus nidulans, the MAPK SakA and the transcription factor AtfA are components of a central multiple stress-signaling pathway that also regulates development. Here we characterize SrkA, a putative MAPK-activated protein kinase, as a novel component of this pathway. ΔsrkA and ΔsakA mutants share a derepressed sexual development phenotype. However, ΔsrkA mutants are not sensitive to oxidative stress, and in fact, srkA inactivation partially suppresses the sensitivity of ΔsakA mutant conidia to H2O2, tert-butyl-hydroperoxide (t-BOOH), and menadione. In the absence of stress, SrkA shows physical interaction with nonphosphorylated SakA in the cytosol. We show that H2O2 induces a drastic change in mitochondrial morphology consistent with a fission process and the relocation of SrkA to nuclei and mitochondria, depending on the presence of SakA. SakA-SrkA nuclear interaction is also observed during normal asexual development in dormant spores. Using SakA and SrkA S-tag pulldown and purification studies coupled to mass spectrometry, we found that SakA interacts with SrkA, the stress MAPK MpkC, the PPT1-type phosphatase AN6892, and other proteins involved in cell cycle regulation, DNA damage response, mRNA stability and protein synthesis, mitochondrial function, and other stress-related responses. We propose that oxidative stress induces DNA damage and mitochondrial fission and that SakA and SrkA mediate cell cycle arrest and regulate mitochondrial function during stress. Our results provide new insights into the mechanisms by which SakA and SrkA regulate the remodelling of cell physiology during oxidative stress and development.

We have proposed that when life was confronted with oxidative stress, cells evolved mechanisms not only to defend against reactive oxygen species (ROS) but also to use this ancestral form of stress to regulate their own growth and differentiation (1, 2). Indeed, the regulated production of ROS by enzymes of the NADPH oxidase family (NOX) is essential for sexual differentiation in Aspergillus nidulans (3) and Neurospora crassa and for polar growth and cell fusion in N. crassa (4), and NOX enzymes play multiple signaling functions in other fungal (5–10), animal, and plant species (11). However, little is known about ROS perception and the mechanisms by which ROS exert their signaling functions.

The use of phosphorylation systems to perceive oxidative stress and other types of environmental stress is conserved in bacteria, plants (12), and fungi (13). The fission yeast Schizosaccharomyces pombe uses a multistep phosphorylation composed of the Mak2/3 sensor histidine kinases, Mpr1 HPt protein, and Mcs4 response regulator to transduce H2O2 stress signals to the Spc1 (also known as Sty1) mitogen-activated protein kinase (MAPK) cascade (14, 15). S. cerevisiae Hog1 and mammalian p38 MAPKs, which are also involved in stress sensing. Phosphorylated S. cerevisiae Hog1 and mammalian p38 MAPKs, which are also involved in stress sensing. Phosphorylated Spc1 phosphorylates the transcription factor Atf1, which mediates most of the transcriptional responses regulated by Spc1, including the induction of many genes involved in the antioxidant response (14). Spc1 also promotes meiosis by inducing the expression of the transcriptional factor Ste11, a regulator involved in sexual development (16). Under osmotic stress, Spc1 interacts with and phosphorylates the Ser/Thr kinase Srk1, which results in a transitory G2/M cell cycle arrest (17), while srk1 overexpression inhibits the cell cycle arrest in G1, under nitrogen starvation. In addition, Srk1 has a regulatory role in meiosis, as null srk1 mutants enter meiosis earlier than the wild-type strain (18).

In S. cerevisiae, the Rck2 kinase, homologous to Srk1, is phosphorylated by Hog1 under oxidative and osmotic stress conditions (19, 20). However, Δrck2 mutants are sensitive to oxidative but not to osmotic stress (19), and a deletion of rck2 suppresses the lethality caused by overactivation of the Hog1 pathway (20). Upon osmotic stress, Rck2 phosphorylates the elongation factor EF2 and transiently attenuates protein synthesis (20, 21). In the pathogenic fungus Candida albicans, ΔacaRck2p mutants are not sensitive to osmotic stress but show cell wall instability and attenuated virulence in mice (22). Although filamentous fungi contain homologous stress-sens-
AtfA, which activates the catalase genes catA and catB. Indeed, SakA accumulates in conidia in an AtfA-dependent way, is phosphorylated for germination. Therefore, SakA phosphorylation for germination. Accordingly, SakA interacts with the b-Zip transcription factor AtfA, which activates the catalase genes catA and catB during oxidative stress (25) and both ΔsakA and ΔatfA mutants are sensitive to oxidative stress. SakA was also identified as HogA (26) and together with AtfA was shown to be involved in gene regulation in response to osmotic stress (27). In many other filamentous fungi, SakA orthologs have been found to be involved in osmotic and/or oxidative-stress resistance and the regulation of development and/or pathogenicity (28–32). A. nidulans sakA-null mutants also show premature sexual development and produce asexual spores (conidia) that progressively lose their viability (24, 25). Indeed, SakA accumulates in conidia in an AtfA-dependent way, is phosphorylated during conidium development, and requires dephosphorylation for germination. Therefore, SakA phosphorylation regulates the transition between latency (spore) and growth (germination), in a process that is conserved in other fungi (25).

As not all the mechanisms by which SakA phosphorylation regulates stress responses, sexual development, and spore functions are known, this work was aimed at identifying other SakA targets that could mediate these and other SakA functions. We report that SrkA, a member of the CAMK (Ca2+/calmodulin-dependent kinase) family, is a novel component of the SakA stress MAPK pathway and identify potentially new protein targets for both kinases. We demonstrate that SakA and SrkA show functional and physical interactions and that the SakA–SrkA pathway plays differential roles in the antioxidant response and development. Furthermore, we show that H2O2 induces mitochondrial fragmentation, consistent with a fission process and the relocation of SakA to nuclei and mitochondria, depending on the presence of SakA.

### MATERIALS AND METHODS

#### Strains, media, and growth conditions.

*Aspergillus nidulans* strains used in this work are listed in Table 1. All strains were grown at 37°C in 1% glucose minimal medium containing nitrate as the nitrogen source (33) and needed supplements. For oxidative-stress sensitivity experiments, H2O2, tert-butyl-hydroperoxide (t-BOOH), menadione, paraquat, and methyl-glyoxal were filter sterilized and added to agar medium before solidification. ΔsakA, ΔsrkA, and ΔsakA ΔsrkA strains in a veA+ background were obtained from sexual crosses with strain FGSCA4 (Table 1). The presence of the veA+ allele was confirmed by PCR using genomic DNA from selected progeny and the primers veA+ forward and veA+ reverse, as reported elsewhere (34). For sexual induction, 1 × 107 conidia were homogeneously inoculated onto plates containing 2% glucose agar minimal medium, and plates were sealed with masking tape and incubated at 37°C. The number of cleistothecia per square centimeter was determined as previously described (24).

