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X-ray survival characteristics and genetic analysis for nine *Saccharomyces* deletion mutants that affect radiation sensitivity.

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ABSTRACT
The availability of a genome-wide set of Saccharomyces deletion mutants provides a chance to identify all the yeast genes involved in DNA repair. Using X-rays, we are screening these mutants to identify additional genes that show increased sensitivity to the lethal effects of ionizing radiation. For each mutant identified as sensitive, we are confirming that the sensitivity phenotype co-segregates with the deletion allele and are obtaining multipoint survival-versus-dose assays in at least two haploid and one homozygous diploid strains. We present data for deletion mutants involving the genes $DOT1$, $MDM20$, $NAT3$, $SPT7$, $SPT20$, $GCN5$, $HF11$, $DCC1$ and $VID21/EAF1$, and discuss their potential roles in repair. Eight of these genes have a clear radiation-sensitive phenotype when deleted, but the ninth, $GCN5$, has at most a borderline phenotype. None of the deletions confer substantial sensitivity to ultra-violet radiation, although one or two may confer marginal sensitivity. The $DOT1$ gene is of interest because its only known function is to methylate one lysine residue in the core of the histone H3 protein. We find that histone H3 mutants (supplied by K. Struhl) in which this residue is replaced by other amino-acids are also X-ray sensitive, seeming to confirm that methylation of the lysine-79 residue is required for effective repair of radiation damage.
Yeast mutants initially isolated on the basis of sensitivity to ionizing radiation (IR) have proved invaluable for understanding many aspects of DNA transactions in eukaryotes. Despite this, pathways and mechanisms of cellular recovery from ionizing radiation (IR) damage are less well understood than many other aspects of DNA repair. To fully understand IR repair, it is important to identify all the genes involved. The availability of a genome-wide set of deletion mutants (WINZELER et al. 1999) now makes it possible to identify virtually all the non-essential genes in *Saccharomyces* that play a role in conferring resistance to ionizing radiation. We and others have begun a systematic search for such genes that were missed in classical screens of mutagenized cells. These screens, summarized by Game and Mortimer (1974), were apparently very effective in identifying mutants that confer a high degree of sensitivity. Few or no new genes have been found in the last thirty years whose mutants confer the extreme IR sensitivity of deletion alleles in the *RAD51* epistasis group. However, classical screens were less effective at identifying mutants with moderate IR-sensitivity, and a significant number of such mutants remain to be characterized (BENNETT et al. 2001; GAME et al. 2003).

Mutants that combine a growth defect with modest radiation-sensitivity can be especially hard to identify in replica-plating screens, since they will form small colonies whose sensitivity is hard to identify compared to poor growth on the
control plate. In addition, assigning novel mutants in unknown genes to specific loci can be laborious. However, identifying a modest IR-sensitive phenotype regardless of growth rate is not difficult when pure cultures of known mutants are tested for X-ray sensitivity individually. Even modestly sensitive mutants are important in understanding repair, because they can uncover unrecognized or redundant pathways and mechanisms. Double or multiple mutant combinations may serve to expose the full role of such pathways.

We have been using the genome-wide deletion set (WinzeleR et al. 1999) to identify new genes or open reading frame (ORFs) whose deletion alleles confer increased sensitivity to killing by X-rays. Some preliminary information is already available about the IR sensitivity of many of the catalogued yeast deletion mutants. Bennett et al. (2001) screened 3,670 diploid deletion strains in plate assays and identified 107 as potentially IR-sensitive. However, follow-up tests were not done and the list includes some false positives where factors other than the deletion allele contributed to IR-sensitivity (Game et al. 2003). In addition, more than a thousand new deletion strains have become available since the work of Bennett et al. (2001). Further information is available from a screen developed in the laboratories of J. Martin Brown and R.W. Davis at Stanford (see Birrell et al. 2001; Game et al. 2003). The screen utilizes a pool of nearly all the deletion
mutants combined into one culture. It involves ranking the relative change in abundance, as judged by ratios of hybridization signals of unique barcode sequences to a microarray plate, of each mutant after irradiation and brief growth of the pool, compared to the starting abundance for that mutant. Mutants with enhanced sensitivity show less relative abundance in the pool after irradiation. Using this methodology more than 4,600 mutants were ranked in order of relative abundance in a pool of mutants 18 hours after IR treatment compared to un-irradiated controls (GAME et al. 2003). However, approximately 9% of deletion mutants in this ranking were not adequately monitored for IR sensitivity using this method because they were insufficiently abundant in the pool prior to irradiation to allow adequate assessment of radiation effects (see GAME et al. 2003).

