Overlapping Functions between SWR1 Deletion and H3K56 Acetylation in Candida albicans

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Nucleosome destabilization by histone variants and modifications has been implicated in the epigenetic regulation of gene expression, with the histone variant H2A.Z and acetylation of H3K56 (H3K56ac) being two examples. Here we find that deletion of SWR1, the major subunit of the SWR1 complex depositing H2A.Z into chromatin in exchange for H2A, promotes epigenetic white-opaque switching in Candida albicans. We demonstrate through nucleosome mapping that SWR1 is required for proper nucleosome positioning on the promoter of WOR1, the master regulator of switching, and that its effects differ in white and opaque cells. Furthermore, we find that H2A.Z is enriched adjacent to nucleosome-free regions at the WOR1 promoter in white cells, suggesting a role in the stabilization of a repressive chromatin state. Deletion of YNG2, a subunit of the NuA4 H4 histone acetyltransferase (HAT) that targets SWR1 activity through histone acetylation, produces a switching phenotype similar to that of swr1, and both may act downstream of the GlcNAc signaling pathway. We further uncovered a genetic interaction between swr1 and elevated H3K56ac with the discovery that the swr1 deletion mutant is highly sensitive to nicotinamide. Our results suggest that the interaction of H2A.Z and H3K56ac regulates epigenetic switching at the nucleosome level, as well as having global effects.

Chromatin-level changes, such as histone modifications, variants, and nucleosome remodeling, have been implicated in the epigenetic regulation of gene expression in many systems. In recent years, focus has shifted toward the role of nucleosome dynamics in epigenetic regulation, in particular the importance of nucleosome destabilization in the establishment and inheritance of active chromatin states (1). Increasing evidence has shown that numerous histone modifications affect nucleosome stability and dynamics by altering the rate of nucleosome turnover and DNA access (2).

One such example of a histone modification altering nucleosome dynamics is the acetylation of H3 lysine 56. H3K56 acetylation (H3K56ac) occurs during S phase on newly synthesized histones and facilitates histone deposition onto replicating DNA as well as nucleosome assembly (3). Consequently, H3K56ac is found at high levels on newly synthesized chromatin and is involved in chromatin packing after DNA replication and repair in Saccharomyces cerevisiae (3–5). During transcriptional activation, H3K56ac promotes chromatin disassembly (6, 7). Replication-independent deposition of histones is also associated with H3K56ac (8). In addition, H3K56 is located near the DNA entry and exit points on the nucleosome core particle (9), further implicating its role in nucleosome dynamics. In yeast, the acetylation of H3K56 is performed by the histone acetyltransferase (HAT) Rtt109 (10, 11), and deacetylation occurs by the sirtuin class histone deacetylases (HDACs) Hst3 and Hst4 (12, 13).

H3K56 acetylation has been shown to regulate the epigenetic process of white-opaque switching in Candida albicans. A major fungal pathogen also found as a commensal with humans, C. albicans switches reversibly between two phenotypic states, white and opaque (14, 15). The two states differ in morphologies, transcriptional profiles, and responses to host defenses, and epigenetic switching may enhance the adaption of C. albicans to host environments (16–19). As in S. cerevisiae, H3K56 acetylation in C. albicans is regulated by Rtt109 and the sirtuin Hst3 (20, 21). Deletion of RTT109 in C. albicans, which prevents acetylation of H3K56, has been shown to impair white-opaque switching, while the HST3/hst3 mutant promotes switching. Treatment with nicotinamide (NAM), which can inhibit sirtuin activity noncompetitively (22, 23) and increases H3K56ac levels, also promotes switching to the opaque form, and this activity has also been shown to be dependent on RTT109 (24). Furthermore, hyper-acetylation of H3K56 is toxic to C. albicans (21, 25).