#### Deletion of the srkA gene and tagging of SakA and SrkA.

A cassette for srkA gene deletion was obtained by double joint PCR (35). 5′ and 3′ srkA fragments were amplified with primers 5′SrkAFor–5′SrkARev and 3′SrkAFor–3′SrkARev, respectively (see Table 2 for primer sequences). The *A. fumigatus* pyrG marker was amplified from plasmid PFNO3 with primers pyrGforward and pyrGreverse (36). These three fragments were used in a fusion PCR with primers 5′Nest AN4483 and 3′Nest AN4483. The final 4,600-bp 5′SrkA-AfpyrG–3′SrkA product was purified and used to transform *A. nidulans* ΔnkuA strain 1155 by protoplast fusion (37). Twenty pyrG+ transformants were obtained, and 10 were analyzed by PCR restriction analyses to confirm the elimination of srkA. Strain TRJ4 was chosen for further analysis and crossed with strain CLK43 to get rid of the ΔnkuA mutation. Strain CRJ2 was confirmed by PCR restriction analysis and used in further experiments (see Fig. S2 in the supplemental material). A similar strategy was used to generate SrkA::GFP, SrkA::S-tag, and SakA::S-tag constructs. For the SrkA C-terminal GFP construct (38), 5′ and 3′ PCR fragments were obtained with primers GSP1AN4483–GSP2AN4483 and GSP3AN4484–GSP4AN4483, respectively. The *A. fumigatus* pyrG cassette was amplified with primers GPF1AN4483–GPF2AN4483, using plasmid PFNO3 as the template. The final PCR product was obtained with primers AN4483N51 and AN4483N52 and the resulting 6,747-bp

| Strain | Genotype | Reference or source |
|--------|----------|---------------------|
| CLK4A  | pabaA1 yA2 veA1 | 24 |
| FGSCA4 | biA1      | FGSC |
| TOL1   | pabaA1 yA2 ΔargB::trpCΔB ΔsakA::argB trpC801 veA1 | Fungal Genetics Stock Center |
| 1155   | pyrG89 pyroA4 ΔnkuA::bar veA1 | This work; 1155 transformed with PCR construct srkA-gfp-AfpyrG |
| TRJ1   | pyrG89 pyroA4 srkA::GFP ΔnkuA::bar veA1 | This work; 1155 transformed with PCR construct srkA-s-tag-AfpyrG |
| TRJ2   | pyrG89 pyroA4 srkA::GFP ΔnkuA::bar veA1 | This work; TRJ1 transformed with construct bi-pyroA-gpdA-h2A-mrfp-bio |
| TRJ4   | pyrG89 pyroA4 ΔsakA::AfpyrG ΔnkuA::bar veA1 | This work; CRJ3 transformed with the construct ph2-h2A-mrfp-ptra |
| TRJ5   | pyrG89 pyroA4 srkA::GFP bio-pyroA::gpdA::h2A::mrfp-bio ΔnkuA::bar veA1 | This work; 1155 transformed with construct bi-pyroA-gpdA-h2A-mrfp-bio |
| TRJ6   | pabaA1 yA2 ΔargB::trpCΔB ΔsakA::argB srkA::GFP ph2A::h2A::mrfp-ptra trpC801 veA1 | This work; progeny from TRJ1 × CLK43 |
| TRJ7   | pyrG89 pyroA4 bio-pyroA::gpdA::h2A::mrfp-bio ΔnkuA::bar veA1 | This work; progeny from TRJ1 × TOL1 |
| CRJ2   | pabaA1 yA2 ΔsrkA::AfpyrG veA1 | This work; progeny from TOL1 × TRJ4 |
| CRJ3   | pabaA1 yA2 ΔargB::trpCΔB ΔsakA::argB srkA::gfp trpC801 veA1 | This work; progeny from TOL1 × TRJ4 |
| CRJ5   | pabaA1 yA2 ΔsakA::argB ΔsrkA::AfpyrG veA1 | This work; progeny from TOL1 × TRJ4 |
| TFL22  | pyrG89 pyroA4 sakA::s-tag::AfpyrG ΔnkuA::bar veA1 | This work; 1155 transformed with PCR construct sakA-s-tag-AfpyrG |
| TRJ6   | pabaA1 yA2 ΔsakA::argB | This work; progeny from TOL1 × FGSCA4 |
| CRJ7   | pabaA1 yA2 ΔsrkA::AfpyrG | This work; progeny from CRJ2 × FGSCA4 |
| CRJ8   | pabaA1 yA2 ΔsakA::argB ΔsrkA::AfpyrG | This work; progeny from CRJ5 × FGSCA4 |
| CRJ9   | pabaA1 yA2 | This work; progeny from CRJ2 × FGSCA4 |

| Strains, media, and growth conditions. | A. nidulans strains used in this work are listed in Table 1. All strains were grown at 37°C in 1% glucose minimal medium containing nitrate as the nitrogen source (33) and needed supplements. For oxidative-stress sensitivity experiments, H2O2, tert-butyl-hydroperoxide (t-BOOH), menadione, paraquat, and methyl-glyoxal were filter sterilized and added to agar medium before solidification. ΔsakA, ΔsrkA, and ΔsakA ΔsrkA strains in a veA+ background were obtained from sexual crosses with strain FGSCA4 (Table 1). The presence of the veA+ allele was confirmed by PCR using genomic DNA from selected progeny and the primers veA+ forward and veA+ reverse, as reported elsewhere (34). For sexual induction, 1 × 107 conidia were homogeneously inoculated onto plates containing 2% glucose agar minimal medium, and plates were sealed with masking tape and incubated at 37°C. The number of cleistothecia per square centimeter was determined as previously described (24).

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SakA interacts with SrkA and other Proteins

For 2 min (Invitrogen, Carlsbad, CA) as reported elsewhere (TRJ1 and TOL1, was transformed with the fragment ph2A::h2A::mrfp-sakA-GFP fragment was used to transform strain 1155. Plasmid = Primer Sequence 5’ to 3’