We have been directly assaying IR sensitivity in some of the 1,000 or so mutants that were not in the collection surveyed by Bennett et al. (2001), focusing especially on those that also could not be adequately ranked by the pool method (BIRRELL et al. 2001; GAME et al. 2003). In addition, we have used quantitative survival assays in combination with genetic analysis to more rigorously test and characterize X-ray sensitivity in several other mutants that were identified as potentially sensitive either in the pool assay or by Bennett et al. (2001), or were identified by us as interesting based on relationships to other known mutants.
Secondary factors unrelated to the created deletions can sometimes be responsible for IR sensitivity in mutant strains from the genomic library (GAME et al. 2003). These can include independent mutations, polyploidy, and in diploids, homozygosity for the Mating Type locus. Hence it is necessary to verify that the phenotype of each newly identified IR-sensitive mutant is truly conferred by the deletion. In addition, it is important to obtain survival curves for mutants initially identified on the basis of qualitative tests.

In this report, we present survival characteristics for nine deletion mutants, eight of which we have confirmed genetically to confer X-ray sensitivity. The ninth, gcn5Δ, may confer marginal sensitivity. Six of these mutants, involving deletions of the genes MDM20, DOT1, SPT7, SPT20, HFII and GCN5, were initially identified as sensitive in spot tests in our own laboratory. We chose the remaining three, deleted for the NAT3, VID21 and DCC1 genes, based on previously reported sensitivity in spot tests (BENNETT et al. 2001). We discuss the possible significance of these genes in DNA repair, and also report difficulties in confirming the radiation sensitivity of two additional mutants. We also tested the mutants for cross-sensitivity to ultraviolet radiation, and we present data suggesting either no sensitivity or at most minor UV-sensitivity.
MATERIALS AND METHODS

**Yeast strains:** We obtained a library of ~ 4,700 individual haploid deletion strains in the alpha Mating Type (background strain BY4742) from Research Genetics, Huntsville, AL (now Invitrogen Life Technologies). These deletion strains can also be obtained from EUROSCARF (Frankfurt, Germany). Genotypes of the parental yeast strain BY4742 and construction of the deletion strains have been described (BRACHMANN *et al.* 1998; WINZELER *et al.* 1999). Information is also available at the Saccharomyces Genome Deletion Project website, [http://www-sequence.stanford.edu/group/yeast_deletion_project/deletions3.html](http://www-sequence.stanford.edu/group/yeast_deletion_project/deletions3.html). The prototrophic wild-type strains X2180-1A and X2180-1B were available to us from R.K. Mortimer. They are haploid spore-clones derived from diploid X2180, which was identified by Mortimer as a spontaneous diploid $MAT_a/MAT_\alpha$ derivative of haploid strain S288C (see MORTIMER and JOHNSTON 1986). They are thus isogenic in background to the strains used to generate the deletions, which were derived from S288C by a series of transformations and subsequent background-isogenic crosses (BRACHMANN *et al.* 1998).

**Genetic methods and media:** Genetic methods including tetrad dissection were as described (SHERMAN *et al.* 1982). Cultures were incubated at 30° unless a temperature-conditional phenotype was segregating, in which case 25° was used.
Rich media (YPD) and supplemented minimal media were prepared as described
(SHERMAN et al. 1982). To make inositol-less medium, we used yeast nitrogen base
(YNB) without inositol, obtained from Q-biogene, in place of regular YNB. To
induce meiosis, we incubated cultures for four or more days, usually at 30°, on
solid Fogel’s sporulation medium. This contains 9.65 g potassium acetate, 1g
glucose, 2.5 g yeast extract (Difco) and 2% agar made up to one liter in water and
autoclaved. To score geneticin-resistance, we used YPD plates supplemented with
geneticin (obtained from Sigma) added from filter-sterilized solution shortly before
pouring plates, to give a final concentration of 150 µg/ml.

**Spot-testing the mutants for X-ray sensitivity:** We retrieved mutants from
cold storage and grew up cultures. We arrayed fresh cultures in thin patches of
twenty per plate on YPD medium and replica-stamped each plate immediately to
six more YPD plates. We irradiated two plates from each set with 78 kilorads (7.8
Gray) and two more with 156 kilorads (15.6 Gray) of X-rays. We incubated one
plate from each pair at 25° and one at 37°, together with the un-irradiated plates.
We monitored each set at one day and two days after irradiation for evidence of
sensitivity in any mutant, as evidenced by less than average growth or survival
compared to the un-irradiated plate at the same temperature.
**X-ray treatments:** For all X-ray exposures, we used a Machlett OEG 60 X-ray tube with a beryllium window and a Spellman power supply operated at 30 kilovolts and 15 milliamps to deliver a dose-rate of 130 rads/second of “soft” X-rays. For survival curves, unless otherwise noted, log-phase cells from overnight liquid YPD cultures grown at 30°C were diluted appropriately in fresh YPD and grown for several more hours with vigorous shaking. When a cell density of $1 \times 10^7$ to $2.5 \times 10^7$ cells/ml was reached, as determined with a hemocytometer, serial dilutions were made in distilled water cooled in ice. Cells plated from the appropriate dilution were irradiated at room temperature on YPD plates, to yield (ideally) about 200 surviving colonies/plate, with two plates per dose. Cultures were inspected for clumpiness. If clumps were observed, cultures were sonicated briefly to disperse them. Colonies were counted after incubation for 5 to 6 days at 30°C unless otherwise noted.