In S. cerevisiae, high H3K56ac levels have been shown to reduce chromatin levels of the histone variant H2A.Z and increase the eviction of H2A.Z-containing nucleosomes (26). This is notable as H2A.Z itself has been implicated in altering nucleosome dynamics and stability. In addition, H3K56ac and H2A.Z have shared roles in genome stability through regulation of chromosome condensation (27, 28). H2A.Z is a highly conserved variant of H2A and is essential in a number of eukaryotic organisms but not in yeast (29–31). H2A.Z is enriched in euchromatin at the promoters of both actively expressed and repressed genes and prevents the spread of heterochromatin (32–34). Nucleosomes containing H2A.Z are enriched in euchromatin at the promoters of both actively expressed and repressed genes and prevents the spread of heterochromatin. Nucleosomes containing H2A.Z are enriched at the nucleosome-free regions (NFRs) at promoter regions, in particular those adjacent to the +1/−1 nucleosomes at the transcriptional start site of genes (32, 35). H2A.Z-containing nucleosomes have been noted to have altered stability; however, separate studies have shown H2A.Z nucle-
TABLE 1 Strains used in this study

<table>
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<th>Strain</th>
<th>Description</th>
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<td>SWR1/swr1</td>
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</tr>
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MATERIALS AND METHODS

Strains and culturing conditions. Strains used in this study are listed in Table 1. Strains were maintained on YEP (1% yeast extract, 2% peptone) or SC (synthetic complete medium) with the appropriate carbon sources.

Strain construction. SWR1 was deleted by using the deletion cassettes described previously by Noble and Johnson (50). PCR amplification of Candida dubliniensis HIS1 from plasmid pSN52 or of Candida dubliniensis ARG4 from plasmid pSN69 was performed by using long primers containing sequences flanking SWR1, such that the PCR product was flanked by 90-bp sequences homologous to flanking sequences of SWR1. The PCR product was then transformed into wild-type (WT) (JYC1) C. albicans to replace SWR1 by homologous recombination. Transformants were selected for survival on SC dextrose histidine or arginine dropout medium, and deletion of SWR1 was verified by PCR.

H2A.Z (HTA3) was hemagglutinin (HA) tagged by PCR amplification of the HTA3 coding sequence with a XHA tag at the 5′ end of the sequence, with HindIII and PstI sites introduced at the 5′ and 3′ ends of the amplicon, respectively. The HTA3 promoter was amplified in a separate reaction, flanked by Xhol and HindIII sites. Subsequently, the HA-HTA3 and HTA3 promoter sequences were inserted into the pWOR1-GFP-SAT1 plasmid (24), replacing the GFP and WOR1 promoter sequences, respectively. The plasmid was digested with MscI prior to transformation into the WT or swr1 strain. All primers used for cloning are listed in Table 2.

Mating type conversion. The MTLa/a yng2 deletion mutant (CLY4) (51) and the yng2+YNG2 strain (HLY4035) (52) were converted to MTLa/a by growth on solid SC medium with 2% sorbose at a density of 10^5 cells per plate for 6 days (53). The mating type locus was verified by PCR.

Switching assays. Stable white or opaque cells from log-phase cultures were spread onto agarose plates of Lee’s medium (modified from reference 54) supplemented with 25 μg/mL uridine and 50 μg/mL arginine, with 1.25% dextrose or N-acetyl-L-glucosamine (Spectrum Chemical) as the carbon source. For CO2 assays, plates were incubated in a Thermo Forma series II water-jacketed CO2 incubator at 25°C with 5% CO2. Colony morphology was scored after 7 days. Both whole-colony and sectored switching events were counted.

Reverse transcription-quantitative PCR (RT-qPCR). RNA was isolated from log-phase cultures by using the Qiagen RNaseasy kit. cDNA was synthesized from 2 μg total RNA by using the Bio-Rad iScript reverse
transcription kit. Quantitative PCR (qPCR) was performed on the Bio-Rad iCycler instrument by using Bio-Rad SYBR green mix. Cycle parameters were 95°C for 1 min and then 39 cycles of 95°C for 10 s, 56°C for 45 s, and 68°C for 20 s. Oligonucleotides used for amplification are listed in Table 2.