| Primer               | Sequence 5’ to 3’               |
|---------------------|--------------------------------|
| 5’SrkA For          | TCCGACGCGGAGGAGGTCAAG           |
| 5’SrkARev+t         | GGTGAAAGGACATTGTGTGAGGCTGTGCTACATGGAAAGG |
| 3’SrkAFor+t         | GATCACTGTGCTCCTCTEACAGGCGCGCCATCTTCTTCGATC |
| 3’SrkA Rev          | AGGCGGGCTGCTCTGTGTCG           |
| 5 Nest AN4483       | GTTGGAGGACAGCCACAGG             |
| 3 Nest AN4483       | TTTAACGCGAGACAGCAG              |
| AN4483 GSP1         | ATGGCCCTGCTCCTCGACCTTTTCC      |
| AN4483 GSP2         | CATGCGAGGCTGCTCTGTGACCTTTC    |
| AN4483 GSP3         | GGCTCTAGCTAGCTTGATAGGTTTC     |
| AN4483 GSP4         | TTCAAGTGTGAAACCGGTTCATCATGACC |
| AN4483 GFP1         | AGAGACAGATTCAAGTCGTAGAGGCGGCGCTGAGG |
| AN4483 GFP2         | GTGAACTCTATTAGCAATGCTGAGGACGGCGCTGAGG |
| AN4483Nes1          | CCTCCTCTTCTACCATGAG             |
| AN4483Nes2          | TACCGCAATTGCGGATTAC             |
| GspiSakA            | GCGCGGCTCAGCTACAGGGATTACCTATGATG |
| Gsp2SakA            | TGTGTTATCCCATAAAGGTGCGGGCT     |
| Gsp3SakA            | AGGCCCAAACTGCGGTGGATGGGCGCGCT |
| Gsp4SakA            | CATGCAATGCGTGACATTGACGCGGCG  |
| Gfp1SakA            | GGAGCGGGGCTCTACCAAGGCGCTGAGGCGCTGAGG |
| Gfp2SakA            | AGGCGGCCGGCTCAGCTGGATGGGCGGGCT |
| 5’Nest-sakA         | TGGAGCGGTAAACGGGTCC            |
| 3’Nest-sakA         | TCAGCAAGACATCCCAAGG           |
| pyr6Forward         | GCCTCAAACATTGCTGTCAC          |
| pyrGReverser        | GTCTGAGAGGACAGCTGTTGAGGACGGCTGAGG |
| veA+ forward        | TACGGCAATTGCGGATTAC            |
| veA+ reverse        | TCTCCTCCTGCGGTCTCAC          |

DNA primers used in this study

S-tag protein purification and identification by LC-MS/MS. To precipitate S-tag-labeled proteins, protein crude extracts were prepared from cultures incubated with or without H2O2 as follows. A total of 2.5 × 10^6 spores were used to inoculate 200 ml of liquid culture and incubated for 12 h at 37°C, with shaking. After this, the culture was treated with 10 mM H2O2 for 10 min or left untreated. Protein purification was performed as reported previously (40). Briefly, samples were frozen with liquid nitrogen, ground, and resuspended in 5 ml of protein extraction buffer (50 mM Tris [pH 7.5], 100 mM KCl, 10 mM MgCl2, 0.1% NP-40, 10% glycerol, 20 mM β-glycerophosphate, 2 mM NaN3, 5 mM NaF, 0.5 mM phenylmethysulfonyl fluoride [PMF], 1 mM benzamidine, 1 mM EGTA, 1 mM diithiotheritol [DTT], and 2X protease inhibitors [Roche]). After two centrifugations at 4°C, the supernatant was transferred to a new tube and incubated at 4°C with 300 μl of S-protein agarose slurry (Novagen) per 100 mg of protein in a rotary shaker for 2 h. After this, S-protein beads were collected by centrifugation and incubated at 4°C with 300 μl of S-protein agarose slurry (Novagen) per 100 mg of protein in a rotary shaker for 2 h. After this, S-protein beads were washed twice and resuspended in 1 ml of protein extraction buffer. Protein extraction was performed twice using 1 ml of extraction buffer. Purified supernatant was incubated with 50 μl of 3× Laemmli gel loading dye, boiled at 95°C for 10 min, and stored at −80°C until used. Liquid chromatography-tandem mass spectrometry (LC-MS/MS) protein identification was done as described by Bayram et al. (42).

Immunoblot detection. A total of 2.5 × 10^6 spores were used to inoculate 200 ml of liquid medium and incubated at 37°C with shaking for 12 h. After this, mycelium was filtered, rinsed with distilled water, frozen with liquid nitrogen, and ground with a mortar. Mycelial powder was resuspended in protein extraction buffer (see above) and used as total crude extract or processed for protein purification (see above). Thirty micrograms of protein was used for immunoblotting as reported elsewhere (24), using anti-Hog1 (y-215) polyclonal (Santa Cruz Biotechnology), anti-phospho-p38 MAP kinase (Cell Signaling Technology), and anti-S-tag (ICL Laboratories) antibodies. Horseradish peroxidase (HRP)-conjugated secondary antibodies (Zymed Laboratories) and Pierce Super-
Signal chemiluminescent substrate (Thermo Scientific) were used for detection.

RESULTS
The elimination of the srkA gene does not result in oxidative-stress sensitivity, and its inactivation partially suppresses oxidative-stress sensitivity of ΔsakA conidia. As a strategy to detect other components of the SakA MAPK pathway in filamentous fungi, we focused on the A. nidulans gene AN4483, encoding a homolog of S. pombe Srk1 MAPK-activated protein kinase, which acts downstream of the SakA ortholog Sty1/Spc1 (18). AN4483 encodes a 611-amino-acid protein that shows 59% identity to Srk1 and 49% identity to S. cerevisiae Rck2. A protein alignment of AN4483 with other members of the CAMK (Ca2+/calmodulin-dependent kinase) family, including C. albicans CaRck2 and proteins from N. crassa and from other aspergilli is shown in Fig. S1 in the supplemental material. All these proteins contain a kinase-regulatory domain, with a glycine-rich sequence not found in any other kinases (43), as well as a putative MAPK-binding site near the C terminus. In addition, we determined that AN4483 and the homologs from filamentous fungi contain a highly conserved N-terminal putative mitochondrial targeting sequence (see Fig. S1 in the supplemental material). A recent publication identified the AN4483 gene as cmkD and reported that its deletion did not produce any obvious phenotype (44). Here, we propose renaming the A. nidulans AN4483 protein SrkA, based on the fact that S. pombe Srk1 is the best-characterized ortholog of this family. In assessing SrkA function, we first deleted the srkA gene by homologous recombination gene replacement. We transformed the nkuA-lacking strain 1155 using a double-joint PCR strategy and the A. fumigatus pyrG gene as a selective marker (see Fig. S2A in the supplemental material). Ten pyrG + transformants, out of 20 transformants obtained, were subjected to PCR and restriction analysis to confirm srkA elimination (see Fig. S2B in the supplemental material), and ΔsrkA strain 26 was renamed TRJ4 and chosen for further characterization. The most evident phenotype in all ΔsrkA strains was the production of high numbers of Hülle cells and a derepression of sexual development (see Fig. S2; also, see Fig. S3 and S6 in the supplemental material). When strain TRJ4 was crossed to strain CLK43, the linkage between this phenotype and the pyrG gene marker was confirmed. Furthermore, the deletion of the srkA gene using the A. fumigatus pyrA gene also produced a sexual-derepression phenotype that was linked to this marker (data not shown).

As a first step to determine if SrkA acted downstream of SakA, we compared the sensitivities of ΔsakA and ΔsrkA single and double mutants to different types of stress. We found that in contrast to ΔsakA strains, ΔsrkA mutants were not sensitive to the cell wall-stressing compound calciofluor (see Fig. S4 in the supplemental material). Likewise, ΔsakA but not ΔsrkA mutants were partially resistant to the fungicide fludioxonil (see Fig. S5 in the supplemental material), which induces constitutive activation of SakA (25). These results indicate that the potential role of SrkA as a downstream component of the SakA pathway does not involve the regulation of cell wall integrity or fludioxonil sensitivity.