**Ultraviolet Radiation treatments:** Cells were prepared in log phase for UV survival curves as outlined above for X-rays. They were irradiated on YPD plates using a shielded apparatus containing five General Electric G8T5 tubes giving most of their radiation at 254 nm. Plates were incubated in the dark and colonies counted as for X-ray curves.
RESULTS and DISCUSSION

**Spot-testing individual mutants:** To identify additional yeast genes that might be involved in IR repair, we began by spot-testing 357 mutants, selected by criteria described earlier, for sensitivity to X-rays at 37°C and at 25°C using two doses as described. We also noted temperature effects on growth in the absence of radiation. It is important to assess IR-sensitivity at more than one temperature, even in deletion mutants, since some yeast proteins play a role in repair that is temperature-dependent (LOVETT and MORTIMER 1987).

Of the 357 mutant cultures initially tested, 25 were chosen for re-testing from those that appeared the most convincing candidates for X-ray sensitivity at one or both temperatures in the first test. After these 25 were re-tested in similar plate tests, three mutants, the *dot1*, *mdm20* and *spt20* deletion strains, were chosen for further study. Three more mutants, those carrying the *spt7*, *hfi1* and *gcn5* deletions, were also chosen for study, based on their known relationship (GRANT *et al.* 1997; HORIUCHI *et al.* 1997) to the identified *spt20* mutant. Two of these, the *spt7* and *hfi1* deletion strains, showed sensitivity in spot tests. The third, the *gcn5* deletion, showed no clear sensitivity in spot tests, but showed a mild sensitivity (less than
the other mutants) in survival curves. These three mutants were also amongst the approximately 1,000 deletions absent from the initial set. One was also absent from the pool of mutants studied in the Brown laboratory. The other two showed a borderline low score or a borderline low signal in the pool assay but were not selected in our initial list of 357 cultures.

In addition to the above six mutants, we chose to study five mutants reported by Bennett et al. (2001) to be sensitive to Cesium-137 gamma rays. These were the deletions of NAT3, VID21 (ORF YDR359C), DCC1, HTL1 and DEF1 (VID31). We chose the five for which the authors presented the most convincing observations of sensitivity in a diploid strain and in both haploid parents. We confirmed that the deletion library strains listed as MATα haploids containing each of these five deletions were X-ray sensitive in spot tests.

**Genetic analysis of mutants:** As shown previously (GAME et al. 2003), some mutant strains from the genomic library contain secondary genetic changes in addition to the created deletion. To determine if the deletion by itself is both necessary and sufficient to confer X-ray sensitivity, we crossed each deletion mutant with a wild-type MATα strain. We determined whether the X-ray sensitive phenotype co-segregated with the deletion in meiotic tetrads from these crosses,
using resistance to geneticin conferred by the \textit{KanMX4} marker to score the deletion allele. These crosses also served to generate new spore-clones carrying the deletions in each mating type and with different combinations of auxotrophic markers. We used these spore-clones to determine the consistency of the survival characteristics in two or more haploid strains for each mutant, as shown in Figures 1 through 7, and to construct our own homozygous diploids for testing, as shown in Figures 8 and 9.

Table 1 shows spore-viability data for each of the 11 deletion mutants we chose for further study, crossed with our \textit{MATa} wild-type strain, g1201-4C. This strain is isogenic in background with the strains used for constructing the deletion library. It was made by crossing the deletions strains carrying multiple auxotrophic markers with the prototrophic strain X2180-1B, which shares the same strain background (see Materials and Methods). Crosses generated haploid spores in each mating type carrying only the \textit{lys2Δ} marker (from BY4742) or the \textit{met15Δ} marker (from BY4741). These single-auxotroph strains can be mated with the deletion mutants created in the BY4741 or BY4742 strains respectively, and the resulting diploids can be selected on minimal medium. These diploids are heterozygous for four auxotrophic mutations in addition to the deletion of interest.
In tetrad analysis these segregating markers, along with Mating Type, help to identify polyploid or aneuploid cells and false tetrads.