### Nucleosome mapping

Micrococcal nuclease (MNase) digestion was performed with modifications of methods described previously (55, 56). Cells were grown to an optical density at 600 nm (OD\textsubscript{600}) of 2 and then cross-linked with 2% formaldehyde at a growth temperature for 30 min before treatment with zymolyase to spheroplast cells. Spheroplasts were then treated with a titration of 2 to 8 units of MNase, and digested samples were used for further analysis. DNA from these samples was isolated by using phenol-chloroform extraction and used for qPCR for nucleosome mapping.

### Fluorescence-activated cell sorting

Fluorescence-activated cell sorting (FACS) was conducted by using the BD FACSCalibur system, using cells taken from actively growing liquid cultures. The FL1-H channel was used for green fluorescent protein (GFP) detection, and 10,000 cells in suspension were counted per sample. Results were analyzed with FlowJo cytometry analysis software.

### RESULTS

The swr1 deletion mutant increases white-to-opaque switching frequency and stabilizes the opaque phase. To investigate the role of chromatin remodeling by the SWR1 complex in white-opaque switching, we deleted the SWR1 gene in C. albicans using homologous recombination to replace it with auxotrophic markers as described previously by Noble and Johnson (50). In the resulting swr1 deletion mutant, chromatin immunoprecipitation confirmed that the deposition of H2A.Z into chromatin was abrogated (not shown). High rates of spontaneous switching to the opaque phase in white colonies of the swr1 mutant were observed at room temperature (RT), often occurring as multiple opaque sectors per white colony (Fig. 1A). The white-opaque switching percentage of the swr1 mutant at room temperature (25°C) was 82%, compared to 2 to 4% for the wild type. Opaque cells of the swr1 mutant are more stable than those of the wild type, with 0% switching to white after 7

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**Table 2 Primers used in this study**

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<tr>
<td>SWR1D-R</td>
<td>AGACTTATCTGAGGTCGACGTCTGAGATTCGAGACGGGTCTCAAGAAACACATCAGGA</td>
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<td>C. dubliniensis HIS1 check</td>
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<tr>
<td>C.dubHIS-R</td>
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<td>C. dubliniensis HIS1 copy check</td>
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<td>HTA3_F</td>
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<td>Amplification of HTA3 promoter</td>
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**RESULTS**

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days of growth at RT, compared to 34% for the WT (Fig. 1B). We next sought to determine the effect of temperature on the swr1 white-opaque phenotype. At 37°C, white-opaque switching of the swr1 mutant increased to 97%, while WT cells no longer switched. We also compared the phenotype of the swr1 mutant to that of the efg1 mutant, the deletion mutant of the transcriptional regulator EFG1 which is known to have high rates of white-opaque switching. Unlike the swr1 mutant, the efg1 mutant was not able to switch to opaque at high temperatures. At 37°C, opaque stability of the swr1 mutant was reduced but still greater than that of the WT, with 30% of opaque cells remaining opaque, while all WT opaque cells switched to white. On the other hand, efg1 opaque cells were less stable than swr1 cells and switched to white cells readily at 37°C (Fig. 1B). To test if SWR1 can restore function to the swr1 mutant, we assessed the white-opaque phenotype of the swr1/Tet-SWR1 mutant, a conditional mutant in which SWR1 expression is shut down in the presence of doxycycline (58). When grown on medium containing doxycycline, the strain displayed high levels of white-opaque switching and opaque stability, similar to the swr1 deletion mutant. In the absence of doxycycline, the strain did not readily switch to opaque and also had low opaque stability at 37°C (see Fig. S1 in the supplemental material). This demonstrates that the expression of SWR1 can restore the wild-type phenotype to an swr1 mutant. From these results, we find that white-opaque switching and opaque stability are enhanced in the swr1 mutant even at high temperature.