As SakA regulates antioxidant responses through the transcription factor AtfA (25) and ΔsakA and ΔatfA mutants are both sensitive to oxidative stress, we evaluated SrkA function during oxidative stress. For this, we grew spores and mycelia from ΔsakA and ΔsrkA single and double mutants in the presence of H2O2, the organic peroxide tert-butyl-hydroperoxide (t-BOOH), menadione, paraquat (Fig. 1), and methylglyoxal (not shown). As shown in Fig. 1A, ΔsakA mutant conidia were sensitive to the oxidative-stress-causing agents H2O2, t-BOOH, and menadione, while ΔsrkA mutant mycelia were more sensitive only to t-BOOH (Fig. 1B). In contrast, ΔsrkA conidia displayed a pattern of resistance to all these compounds that was similar to the one shown by the wild-type strain. Unexpectedly, conidia from ΔsakA ΔsrkA mutants showed higher resistance to H2O2 (4.5 mM), t-BOOH (0.5 mM), and menadione (60 μM) than the ΔsakA single mutant (Fig. 1A). Mycelia from single and double mutants showed similar patterns of resistance to these compounds, except that the ΔsakA ΔsrkA mutant displayed decreased resistance to 0.5 mM t-BOOH. These results indicate that the MAPK SakA and the CAM kinase Srk1 play antagonistic roles in the response of conidia to the oxidative stress caused by H2O2, t-BOOH, and menadione.

SrkA represses sexual development independently of SakA. The SakA MAPK not only regulates stress responses but also represses sexual development (24, 25). To determine if SrkA mediated this repression, we followed sexual development of ΔsakA and ΔsrkA single and double mutants and determined the number of fruiting bodies or cleistothecia. Results in Fig. 2 show that, as reported before (24), a ΔsakA mutant produces higher numbers of cleistothecia than a wild-type (WT) strain. The ΔsrkA strain also developed more cleistothecia than the WT strain but not as many as the ΔsakA mutant. Notably, the ΔsakA ΔsrkA strain showed an additive phenotype, forming about 7 times more cleistothecia than the WT strain after 7 days of induction of sexual development.

The A. nidulans veA gene encodes a member of a protein family conserved in fungi which is required for cleistothecium formation (45) and regulation of secondary metabolism (42). As our laboratory strains contain a veA1 allele that results in higher production of conidia and lower numbers of cleistothecia (46), we also evaluated the ΔsakA and ΔsrkA sexual-derepression phenotypes in the presence of a wild-type veA allele. Results in Fig. S3 in the supplemental material show that in the veA + background, all strains produced much higher numbers of cleistothecia than equivalent veA1 mutants after 5 days of induction (Fig. 2). As before, ΔsakA and ΔsrkA mutants showed sexual-derepression phenotypes. In this case, the double mutant did not show an additive phenotype in the production of cleistothecia. However, there was a massive production of Hülle cells, suggesting that many structures initiate sexual development but some fail to complete the process and that SrkA repression of sexual development also occurs in a veA + background. These and the oxidative-stress sensitivity results (Fig. 1) indicate that SakA and SrkA regulate both the antioxidant response and sexual development and suggest antagonistic and non-antagonistic SakA-SrkA interactions during these two processes, respectively.

H2O2 induces mitochondrial fragmentation and a relocalization of SrkA that depends on the presence of SakA. In response to stress, SakA is phosphorylated and accumulates in the nucleus (25). To further explore SakA-SrkA interactions, we determined SrkA localization with and without oxidative stress. For this purpose, we generated strains in which srkA was replaced by a functional (see Fig. S6 in the supplemental material) srkA::GFP allele, in WT and ΔsakA genetic backgrounds. In addition, a H2A::RFP construction was introduced in these strains, as a nuclear marker. Results in Fig. 3 show that without H2O2, SrkA::GFP was excluded...
from nuclei and was found to be homogenously localized throughout the cytosol. Treatment with 30 mM H$_2$O$_2$ resulted in a clear accumulation of SrkA::GFP in nuclei and a redistribution of the nonnuclear signal. In the absence of SakA and H$_2$O$_2$, SrkA::GFP nonnuclear localization changed to a nonhomogenous pattern, characterized by the presence of tubular and small-vesicle structures. Notably, in this case H$_2$O$_2$ treatment did not result in SrkA::GFP nuclear accumulation, and instead, the protein was redistributed into round structures throughout the hyphae. These results indicate that SrkA translocates to the nucleus in response to oxidative stress and that both nuclear and nonnuclear localizations of SrkA are determined by the presence of the SakA protein. Since SakA becomes activated during asexual development, we decided to also detect the localization of SrkA in intact conidia. As shown in Fig. 3B, SrkA::GFP appears in a nonhomogenous vesicular pattern, and part of the fluorescence colocalizes with the H2A::mRFP nuclear signal. In a ΔsakA background, SrkA is no longer localized in the nucleus, and the protein appears to be localized mainly at the plasma membrane.

In the absence of SakA, the nonnuclear pattern of SrkA::GFP changed from homogenous to reticular structures that became granular after H$_2$O$_2$ treatment (Fig. 3A). A similar change from network and filaments to punctuate units has been reported to occur in mitochondria during ageing in *Podospora anserina* and *S. cerevisiae*, where decreased mitochondrial fission has been linked to extended life span (41). This led us to test if H$_2$O$_2$ can induce mitochondrial fission in *A. nidulans* and if SrkA could be partially localized in mitochondria, by using the red fluorescent dye MitoTracker to stain mitochondria in living cells treated with H$_2$O$_2$ or left untreated. Results in Fig. 4 show that, indeed, a 30-min treatment of the wild-type strain with H$_2$O$_2$ induced a drastic change in mitochondrial morphology, probably caused by a fission process, and a similar phenomenon was observed in strains containing SrkA::GFP, particularly when SakA was not present. As shown in Fig. 4 (bottom [arrowheads]), H$_2$O$_2$ induced very similar patterns of fragmentation for both SrkA::GFP and mitochondria, which colocalized in many but not all cases. To learn more about the kinetics of H$_2$O$_2$-induced mitochondrial fragmentation, we carried out a time course analysis. As shown in Fig. 5, in the absence of H$_2$O$_2$ the initial reticular mitochondrial morphology was preserved during the course of the experiment. In contrast, H$_2$O$_2$ induced mitochondrial fragmentation as early as 5 min, which became more evident after 15 min. We did not observe a recovery of the tubular mitochondrial morphology for as long as 2 h, sug-

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**FIG 1** ΔsakA mutants are not sensitive to oxidative stress, and the lack of srkA partially suppresses the H$_2$O$_2$ sensitivity of ΔsakA mutant conidia. (A) Conidia (1 × 10$^4$) from strains CLK43 (WT), TOL1 (ΔsakA), CR2 (ΔsakA), and CRJ5 (ΔsakA ΔsrkA) were inoculated on supplemented minimal medium plates containing hydrogen peroxide (H$_2$O$_2$), t-butyl-hydroperoxide (t-BOOH), or menadione at the indicated concentrations and incubated at 37°C for 4 days. (B) Mycelial plugs from strains CLK43, TOL1, CRJ2, and CRJ5 cut from the growing edge of 5-day colonies were transferred to plates containing the indicated compounds and incubated as for panel A. This experiment was repeated at least three times, with the same results.
gesting that this process is irreversible under these experimental conditions. These results indicate that H$_2$O$_2$ induces mitochondrial fragmentation and suggest that H$_2$O$_2$ also induces the partial localization of SrkA to mitochondria particularly when SakA is not present. This is consistent with the presence of a highly conserved mitochondrion-targeting signal in SrkA homologs from filamentous fungi (see Fig. S1 in the supplemental material). As fragmented mitochondria are often related to mitophagy, autophagy, and/or apoptosis, further research would be required to determine the possible involvement of SakA and SrkA in these processes.