Table 1 reveals that in 9 of 11 deletion strains analyzed, meiotic spore viability from the heterozygous diploids was high, and the deletion alleles as scored by geneticin resistance segregated 2+:2- per tetrad, as expected. In eight mutants, the geneticin-resistance phenotype co-segregated with an X-ray sensitive phenotype that could be readily observed on replica plates given 156 kilorads of radiation. Fifteen or more tetrads with four viable spores were monitored for co-segregation for each mutant. In the case of the spt7 deletion, a second cross was needed, since poor spore viability led to only three tetrads with four live spore-clones in the first cross. Since these three tetrads and other partial tetrads showed convincing segregation for X-ray sensitivity, we hypothesized that the poor viability was unrelated to the deletion. A back-cross to wild-type using an spt7Δ spore-clone from one of these tetrads confirmed this by giving high spore-viability, and also confirmed the co-segregation relationship, as shown in Table 1. The tetrad data in Table 1 show that an unlinked secondary marker is not responsible for the X-ray sensitivity in these 8 mutants, and the high spore viability and 2+:2- segregation of recessive markers from each parent effectively rules out polyploidy. The possibility of a secondary mutation closely linked to the deletion itself is not
excluded, but in *Saccharomyces* the probability of such close linkage of mutations by chance is less than 1%. We conclude that at least for this genetic background, the deletion allele is both necessary and sufficient to confer the observed X-ray sensitivity in each of the first eight mutants in Table 1. For a ninth mutant, the *GCN5* deletion, a minimal X-ray sensitivity that was apparent in survival curves (Figure 3) was insufficient to permit reliable scoring of this phenotype in replica-plated tetrad sets, as discussed below.

Two mutants, those with deletions in the *HTL1* and *DEF1* genes, failed to behave in the same way as those discussed above. Spore viability from the crosses with wild-type was poor in each case (see Table 1). In addition there was wide variation in the size of the germinating spore colonies, with many weak spore-clones that could not be reliably scored for IR-sensitivity. Aneuploidy or polyploidy is a likely possibility in these crosses, especially in the case of *htl1Δ*, which is itself known to lead to increased frequencies of spontaneously polyploidized cells (LANZUOLO et al. 2001). Since polyploidy by itself is well known to affect IR-sensitivity (MORTIMER 1958; LASKOWSKI 1960), it is difficult to assess without reconstructing the strains whether these deletion mutations also confer sensitivity. We have not pursued the *htl1Δ* and *def1Δ* mutants further.
**X-ray survival curves:** We performed X-ray survival curves for at least two haploids and one homozygous mutant diploid strain for the nine out of eleven deletion mutants in Table 1 that showed 2+:2- segregation for geneticin resistance when crossed to wild-type. The results are shown in Figures 1 through 9. Additional whole or partial survival assays for many of the mutants (not shown) served to confirm these data. We prefer to present individual survival assays instead of averaging measurements at each dose from separate curves, in part because dose-points within a curve are related based on serial dilutions and are not independent measurements. In addition, their accuracy in different curves will vary according to colony count. Hence, taking mean values may be misleading.

We include two haploid wild-type strains with a genetic background isogenic to the mutants. These are g1201-4C and MW5067-1C, each derived from crosses as described above. These strains were isolated as fresh spore-clones from crosses with high viability and from tetrads with four viable spores, hence the presence of any gross chromosomal abnormalities that could have accrued in the parent strain over time is unlikely. The wild-type curves shown are representative of several done during the course of this project. A survival curve (not shown) for strain BY4742, the \( {\text{MAT}}\alpha \) haploid wild-type from the deletion collection, was almost identical to that of MW5067-1C. The diploid shown, B4743, is the wild-type from the deletion collection.
It can be seen that eight of the mutant strains are significantly more X-ray sensitive than wild-type in both haploid and diploid configurations. The ninth mutant, deleted for GCN5, appears to show marginal sensitivity. None of these mutants show such strong sensitivity as the major recombinational repair mutants. These are represented by the rad51null haploid and diploid strains shown in the figures for comparison. Results and discussion for each mutant are detailed below.

**DOT1: Histone methylation is involved in IR-repair:** We find that haploid and homozygous diploid strains deleted for the DOT1 gene (SINGER et al. 1998) show significant X-ray sensitivity (see Figure 1 and Figure 8). It can be seen that the dot1Δ haploid survival curves are about equal to that of a deletion mutant of the RAD5 gene. This typifies mid-range sensitivity that is substantially less than that of the rad51Δ mutant (Figure 1). Interestingly, the homozygous dot1Δ/dot1Δ mutant diploid (Figure 8) is comparatively less sensitive compared to the wild-type diploid than the dot1Δ haploid strains are to haploid wild types (Figure 1). This could imply a role in repair of recessive lethal damage, such as base damage rather than double-strand breaks (DSBs), which are thought to be dominant lethal lesions in the absence of repair (reviewed in GAME 1983). Alternatively, DOT1 could mediate DSB repair that primarily involves sister-chromatids rather than
homologous chromosomes. The \textit{DOT1} gene is highly conserved throughout eukaryotes (Feng \textit{et al.} 2002) and its product has a single known function, the methylation of histone H3 protein at one residue, lysine-79, in the core of the protein (Ng \textit{et al.} 2002; Feng \textit{et al.} 2002; Van Leeuwen \textit{et al.} 2002). This methylation is required for DNA silencing near telomeres and elsewhere (Ng \textit{et al.} 2002; Ng \textit{et al.} 2003), and \textit{dot1} mutants were initially isolated and named based on loss of this function (disruptor of telomeric silencing) (Singer \textit{et al.} 1998). \textit{DOT1} is important in differentiating heterochromatin from euchromatin (Ng \textit{et al.} 2003). To determine whether the \textit{DOT1} gene functions in repair via its known activity in histone H3 lysine-79 methylation or via some other unidentified function, we obtained three mutants from Dr. Kevin Struhl in which the lysine-79 residue in histone H3 is replaced by a different amino acid (alanine, proline and glutamine respectively) that is not a substrate for methylation (Ng \textit{et al.} 2002). In these strains, the altered histone H3 gene is placed on a CEN plasmid and the two chromosomal genes for histone H3 are deleted. We expected that such mutants would be similar in IR-sensitivity to \textit{dot1null} mutants even in a \textit{DOT1} wild-type background if lysine-79 methylation is required for normal DNA repair.