We proceeded to investigate whether the deletion of SWR1 promotes switching downstream of known pathways. It has been documented that low concentrations of CO2 as well as utilization of N-acetylglucosamine (GlcNAc) as the main carbon source promotes white-opaque switching (59, 60). To assay whether Swr1 acts downstream of either of these pathways, we cultured white
cells of the WT and the swr1 mutant in air or 5% CO₂ on Lee’s medium with dextrose or GlcNAc as the carbon source and tracked switching to opaque over the course of 14 days. In the WT, as previously documented, both CO₂ and GlcNAc promoted white-opaque switching and showed synergy with each other. In the swr1 mutant, we observed a higher level of spontaneous switching than in the WT, even under control conditions of growth in air on dextrose. Notably, switching of the swr1 mutant was elevated in the presence of CO₂ regardless of the carbon source, showing a synergy similar to that of GlcNAc and CO₂ (Fig. 1C). Unlike the swr1 mutant, the efg1 mutant readily switched to opaque without GlcNAc or CO₂ with a timing similar to that of the wild type in the presence of both GlcNAc and CO₂ (data not shown). Thus, SWR1 deletion appears to drive white-opaque switching in a pathway synergistic with the Flo8-mediated CO₂-sensing pathway and may act downstream of the GlcNAc signaling pathway. Although wild-type opaque cells switch to white at 37°C under most conditions, it has been noted that GlcNAc as a carbon source increases switching in a manner synergistic with higher temperatures as well (60). This is consistent with the observation of white-to-opaque switching at high temperature in the swr1 mutant.

We then explored the mechanisms behind the white-opaque phenotype of the swr1 mutant through regulation of WOR1, the master regulator of switching. First, we investigated whether the swr1 mutant had a higher level of expression from the WOR1 promoter by using WT and swr1 strains transformed with the pWOR1-GFP plasmid, which expresses GFP from the native WOR1 promoter. After 4 days of growth on solid SCG medium, starting from white cells, the swr1 mutant showed numerous instances of darker colonies and sectors than those of the WT, indicative of the expression of pWOR1-GFP in cells that had become opaque (Fig. 1D). This further supports elevated white-to-opaque switching in swr1. To determine WOR1 expression levels in white and opaque cells, fluorescence-activated cell sorting (FACS) was performed on WT and swr1 cells carrying pWOR1-GFP. As seen in fluorescence histograms, transcription from the WOR1 promoter in white cells was not greater for the swr1 mutant than for the WT. In opaque cells, the level of GFP in the swr1 mutant was slightly elevated compared to that in the WT (Fig. 1E). Because the basal levels of WOR1 expression in white cells are extremely low, it could be difficult to detect a slight change in Wor1 levels by using FACS analysis. Given the high white-to-opaque switching frequency in the swr1 mutant, it may at least be easier to reach the threshold to initiate the positive self-feedback loop of Wor1 in the mutant than in the WT. Indeed, RT-qPCR analysis of WOR1 mRNA levels in WT and swr1 white and opaque cells detected a slightly elevated WOR1 expression level in white swr1 cells compared to wild-type cells (Fig. 1F). This difference was not detected by FACS analysis. The WOR1 level in opaque swr1 cells was also slightly higher than that in opaque WT cells, consistent with the FACS data. While WOR1 expression was not greatly elevated in the swr1 mutant, a moderate increase may make it easier to reach the threshold to initiate the positive self-feedback loop of Wor1 and promote white-opaque switching or opaque stability through positive feedback.