**SrkA and SakA show physical interaction independently of SakA phosphorylation.** The above results suggest that without stress, SrkA interacts with SakA outside the nucleus when SakA is not phosphorylated and that SakA activation results in translocation of both proteins to the nucleus. To directly address this possibility, we generated strains in which either srkA or sakA genes were replaced by alleles that result in tagging of the proteins with the S-tag epitope (39). After confirming the strains and showing that S-tagging did not affect SrkA or SakA functions (see Fig. S6 and S7 in the supplemental material), we carried out protein pulldown experiments (see Materials and Methods) to identify the interaction patterns of both proteins by Western blot and mass spectrometry assays. Protein extracts were prepared from WT, SakA::S-tag, and SrkA::S-tag strains that were untreated or were treated with 10 mM H$_2$O$_2$ at different times. S-tag purified proteins were used for Western blot analysis using antibodies that specifically recognize phosphorylated SakA, nonphosphorylated SakA, or the S-tag. Results in Fig. 6 show that pulldown of SrkA::S-tag results in copurification of SakA only in the strain expressing SrkA::S-tag and not in a WT strain. Moreover, results show that this interaction occurs even in the absence of SakA phosphorylation (without H$_2$O$_2$). We showed before that nonphosphorylated SakA is excluded from nuclei in the absence of oxidative stress and that H$_2$O$_2$ treatment induces SakA phosphorylation and its translocation to the nucleus (25). Our results show that under nonstressing conditions, SrkA interacts physically with nonphosphorylated SakA, while oxidative stress leads to SakA phosphorylation and the localization of both proteins in the nucleus.

**Different sets of proteins interact with SakA and/or SrkA in the absence and in the presence of H$_2$O$_2$.** To confirm the physical interaction between SrkA and SakA and identify other SakA-interacting proteins, we decided to carry out reciprocal pulldown experiments using protein extracts from strains TFL22 and TRJ2, expressing SakA::S-tag and SrkA::S-tag, respectively, together with mass spectrometry analysis. Purified protein extracts were separated in an SDS-acrylamide gel and stained with silver reagent. As shown in Fig. 7A, lanes corresponding to extracts from SakA::S-tag and SrkA::S-tag have enriched bands corresponding to SakA and SrkA molecular masses of 45 and 70 kDa, respectively, while the WT extract shows only faint, unspecific bands. Proteins excised from the SDS gel were processed for mass-spectrometric analysis as reported elsewhere (42). After subtracting common proteins also detected in WT extracts, we used the Aspergillus genome database AspGD (47, 48), gene ontology terms, and manual annotation to identify and group the proteins that copurified with SakA or SrkA.

The proteins that copurified with SakA or SrkA before and after the H$_2$O$_2$ treatment are listed in Table S1 in the supplemental material. Overall, these results indicate that SakA interacts with 57 proteins, of which 21 were detected only after H$_2$O$_2$ treatment, 15 were detected only in the absence of H$_2$O$_2$, and 21 were common to both sets.

In the case of SrkA, the results suggest that SrkA interacts with 6 proteins without oxidative stress and with 50 proteins in response to H$_2$O$_2$ and that 5 of these proteins are common to both sets. Only 1 of the proteins (AcuN) that copurified with SrkA was specific to no H$_2$O$_2$ treatment. In contrast, 45 pro-
proteins were detected as interacting with SrkA only upon H\textsubscript{2}O\textsubscript{2} treatment (see Table S1 in the supplemental material). Considering SakA and SrkA results together, 14 of the proteins that copurified with SrkA only in the presence of H\textsubscript{2}O\textsubscript{2} were also found to copurify with SakA under H\textsubscript{2}O\textsubscript{2} conditions, suggesting that they represent specific H\textsubscript{2}O\textsubscript{2}-induced interactions. Likewise, the proteins recovered from H\textsubscript{2}O\textsubscript{2}-treated and untreated SakA::S-tag (21 proteins) and SrkA::S-tag (5 proteins) extracts might be considered constitutively associated with the SakA-SrkA protein complex.

**FIG 3** SrkA nuclear localization depends on the presence of SakA. (A) Conidia from strains TRJ7 (WT), TRJ5 (SrkA::GFP), and TRJ6 (SrkA::GFP/ΔsakA) were grown for 12 h in minimal medium at 37°C and then exposed to 30 mM H\textsubscript{2}O\textsubscript{2} for 30 min and observed *in vivo* using confocal spinning disc microscopy. (B) Intact conidia from strains TRJ7 (WT), TRJ5 (SrkA::GFP), and TRJ6 (SrkA::GFP/ΔsakA) were observed using confocal spinning disc microscopy.
SakA interacts with the SrkA kinase, the stress MAPK MpkC, the protein tyrosine phosphatase (PTP) PtpA, and other proteins that can be linked to SakA and SrkA functions. Among the proteins considered constitutively associated with SakA, 17 and 18 peptide sequences corresponding to SrkA (AN4483) were identified under no-stress and oxidative-stress conditions, respectively. Consistent with this, 10 and 12 SakA (AN1017) peptide sequences were identified in non-H$_2$O$_2$-treated and H$_2$O$_2$-treated SrkA extracts, respectively. These results confirm that SrkA is as a major SakA interactor even in the absence of H$_2$O$_2$ and validate our approach to identify SakA and SrkA interacting proteins.