We found that all three of these mutant strains showed X-ray sensitivity in spot tests that is similar to that of the \textit{dot1}\textDelta mutant. Figure 1 shows a survival
curve for a mutant in which lysine-79 is replaced by glutamine. In the same Figure, it can be seen that no IR-sensitivity is present in a strain (UCC1111) in which a wild-type histone H3 gene is provided on a plasmid to cover the chromosomally deleted histone H3 genes. This confirms that the mutant alleles themselves, rather than the location of the histone H3 gene on a plasmid, are responsible for the IR-sensitivity of the H3 lysine-79 replacement mutants. In comparing the hht2-K79Q mutant with the dot1Δ mutant, we are comparing the effect of histone H3 containing a glutamine at residue 79 versus histone H3 containing an unmethylated lysine at residue 79. While these altered histone proteins may not be exactly equivalent, the fact that both strains are significantly sensitive to ionizing radiation provides strong evidence of a repair function for lysine methylation in the core of histone H3. We are currently determining which repair pathways are affected in the dot1 mutant by constructing and studying dot1 rad double mutant strains carrying blocks in each of the currently known IR-repair mechanisms.

**SPT7, SPT20, HFI1 and GCN5: Components of the SAGA complex:** Figures 2 and 9 show that deletions of the SPT7 and SPT20 genes each confer modest but consistent IR sensitivity in haploids and detectable sensitivity in diploids. The SPT genes in yeast were identified by Winston et al. (1984) based on a mutant
phenotype that involves suppression of the effects of Ty elements inserted into the promoters of other yeast genes. *SPT7* and *SPT20* code for two components of the yeast Spt-Ada-Gcn5-acetyltransferase (SAGA) complex (Grant et al. 1997). SAGA is a conserved multi-protein complex involved in normal transcription in yeast. Loss of the complex results in altered mRNA levels for about 10% of the genes in Saccharomyces (reviewed in Wu and Winston 2002). Its components include the catalytic subunit Gcn5p, which is a histone acetyltransferase (Brownell et al. 1996). The histone acetylation activity of Gcn5p is modulated by the associated adaptor proteins Ada2p and Ada3p (Marcus et al. 1994; Horiuchi et al. 1995) and these three proteins also occur as parts of a second complex called ADA ((Eberharter et al. 1999). In addition, the SAGA complex interacts with TATA box binding protein (TBP) and, in the classical form of SAGA that contains the Spt8 protein, inhibits its interaction with the TATA box at some promoters (Sterner et al. 1999; Belotserkovskaya et al. 2000). The Spt7 and Spt20 proteins, together with the product of the *HFI1* gene, (also known as *ADA1* (Horiuchi et al. 1997) and originally identified as *SUP110* (Brown 1994)), are each believed to be essential for the structural integrity of the SAGA complex, which does not form if any of them are absent (Sterner et al. 1999). SAGA includes additional known proteins and can also exist in one or more alternate forms (Wu and Winston 2002; Sterner and Berger 2000).
Because of the functional relationship of \textit{GCN5} and \textit{HFI1} with the \textit{SPT7} and \textit{SPT20} genes, we also undertook genetic crosses to wild-type with the \textit{gcn5} and \textit{hfi1} deletion mutants and performed survival assays of haploid and diploid strains, as with the other mutants. As shown in Figure 3, there is unequivocal X-ray sensitivity for the \textit{hfi1} deletion strains. The haploid \textit{hfi1} survival curves in Figure 3 show a slightly greater sensitivity than the \textit{gcn5} curves in the same figure or the \textit{spt7}Δ and \textit{spt20}Δ strains in Figure 2. The homozygous diploid \textit{hfi1}Δ/\textit{hfi1}Δ strain is very close in survival to the \textit{spt7}Δ/\textit{spt7}Δ and \textit{spt20}Δ/\textit{spt20}Δ diploids (Figure 9). We found that the IR sensitivity phenotype of the \textit{hfi1}Δ mutant could be readily scored in irradiated replica-plate assays and co-segregates with the deletion allele. We also confirmed that the \textit{hfi1} deletion strain is auxotrophic for inositol, as expected for this mutant (HORIUCHI \textit{et al.} 1997), and that inositol auxotrophy co-segregates with X-ray sensitivity and the \textit{KanMX4} marker. While this work was in progress, a new mutant (\textit{srm12}) that was identified in a screen for decreased spontaneous mutagenesis to the mitochondrial rho− state was shown to be a nonsense allele of the \textit{HFI1} gene, and was also shown to confer IR-sensitivity (KOLTOVAYA \textit{et al.} 2003). A diploid homozygous for this mutation showed sensitivity to Co\textsuperscript{60} gamma rays (KOLTOVAYA \textit{et al.} 2003) that was comparable to
our observations (Figure 9) for the \textit{hfi1}Δ homozygous mutant diploid treated with X-rays.