Nucleosome positioning on the WOR1 promoter differs between white and opaque cells and is altered in the swr1 mutant. We next sought to investigate whether deletion of SWR1 altered the white-opaque phenotype by changing the regulation of WOR1 through chromatin remodeling at the WOR1 promoter. As WOR1 has a long 8-kb promoter as well as a long 5’ untranslated region (UTR), nucleosomal dynamics upstream of WOR1 may be crucial to the regulation of its transcription. Since H2A.Z-containing nucleosomes have been shown to have altered stability and dynamics (36–38, 41), we proceeded with a nucleosome map of the WOR1 promoter in WT and swr1 cells, both of which carry HA-tagged HTA3 (H2A.Z), to facilitate further studies. To obtain nucleosomal DNA, Staphylococcus aureus micrococcal nuclease digestion was performed in order to cleave non-nucleosome-bound DNA while leaving nucleosome-bound DNA intact. qPCR was then performed on the nucleosomal DNA, amplifying staggered 100-bp regions along the WOR1 promoter and providing a map of nucleosomal enrichment in this region. We found that even in the WT, white and opaque cells showed a difference in nucleosome occupancy and positioning along the WOR1 promoter. While regular nucleosome peaks were observed at similar positions in both cell types, notably, nucleosome peaks were more defined in white cells. In particular, this was true of the +1/−1 nucleosomes adjacent to the transcriptional start site −1,997 bp upstream of the WOR1 ATG start codon. In white cells, there is a nucleosome-free region (NFR) between the +1 and −1 nucleosomes as well as one −2,550 to 2,350 bp upstream of the WOR1 ATG codon, absent in opaque cells. In the swr1 mutant, we saw a marked change in nucleosome positions on the WOR1 promoter compared to those in the WT. Nucleosome positioning was altered from that of the wild type, particularly in white cells, and the NFRs were abolished, with nucleosome occupancy being highly elevated in the region spanning bp −2,550 to −2,350 instead. The highly elevated levels of nucleosome occupancy at NFRs of the WOR1 promoter in white swr1 cells likely reflect slower nucleosome turnover, which is consistent with the known function of H2A.Z. In contrast, nucleosome occupancy at the NFRs of the WOR1 promoter is much lower in opaque swr1 cells than in wild-type white or opaque cells (Fig. 2). Overall, nucleosome mapping suggests that Swr1 is required for proper nucleosome positioning and stability at the WOR1 promoter and for the differential regulation of promoter nucleosomes in white and opaque states. Our data therefore support the importance of H2A.Z deposition in epigenetic regulation of transcription in cell fate determination.

H2A.Z is enriched at the WOR1 promoter in white cells. H2A.Z is known to be enriched at developmentally regulated regions. To further investigate nucleosomal H2A.Z content, we mapped H2A.Z enrichment along the WOR1 promoter in white and opaque WT cells. In addition, swr1 cells were used as a control. H2A.Z was HA tagged in all strains used. H2A.Z enrichment was assayed by immunoprecipitation of H2A.Z-containing nucleosomes using anti-HA- on micrococcal nuclease-treated nucleosomes (Fig. 2), followed by qPCR using the same WOR1 primers as those used for nucleosome mapping to provide coverage along the WOR1 promoter. As expected, H2A.Z levels on promoter chromatin were very low in the swr1 mutant. In the wild type, notably, the H2A.Z level was higher in white cells than in opaque cells. Particularly of interest is that H2A.Z was enriched in the −2 and −1 nucleosomes at two NFRs on the WOR1 promoter (Fig. 3). The location of H2A.Z-enriched nucleosomes at NFRs is consistent with the role of H2A.Z in promoting nucleosome dynamics, as shown in yeast and high eukaryotes (61).
elevated H2A.Z deposition by the SWR1 complex at the WOR1 promoter in white cells indicates a role for H2A.Z in stabilizing the repressive chromatin state in white cells, potentially by maintaining NFRs and permitting the binding of repressive factors.