Other proteins that copurified with SakA or SrkA include several potential interactors that can be clearly connected to the func-

FIG 4 H$_2$O$_2$ induces mitochondrial fragmentation and mitochondrial relocalization of SrkA. Strains CLK43 (WT), TRJ1 (SrkA::GFP), and CRJ3 (SrkA::GFP/ΔsakA) were incubated with MitoTracker for 5 min, treated with 30 mM H$_2$O$_2$ for 30 min or left untreated, and observed in vivo using epifluorescence microscopy. Arrowheads highlight some of the regions where Mitotracker and SrkA::GFP signals colocalize. Bar = 10 μm.
tions of these kinases. These comprise MpkC (AN4668), a stress MAPK homologous to SakA that, like SakA, is a substrate of the upstream MAPKK PbsB (46), and the PTP PtpA (AN6982), which is homologous to *S. pombe* PyP2, involved in dephosphorylation of SakA homolog StyI/Spc1 (49). Both MpkC and PtpA were found to be associated with SakA with and without oxidative stress. AN8269, AN6089, and AN2026 are three putative heat shock proteins identified in the SakA and/or SrkA interactomes (see Table S1 in the supplemental material). AN8269, found to be constitutively associated with SakA and SrkA, corresponds to chaperone HSP90, which plays signal transduction functions in many organisms and has been found to interact with Hog1 (50) and be involved in cell cycle progression in *C. albicans* (51).

Among the *H₂O₂*-specific proteins (Table 3), AN7254, an ortholog of the *S. cerevisiae* Cdc48 ATPase that regulates numerous cellular processes, including protein quality control, DNA repair, and the cell cycle (52), was identified as interaction partner of SakA and SrkA only in the presence of *H₂O₂*. Consistent with this, AN7254 is induced by conditions that result in SakA activation, such as osmoadaptation (53), farnesol treatment (54), and nutrient starvation (55).

ArtA (AN4501) was found as a SakA-interacting protein and AN5744 as a SrkA interaction partner. ArtA and AN5744 are two of three 14-3-3 signal transduction proteins present in the *A. nidulans* genome, and both are homologs of *S. pombe* Rad24/Rad25. Rad24 is directly related to Srk1 function in *S. pombe* (17), while ArtA is induced by *H₂O₂* in *A. fumigatus* and by compounds that induce DNA damage in *A. nidulans* (56).

In response to *H₂O₂*, SakA and SrkA were also found to be associated with other proteins involved in the response to different types of stress, such as the response to DNA damage, mRNA stability, and protein biosynthesis and mitochondrial function and energy metabolism (Table 3). We think most of these proteins are connected to SakA and SrkA functions (see Discussion).

**FIG 5** Time course of mitochondrial fragmentation induced by *H₂O₂* treatment. Mitochondria from wild-type strain CLK43 were stained with MitoTracker and treated with 30 mM *H₂O₂* or left untreated, and single hyphae were photographed every 5 min under epifluorescence microscopy. Arrowheads highlight early fragmented mitochondria.

**FIG 6** SakA and SakA interact independently of the SakA phosphorylation state. Mycelia from strains 1155 (WT) and TRJ2 (SrkA::S-tag) were treated with 10 mM *H₂O₂* for the indicated times or left untreated, immediately frozen with liquid nitrogen, and processed for S-tag protein purification as described previously (40). Samples (30 μg) were processed for immunoblotting using anti-phospho-P38 (α-P-SakA), anti-Hog1 (α Total SakA), and anti-S-tag (α S-tag) antibodies. A blot from the crude extracts using anti-Hog1 (α Total SakA) is included as a protein loading control.
In summary, we have demonstrated that SakA and SrkA show both functional and physical interactions and that the SakA-SrkA pathway plays differential roles in the antioxidant response and development. We have also shown that H$_2$O$_2$ induces mitochondrial fragmentation, consistent with a fission process, and the re-localization of SrkA to nuclei and mitochondria, depending on the presence of SakA. Moreover, we identified potentially new protein targets for SakA and SrkA, suggesting novel functions for these kinases.

**DISCUSSION**

SrkA inactivation partially suppresses the sensitivity of $\Delta$sakA mutant conidia to oxidative stress. Our results show that *A. nidulans* mutants lacking the CAMK SrkA are not sensitive to os-
motic, oxidative, or cell wall stress and that SrkA does not mediate the sensitivity to the fungicide fludioxonil. This is in contrast to what occurs in some other fungi, where SrkA orthologs are important in dealing with different types of stress. In \textit{S. cerevisiae}, \textit{hrk2} mutants are sensitive to oxidative stress (19). In \textit{Cryptococcus neoformans}, Hrk1 has Hog1-dependent and -independent functions and \textit{hrk1} mutants are resistant to fludioxonil and not affected in virulence (57). In \textit{C. albicans}, \textit{CaRck2} is required for cell wall stress resistance, although its kinase activity does not seem necessary for this function. In contrast, \textit{CaRck2} protein and kinase activity are required for normal virulence in mice (22). In \textit{S. pombe}, there is some controversy as to whether (17) or not (18) \textit{srk1} mutants are sensitive to osmotic stress. Nevertheless, part of our results seem more comparable to what has been found in this yeast, where Srk1 is a substrate of the MAPK StyI and upon different types of stress Srk1 translocates from the cytoplasm to the nucleus, in a StyI-dependent process (18). We found not only that SrkA is not required for stress resistance but also, more importantly, that its elimination results in partial rescue of the oxidative-stress sensitivity of \textit{sakA} strains. Based on this, and the fact that in response to H$_2$O$_2$ SakA and SrkA interact with proteins involved in cell cycle control and the DNA damage stress response, we propose that SrkA mediates a decreased survival response in response to oxidative stress (see below).

| Putative function and protein ID | Protein name and/or description | No. of peptides$^a$ |
|---------------------------------|---------------------------------|--------------------|
|                                 |                                 | SakA | SrkA |
| **Cell cycle/signal transduction** |                                 |      |      |
| AN7254                          | Protein with a conserved CDC48, cell division protein N-terminal domain | 3 | 2 |
| AN4501                          | ArtA, putative 14-3-3 protein | 2 |      |
| AN5744                          | Putative 14-3-3-like protein | 2 |      |
| **Histone/DNA damage response**  |                                 |      |      |
| AN0734                          | H4.1, histone H4.1 | 3 | 3 |
| AN3468                          | H2A.X, histone H2A | 2 | 2 |
| AN3469                          | H2B, histone H2B; core histone protein | 2 |      |
| **Protein biosynthesis/mRNA stability** |                                 |      |      |
| AN10416                         | Putative 60S ribosomal protein | 2 |      |
| AN1964                          | Ortholog of \textit{S. cerevisiae} RS6B and RS6A; polA-dependent expression | 3 |      |
| AN10681                         | Ortholog(s) has structural constituent of ribosome activity | 2 | 2 |
| AN10740                         | Has domain(s) with predicted structural constituent of ribosome activity | 2 |      |
| AN4475                          | Ortholog(s) has role in ribosomal large subunit assembly | 2 |      |
| AN4916                          | Ortholog(s) has role in ribosome biogenesis | 2 |      |
| AN2275                          | Ortholog(s) has structural constituent of ribosome activity | 2 |      |
| AN0843                          | Ortholog(s) has structural constituent of ribosome activity | 2 |      |
| AN4000                          | FabM protein with similarity to poly(A)-binding proteins | 2 |      |
| AN2932                          | AN2932, putative eukaryotic initiation factor 4A | 2 |      |
| AN5931                          | Putative ATP-dependent RNA helicase | 4 |      |
| **Energy metabolism/mitochondrial function** |                                 |      |      |
| AN2435                          | AcnA, putative ATP citrate synthase | 4 | 3 |
| AN9403                          | FdhC, putative pyruvate dehydrogenase (lipoamide) | 2 | 4 |
| AN9879                          | AlcA, Alcohol dehydrogenase with a role in two-carbon compound metabolism | 2 | 2 |
| AN6717                          | MdbA, putative mitochondrial malate dehydrogenase | 2 |      |
| AN4888                          | PdxA, putative pyruvate decarboxylase | 3 |      |
| AN8275                          | CitA, mitochondrial citrate synthase | 2 |      |
| AN1534                          | Putative F$_F$F$_A$-ATPase complex subunit | 2 |      |
| AN9340                          | TreA, \alpha-\alpha-trehalase with a role in trehalose hydrolysis | 2 | 2 |
| **Fatty acid metabolism**       |                                 |      |      |
| AN9408                          | FasB, fatty acid synthase, beta subunit | 2 |      |
| **Undeclassified**              |                                 |      |      |
| AN4463                          | Ortholog(s) has structural molecular activity | 2 |      |
| AN8870                          | Expression increased in salt-adapted strains | 2 | 2 |
| AN3804                          | Ortholog(s) has IgE binding activity | 2 | 2 |
| AN4865                          | Has domain(s) with predicted nucleic acid binding | 2 | 2 |
| AN7725                          | PyroA protein required for biosynthesis of pyridoxine | 2 | 2 |
| AN0745                          | Putative nucleolar protein | 2 | 2 |
| AN1551                          | BtgE putative beta-glucosidase with predicted role in degradation of glucans | 2 | 3 |