In contrast to \textit{hfi1}Δ, the \textit{gcn5} deletion confers at most marginal IR sensitivity. The strains whose survival is shown in Figures 3 and 9 were consistently more sensitive than wild-type, but the phenotype is sufficiently mild that we were unable to demonstrate that X-ray sensitivity co-segregated with the \textit{gcn5} deletion using replica-plates of spore-clones from meiotic tetrads. We then took 20 spore-clones from five meiotic tetrads and measured survival at a single dose (122.9 kr/12.29 Gy) by counting plated colonies, as in our survival curve assays. We found a small difference between mutant and wild type average survival, but this was largely masked by variation between the individual measurements. The finding that the \textit{gcn5}Δ mutant is scarcely IR-sensitive and certainly less sensitive than the other SAGA mutants we studied may implicate functions other than histone acetylation in mediating the repair functions of this complex. A role for the complex in the transcriptional activation of one or more repair proteins could explain the observation that mutants in genes required for its structural integrity are more sensitive than a mutant deleted only for the histone acetylation activity. Analysis of sensitivity in strains lacking other components of
SAGA and its alternate and related complexes will clarify which of their activities is involved in recovery from IR.

**NAT3 and MDM20: Subunits of the Nat3B protein:** Survival curves for two haploid strains containing the deletion of *NAT3* and two strains deleted for *MDM20* are shown in Figure 4. Curves for diploid strains homozygous for each of these deletions are shown in Figure 8. The *nat3* and *mdm20* deletions confer comparable sensitivity that is greater than that of the other mutants described here or by GAME et al. (2003). While this work was in progress, it was shown that *NAT3* and *MDM20* code for subunits of a single protein, NatB Nα-terminal acetyltransferase (POLEVODA et al. 2003; see also SINGER and SHAW 2003). Hence, the similarity in their IR-sensitive phenotypes is to be expected. The *NAT3* gene was previously identified as the probable catalytic subunit of this protein (POLEVODA et al. 1999), which is one of three known enzyme-complexes that between them acetylate the N-termini of a large number of yeast proteins. Specifically, the NatB protein acetylates yeast proteins with N-termini consisting of Met-Glu or Met-Asp, and sub-classes of proteins with Met-Asn or Met-Met, and partially acetylates some proteins with other termini (see POLEVODA and SHERMAN 2003).
Previously reported phenotypes for both nat3 and mdm20 deletion strains include increased sensitivity in spot tests to several chemicals that lead to DNA damage, including camptothecin, bleomycin, hydroxyurea and caffeine (POLEVODA et al. 2003), an inability to grow at 37°, reduced growth on nonfermentable carbon sources, diminished mating efficiency, and other effects confirmed and reviewed by POLEVODA et al. (2003). In our hands, at 30° radiation-sensitivity convincingly co-segregated 2+: 2- with the deletion alleles, for both mdm20 and for nat3 deletion strains when crossed with wild-type (see Table 1). Each mutant also showed a temperature-conditional growth phenotype. However, as reported elsewhere (SINGER and SHAW 2003), this phenotype was more pronounced in mdm20∆ strains, which showed essentially no growth at 37°, than in nat3∆ strains, which we found to show limited but real growth at 37° over a period of two or more days.

In the cross of the original temperature-sensitive mdm20∆ mutant to our wild-type strain g1201-4C, a fraction of the tetrads showed a digenic segregation for temperature-sensitive growth, such that one or in some cases both the spore-clones containing the mdm20∆::KanMX4 allele showed wild-type growth at 37°C. None of the MDM20+ spores were inviable at 37°C, indicating that the deletion was necessary but not always sufficient to confer the temperature-conditional
growth phenotype in this cross, and that an unlinked suppressor of the conditional lethality was also segregating in some tetrads. We mated \textit{mdm20\Delta} spore-clones that were able to grow at 37° with those that were inviable at this temperature. The resulting diploids were viable at 37°, indicating that the suppressor phenotype is dominant. However, radiation-sensitivity was apparently unaffected by this suppressor, since \textit{mdm20\Delta} spore-clones that were viable at 37° remained IR-sensitive both at this temperature and at 30°C. Survival curves (at 30°) of a temperature-conditional \textit{mdm20\Delta} strain (g1229-1D) and one able to grow at 37° (g1229-9B) were equivalent (Figure 4).