A deletion mutant of yng2, a subunit of the NuA4 complex, produces a white-opaque switching phenotype and synergy with CO2 similar to those of the swr1 mutant. In exploring the regulation of H2A.Z deposition, we considered the recruitment of the SWR1 complex by NuA4 acetylation of H2 and H4 and the substantial overlap in subunits between the SWR1 and NuA4 complexes. Yng2 is a subunit of the NuA4 HAT module, the deletion of which, as we have shown, severely impairs H4 acetylation (51). Thus, we investigated whether deletion of YNG2 would produce a white-opaque phenotype similar to that of the swr1 mutant. We found that at room temperature, white cells of the yng2 mutant switched to opaque at a very high frequency compared to that of the wild type, while opaque cells of the yng2 mutant were highly stable. A complemented yng2 + YNG2 strain showed a phenotype similar to that of the wild type (Fig. 4A). In addition, opaque yng2 cells were stable at 30°C but not at 37°C (not shown). Because of the relation between NuA4 acetylation of histones and SWR1 deposition of H2A.Z in the same nucleosome, we speculated that the yng2 and swr1 mutants produced their high-switching phenotype through the same pathways and would respond similarly to CO2 and GlcNAc. To test this, white cells of the yng2 mutant were grown at room temperature in air or 5% CO2, with dextrose or GlcNAc as a carbon source, and switching was assessed. We found that yng2 cells began switching to opaque sooner when incubated in CO2, preceding switching in air by several days. This behavior is similar to that of the swr1 mutant. Notably, the yng2 mutant switched more slowly when the carbon source was GlcNAc than when grown on dextrose, showing a more complete lack of synergy with GlcNAc than the swr1 mutant did (Fig. 4B). Therefore, like SWR1, Yng2/NuA4 also functions downstream of the GlcNAc signaling pathway, separate from the CO2-regulated pathway. This is consistent with the known function of NuA4 in histone acetylation, which in turn allows SWR1 recruitment and H2A.Z deposition.

The swr1 mutant is highly sensitive to nicotinamide. In addition to the epigenetic regulation of white-opaque switching, we also sought to investigate the effects of swr1 deletion on additional cellular functions. H2A.Z is enriched in nucleosomes surrounding transcriptional start sites and is involved in gene expression (62).
Proper deposition of H2A.Z has been linked to numerous global effects, such as euchromatin-heterochromatin boundary establishment, centromeric functions, and DNA repair (33, 63–65). Recent work in S. cerevisiae has demonstrated that heightened acetylation of H3K56 is associated with reduced deposition and increased eviction of H2A.Z from chromatin by SWR1, with significant overlap in gene expression profiles between cells with constitutively acetylated H3K56 and htz1 (H2A.Z) deletion (26).

It is known that nicotinamide (NAM) inhibits C. albicans growth by an elevation of H3K56ac levels through inhibition of the HDAC Hst3 (21, 24). To further explore the functional relationship between H3K56ac and H2A.Z deposition, we examined the sensitivities of the WT, swr1, HST3, and rtt109 strains to NAM by a spot assay for growth on solid medium in the presence of nicotinamide. Cells were grown for 3 days at 30°C. The HST3 strain was highly sensitive to NAM and barely grew with 4 mM NAM, while the rtt109 strain was more resistant to NAM at 4 mM than the WT, consistent with previously reported results (24). Interestingly, the swr1 strain was even more sensitive to NAM than the HST3 strain, barely growing even on 2 mM NAM (Fig. 5). Unlike the HST3 strain, NAM sensitivity was not observed for the swr1 strain. The lack of haploid insufficiency indicates that NAM probably does not directly act on Swr1. In contrast to NAM sensitivity, the swr1 and HST3 strains did not show any increased sensitivity to the DNA-damaging agent methyl methanesulfonate (MMS), while the rtt109 strain was sensitive (Fig. 5). In addition, the swr1 mutant showed no increased growth sensitivity to hydroxyurea or heat and osmotic stress (not shown).