$^a$Number of peptides from each protein identified in the sample.
SrkA represses sexual development independently of SakA. Like the S. pombe Sty1-Srk1 pair, A. nidulans SakA-SrkA equivalent partners are involved in regulation of sexual development. However, the specific roles they play in each fungus are different. Sty1 elimination results in impaired sexual development and hyperactivation of meiosis only under nitrogen starvation conditions (18). Our results show that SakA as well as SrkA inactivation results in increased sexual differentiation in an additive way, indicating that SakA and SrkA use different pathways to repress sexual development. This, and the fact that SrkA elimination rescues the sensitivity of ΔsakA mutants to oxidative stress, indicates that SakA and SrkA interact in a complex, not completely epistatic fashion. Part of this complexity might be related to the fact that among the ascomycetes, only the aspergilli contain a second stress MAPK, called MpkC, which we identified here as a SakA interactor.

H₂O₂ induces a dramatic change in mitochondrial morphology and the relocalization of SrkA during oxidative stress, and asexual development depends on the presence of SakA. We have shown that H₂O₂ induces both a mitochondrial fragmentation consistent with a fission process and the relocalization of SrkA to nuclei and mitochondria. By analogy to what is known to occur in S. pombe (17, 58), nuclear SrkA would be involved in stress-induced cell cycle arrest. During A. nidulans asexual development, SakA is phosphorylated in conidia and partially localized in the nucleus, where it interacts with the transcription factor AtfA. More importantly, the dephosphorylation of SakA is necessary for spore germination to take place (25). Therefore, the SakA-dependent nuclear localization of SrkA during oxidative stress would be required for the regulation of cell cycle arrest and for the cell cycle arrest and dormancy of conidia. Such activation of the stress MAPK SakA during normal conidiophore and conidium development supports our long-standing view of development as a response to oxidative stress (1, 2).

A mitochondrial localization of yeast SrkA homologs has not been reported before. However, only the SrkA homologs from filamentous fungi contain a conserved mitochondrion-targeting signal (see Fig. S1 in the supplemental material). In addition, recent data show that Sty1 is partially localized in mitochondria (59), supporting a link between this MAPK pathway and mitochondrial function. The roles of SakA and SrkA in the regulation of mitochrondrial function are yet to be determined. However, this hypothesis is supported by the major role that SakA plays in responding to oxidative stress, together with the fact that H₂O₂ induces SakA phosphorylation, mitochondrial fragmentation, SrkA mitochondrial localization, and the interaction of SakA and/or SrkA with mitochondrial proteins (see below). Direct connections between MAPK signaling and mitochondrial dynamics have been reported very recently in mammalian cells, where stress-induced JNK phosphorylation of mitofusin MFN2, involved in mitochondrial fusion, and ERK2 phosphorylation of dynamin-related protein 1 (DRP1), required for mitochondrial fission, both result in mitochondrial fragmentation (60, 61).

SakA and SrkA interact with each other and with proteins involved in cell cycle regulation and DNA damage response. Our proteomic experiments not only confirmed SakA-SrkA interaction but also identified 33 proteins that potentially interact with SakA and/or SrkA upon oxidative-stress treatment. It is clear that these interactions need to be confirmed using other methods, as some could represent false positives. However, we discuss them in some detail because some of these proteins can be directly linked to SakA and SrkA functions, while others represent potential new targets involved in the response to different types of stress, such as the response to DNA damage, carbon or nitrogen limitation and regulation of the cell cycle. Functions that are all consistent with SakA roles in osmotic, oxidative, and nutrient starvation stress responses (24, 25).

The proteins that might be directly related to SakA and/or SrkA functions include the stress MAPK MpkC (AN4668) and the PTP PtpA (AN6982). In A. fumigatus, MpkC is required for the utilization of sorbitol and mannitol as sole carbon sources (62), and although A. nidulans ΔmpkC mutants do not show any clear phenotype (63), MpkC is the substrate of the SakA-upstream MAPKK PbsB (64). MpkC and SakA belong to the same family of stress MAPKs, and SrkA could also be a MpkC substrate. As MpkC was found to be continuously associated with SakA (stress and no stress), it is likely that in response to H₂O₂, MpkC could be translocated to the nucleus along with SakA. SakA and/or MpkC could be substrates of the PTP PtpA (AN6982), and although mutants lacking PtpA do not show any clear phenotype (65), they have not been characterized in detail yet.

Notably, AN5744 (SakA interacting) and AN4501 (ArtA; SakA interacting) correspond to 14-3-3 proteins homologous to S. pombe Rad24 and Rad25. In this yeast, the phosphorylation of Cdc25 by Srk1 causes Cdc25 binding to Rad24 (17), and in mammalian cells, protein phosphorylation by the functionally homologous kinase MK2 promotes interaction with different 14-3-3 proteins, some connected to the DNA damage response (66). In A. nidulans, the Cdc25 ortholog Nim1 also controls DNA damage checkpoint, regulating NimX (Cdc2 ortholog) activity (67). AN7254, another potential SakA interactor orthologous to the S. pombe cell cycle-regulatory protein Cdc48, could also be related to SakA and SrkA functions in cell cycle control. Upon H₂O₂ treatment, SakA and SrkA also interact with histones H2A.X and H4.1, and SrkA interacts with histone H2B (Table 3). Phosphorylation of H2AX is recognized as a universal epigenetic signal for DNA double-strand-break repair (68), and H4.1 is also associated with histone deposition and DNA damage repair. We have found that H₂O₂ can induce mitochondrial fragmentation, which in turn could induce an increased production of ROS. Either directly or indirectly, H₂O₂ can induce DNA damage. The oxidative-stress-induced interaction of SakA and SrkA with these histones suggests that these kinases function in chromatin remodeling and DNA repair during oxidative stress, which in turn might be related to SakA and SrkA functions in sexual development and meiosis.