We observed a similar phenomenon with \textit{nat3\Delta} strains. In this case, about half the \textit{nat3\Delta} spores showed a growth defect at 37° that was more pronounced than that of the initial \textit{nat3\Delta} mutant culture, although still not as strong as that seen in \textit{mdm20\Delta} strains. We inferred that a weak suppressor of the temperature conditional \textit{nat3\Delta} phenotype was present in our starting culture. We tested whether this influenced IR sensitivity by comparing survival of a strongly temperature-conditional spore-clone with that of a weakly temperature-conditional one. We also tested the effect of temperature on IR sensitivity in each strain by incubating parallel sets of plates at 25°, 30° and 37° immediately after irradiation. (Growth prior to irradiation in this experiment was at 25°). Even the strain with the
stronger temperature-sensitive growth defect was able to form small but countable colonies at 37°C. The results are presented in Figure 5, where it can be seen that there is a small effect of temperature on survival in both strains, but no clear difference between the strains. There is also a minor difference in the survival curves at two temperatures in the wild-type strain (Figure 5). Although this is less than that seen in the two nat3Δ strains, it seems likely that as with mdm20Δ, the IR-sensitive phenotype and the temperature sensitive growth defect in the nat3 deletion are conferred through separate mechanisms.

These observations are consistent with findings of SINGER et al. (2000), who identified and studied nine dominant suppressor mutations of the mdm20 deletion. They found that all nine of these suppressors represent mis-sense alleles in the structural genes for actin or tropomyosin (ACT1 and TPM1 respectively). They argued from this and other evidence that many of the phenotypes of the mdm20 deletion mutant arise from its destabilization of actin-tropomyosin interactions, causing partial loss of function. It has been shown independently that the NatB complex is required for acetylation of both actin (POLEVODA et al. 1999) and tropomyosin (SINGER and SHAW 2003), supporting this hypothesis. However, POLEVODA et al. (2003) point out that several of the many other potential target proteins for the NatB acetyltransferase are involved in repair. In addition, as in the
case of the mdm20 deletion (Singer et al. 2000), they identified suppressors of the nat3Δ temperature-sensitive phenotype that represented alterations in the ACT1 and TPM1 genes (Polevoda et al. 2003). In spot-tests, these suppressors did not suppress the sensitivity of nat3Δ mutants to hydroxyurea and camptothecin, although the TPM1 (but not ACT1) mutants did partially suppress sensitivity of nat3Δ strains to bleomycin (Polevoda et al. 2003). These authors concluded that the increased sensitivity of nat3Δ and mdm20Δ strains to DNA damaging agents in spot-tests may arise from effects of the mutations on other target proteins. If so, this could explain our observation that suppressors of the temperature-conditional phenotype of the mdm20Δ and nat3Δ mutants fail to affect their radiation-sensitive phenotypes. Additional studies of mis-sense mutants involving potential NatB target enzymes that cannot be acetylated, and of mdm20 or nat3 double mutant combinations with these and other mutants should clarify the cause of the IR-sensitivity conferred by these deletions.

**ORF YDR359C (VID21/EAF1):** The name VID21 was standardized for ORF YDR359C by the Saccharomyces Genome Database in August 2003. The name represents a suggested function in vacuolar import and degradation, proposed earlier for twenty other genes numbered VID1 to VID20 (Hoffman and Chiang 1996). Very recently YDR359C has also been shown to be the ORF for an
independently named gene, \textit{EAF1}, identified from a protein (Esa1-associated factor-1) that is a member of the NuA4 histone acetyltransferase complex (Doyon \textit{et al.} 2004). Strains deleted for \textit{VID21} were reported by Bennett \textit{et al.} (2001) to be IR-sensitive. We observed significant IR-sensitivity in the BY4742 \textit{MAT}α strain deleted for ORF YDR359C (\textit{VID21/EAF1}), and confirmed that an IR sensitive phenotype co-segregates with the deletion allele (see Table 1). X-ray survival curves for two haploid and one homozygous diploid \textit{vid21Δ::KanMX4} mutant strains are shown in Figures 6 and 8, respectively. It can be seen that the deletion confers significant X-ray sensitivity in both the haploids and in the homozygous diploid strain. The mutant effect is only slightly less than that shown by the \textit{mdm20} and \textit{nat3} deletion strains in Figure 4.