We have previously shown that the rtt109 mutant has an increased rate of generating aneuploidy (25). However, we did not observe any increase in aneuploidy formation in the swr1 mutant after growth on l-sorbose medium (not shown). Therefore, rtt109 (or blocking of H3K56 acetylation) is associated with aneuploidy and sensitivity to DNA damage, while H3K56ac and swr1 are associated with sensitivity to NAM. From our genetic studies, we suggest that the NAM sensitivity of swr1 and H3K56ac is associated with their roles in gene expression.

**DISCUSSION**

The role of histone variants and modifications on nucleosomal stability is a promising angle for the investigation of epigenetic regulation. In particular, the histone variant H2A.Z as well as the acetylation of H3K56 have been linked to changes in nucleosomal dynamics. Previous studies in our laboratory have demonstrated the effect of H3K56 acetylation on epigenetic regulation of white-opaque switching in C. albicans (24, 25). In this study, we show that epigenetic switching is also regulated by chromatin deposition of H2A.Z by SWR1. Both chromatin modifications affect the switching frequency and stability of cell fates but do not dramatically affect transcriptional levels of key cell fate regulators. A small increase in WOR1 expression was observed in the swr1 mutant, which may facilitate reaching the threshold for positive self-feedback regulation of Wor1. Additionally, we find synergy between the swr1 deletion and H3K56ac in C. albicans.
H2A.Z enrichment at promoter regions is often associated with both active and inactive transcription (32–34). Many studies have found H2A.Z nucleosomes enriched on the promoters of repressed genes, and H2A.Z deposition is important for proper induction of gene expression. Our study finds an example of these properties in demonstrating that H2A.Z is enriched at the WOR1 promoter in white cells and that white-to-opaque switching is enhanced in an swr1 mutant. Thus, H2A.Z is repressive to WOR1 expression or the opaque state. How does H2A.Z exert both positive and negative effects on transcription? One attractive model is that H2A.Z facilitates the binding of either activating or repressive complexes by keeping regions of promoters accessible (61). We find that nucleosome occupancy at the WOR1 promoter in white cells is elevated when SWR1 is deleted. Of particular note, a high H2A.Z level was found at nucleosome-free regions on the WOR1 promoter in WT cells, and in the swr1 mutant, these regions were no longer NFRs and instead had very high nucleosome occupancy. The existence of these NFRs in the white but not opaque state in the WT suggests a role for them in the repression of WOR1 transcription. Chromatin immunoprecipitation with microarray technology (ChIP-chip) studies of C. albicans have demonstrated that Efg1, a repressor of WOR1 and the opaque state, binds to the WOR1 promoter in white cells at only one major peak in the region between −3 kb and −2 kb, while it binds at multiple regions in opaque cells (66). This finding, in conjunction with our results, suggests that H2A.Z deposition in white cells maintains NFRs that facilitate the binding of repressive factors such as Efg1, favoring a repressive state of WOR1 transcription. Deletion of SWR1 may abolish these regions, preventing repressor binding and leading to a more permissive chromatin state for WOR1 transcription and an increased frequency of white-to-opaque switching. Future work is needed to examine this model of reduced accessibility of the WOR1 promoter to negative regulators of white-opaque switching in the swr1 mutant.

In exploring the functional relation of Swr1 with known white-opaque signaling pathways, we also find that the high-switching phenotype of the swr1 mutant showed synergy with CO2 in promoting white-opaque switching. This synergy with CO2 is similar to that of GlcNAC with CO2. Furthermore, the swr1 mutant shows no additional synergy with GlcNAC. Based on these data, we suggest that the SWR1 complex functions in the GlcNAC signaling pathway. A similar high-switching phenotype and synergy with CO2 are seen in the deletion mutant of yng2, a subunit of the NuA4 complex that shares subunits with the SWR1 complex and recruits the NuA4 complex on promoters of gene expression. Nat Rev Genet 9:15–26. http://dx.doi.org/10.1038/nrg2206.

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