SakA and SrkA interaction with proteins involved in mRNA stability and protein synthesis. Different SrkA homologs play central roles in regulation of mRNA stability and translation. In S. cerevisiae Rck2 attenuates global protein synthesis under stress conditions (20, 69). In mammalian cells MK2/3 regulates cytokine mRNA stability and translation (70), and the MAPK-activated protein kinase RSK2 orchestrates stress responses with cell survival and proliferation through the formation of stress granules. Silencing RSK2 reduces stress granule formation by blocking the recruitment of TIA-1 (an RNA-binding protein acting as a translation factor) to stress granules (71). In this context, it is interesting that SakA and/or SrkA interacts with proteins potentially involved in similar processes. Among these, AN5931 corresponds to a putative ATP-dependent RNA helicase, and FabM is a poly(A)-binding protein whose overexpression induces conidiation in A.
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SakA- and/or SrkA-interacting proteins involved in mitochondrial function and energy metabolism. In human mesenchymal stem cells, the SakA-homologous MAPK p38 mediates increased mitochondrial activity in an MK2-dependent manner, higher ROS levels, a persistent DNA damage response, DNA double-strand breaks (DSBs), and activation of the ATM pathway. This feedback loop seems necessary to stop the cell cycle and drive cells into senescence (75). Mitochondrial ROS are produced by partial O2 reduction in the respiratory chain or by damage and loss of membrane potential (76, 77). In the last case, the cell uses a retrograde signaling (RTG) from mitochondria to the nucleus to adjust metabolic and biosynthetic pathways and compensate for the loss of mitochondrial quality (78, 79). Hog1 activates the RTG pathway in yeast at the transcriptional level (80), but a direct interaction or regulation of mitochondrial proteins by this MAPK has not been reported. In this regard, it is interesting that H2O2 induces SakA phosphorylation, mitochondrial fragmentation, SrkA mitochondrial localization, and, as discussed here, the interaction of SakA and/or SrkA with proteins involved in mitochondrial function or carbon, nitrogen, or fatty acid metabolism.

In response to H2O2, SakA interacts with the mitochondrial proteins citrate synthase (AN2435) and MdhA (AN6717), a putative malate dehydrogenase downregulated upon shift from glucose to ethanol (81). These proteins are predicted to play a role in the trichloroacetic acid (TCA) cycle, being implicated in energy metabolism. Furthermore, SakA interacts constitutively with the aldehyde dehydrogenase AldA (AN0554) and during oxidative stress with the alcohol dehydrogenase AlcA, two enzymes required for ethanol utilization. As the aldA and aldld genes are normally subject to glucose repression, the presence of these proteins under our experimental conditions is somewhat unexpected. In addition, the fatty acid synthase alpha (FasA) subunit was associated with SakA with and without stress, while the beta (FasB) subunit was associated with SakA and SrkA upon H2O2 treatment. Fatty acid synthases are involved in the cytosolic NADPH-consuming synthesis of fatty acids.

SakA also interacts with two proteins involved in nitrogen assimilation, the nitrate reductase NiiA (AN1007) and the glutamate dehydrogenase GdhA (AN4376). GdhA is a critical enzyme linking fundamental metabolic pathways such as amino acid metabolism, TCA cycle, and glutathione biosynthesis. S. cerevisiae mutants lacking Gdh3 show accelerated chronological ageing and are hypersensitive to thermal and oxidative stress (82). In S. pombe, StyI is activated after nitrogen starvation and promotes meiosis through transcription factor AtfI (83), but again, a direct interaction or regulation of the enzymes involved in nitrogen metabolism has not been explored.

It is interesting that the abundance of 15 proteins that interact with SakA or SrkA after H2O2 exposure is altered by farnesol or menadione treatment (see Table S2 in the supplemental material), as these compounds induce the generation of ROS (84, 85) and provoke apoptosis and cell cycle arrest in yeasts and filamentous fungi (84, 86, 87). In fact, SakA mediates the induction of the dplA gene by farnesol, which encodes a putative dehydrin involved in conidium resistance to H2O2 (54).

Together, our results support a model in which part of the SrkA pool interacts with nonphosphorylated SakA in the cytosol preventing its accumulation in mitochondria, perhaps by masking its mitochondrial targeting signal. Under oxidative-stress conditions, phosphorylated SakA would phosphorylate bound SrkA, and the interacting proteins would translocate to the nucleus, while a nonnuclear (not bound to SakA) SrkA fraction would interact with stress proteins in the cytoplasm, accumulate in filamented mitochondria, and interact with proteins involved in mitochondrial function. In the absence of SakA, a larger portion of SrkA accumulates in mitochondria with or without oxidative stress. According to the Styl-Srk1 model (17, 58), SakA and SrkA will dissociate inside the nucleus; SakA will then interact with transcription factor AtfA and other proteins. SrkA will regulate cell cycle arrest through phosphorylation of Cdc25, allowing this protein to interact with the 14-3-3 protein ArtA or AN5744 in order to be excluded from the nucleus. Phosphorylated SrkA inside the nucleus would be prone to degradation.

According to this model, SakA and SrkA are part of an oxidative and general stress signal transduction pathway involved in regulation of the cell cycle, the DNA damage response, stability of mRNA and protein synthesis, and the regulation of energy metabolism and mitochondrial function. Our results provide new insights into the mechanisms of MAPK stress signaling and its connections to fungal development, opening new lines of research in this field.

ACKNOWLEDGMENTS

This work was funded by grants CB-2010-01-153256 from CONACYT, IN207913 from PAPIIT-UNAM, DFG-CONACYT Germany-México Collaboration Grant 75306 from CONACYT, and the Deutsche Forschungsgemeinschaft (DFG; Mexican-German research unit 1334). R. Jaimes-Arroyo is a Ph.D. student in the program Posgrado en Ciencias Biológicas from UNAM and recipient of a fellowship (229044) from CONACYT.

We are deeply grateful to Olivia Sánchez (IFC-UNAM) for her technical support, to Ozlem S. Bayram for providing nuclear marker plasmids pOB340 and pON307, and to Luis Cárdenas (IBT-UNAM) for his generous technical support, to O¨ zlem S. Bayram for providing nuclear marker plasmids pOB340 and pON307, and to Luis Cárdenas (IBT-UNAM) for his generous support with in vivo imaging. We also thank the Molecular Biology and Microscopy Units (IFC-UNAM) and Juan Barbosa and Ivette Rosas from the IFC Computer Facility.

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