The recent finding that \textit{VID21/EAF1} encodes a member of the NuA4 HAT complex (Doyon \textit{et al.} 2004) will help to clarify its role in repair. The catalytic unit of this complex is the essential gene \textit{ESA1}, whose product acetylates \textit{in vivo} up to four lysine residues in the tail region of histone H4 and probably some sites on other histone proteins to a lesser degree (Allard \textit{et al.} 1999; Sterner and Berger 2000). Mis-sense mutants that are viable but partially defective in the activity of Esa1 protein, and histone H4 mutants in which the target lysine residues are altered to non-acetylated amino acids, have both been shown to confer
sensitivity to MMS and camptothecin (Bird et al. 2002). Another mutant involving the NuA4 HAT complex, yng2null, has also shown to be sensitive to MMS and camptothecin, and to show a reduction in the repair of MMS-induced DSBs in an assay using pulsed-field gel electrophoresis (Choy and Kron 2002). It has been suggested (Bird et al. 2002) that some NuA4 complex mutants may affect replication-coupled repair, based on their increased sensitivity to camptothecin, which is a topoisomerase I poison known to lead to DSBs during replication (D’Arpa et al. 1990).

**DCC1:** The DCC1 gene is represented by ORF YCL016C. Its gene product was identified as a protein that binds to others involved in sister-chromatid cohesion, and the gene was named DCC1 based on its mutant phenotype of defective sister chromatid cohesion (Mayer et al. 2001). A human homolog, hDCC1, has been cloned and characterized (Merkle et al. 2003). Strains from the genomic deletion library that were deleted for YCL016C (DCC1) were reported as IR-sensitive in spot-tests by Bennett et al. (2001), and we verified that this phenotype is conferred by the deletion (see Table 1). Detailed X-ray survival curves (Figure 7) confirm the IR sensitivity, with two haploid spore-cones showing excellent agreement. A diploid homozygous for the dcc1∆::KanMX4 deletion, constructed by mating two spore-clones, also shows substantial X-ray sensitivity (see Figure 8).
It is likely that recombinational repair involving sister chromatids could be
defective in *dcc1* deletion strains given the known role of *DCC1* in enabling sister-
chromatid cohesion (MAYER et al. 2001). Recombinational repair using sister-
chromatids as templates is believed to be a major route for repair of IR-induced
DSBs in wild-type haploid yeast cells (see KUPIEC 2000; GAME 2000 for reviews).
In addition, work with several organisms including Saccharomyces (SJOGREN and
NASMYTH 2001), Schizosaccharomyces (HARTSUIKER et al. 2001) and Coprinus
(CUMMINGS et al. 2002) has shown that mutants directly affected in sister-
chromatid cohesion are often sensitive to radiation and compromised in
recombinational repair (reviewed by STRUNNIKOV and JESSBERGER 1999). Dcc1p
forms part of an “alternative” replication factor C (RFC) complex (MAYER et al.
2001) that has recently been shown to load the sliding-clamp proliferating cell
nuclear antigen (PCNA) on to DNA (BERMUDEZ et al. 2003). The same clamp-
protein (PCNA) is also loaded on to DNA by the related RFC1 complex, which
contains several proteins in common but lacks Dcc1p (CULLMANN et al. 1995;
reviewed in WAGA and STILLMAN 1998). It has been proposed that the Dcc1p-
containing complex loads PCNA on to DNA at certain sites, and that this effects a
change in the replication-polymerase machinery to enable cohesin proteins to be
laid down at these sites, leading to sister-chromatid cohesion (MAYER et al. 2001).
In addition, modified forms of PCNA are major players in controlling post-replication/translesion synthesis repair. Modification of PCNA is mediated by the RAD6, RAD18, RAD5 and UBC13 gene products in a complex way to provide ubiquitinated and SUMO-ylated forms of this protein, and these modifications are thought to control its roles in different repair mechanisms (reviewed in Matunis 2002; see also Höge et al. 2002; Stelter and Ulrich 2003).

There are six other proteins in the same heptameric alternative RFC complex that includes the Dcc1 protein. These consist of four RFC proteins that are essential and occur in the other RFC complexes, plus the products of the CTF8 and CTF18 genes (Hanna et al. 2001; Mayer et al. 2001; Naiki et al. 2001). We have not yet tested strains deleted for either CTF8 or CTF18, but note that Bennett et al. (2001) have reported that strains deleted for CTF8 showed IR-sensitivity in spot tests. CTF18 was initially identified and named CHL12 based on a screen for mutants with increased chromosome-loss (Kouprina et al. 1993). The deletion mutant was found to show elevated spontaneous mitotic recombination, slow growth, and cold-sensitive phenotypes (Kouprina et al. 1994).

**Testing the mutants for cross-sensitivity to ultra-violet radiation:** Yeast mutants that are sensitive to IR frequently show cross-sensitivity to ultraviolet
radiation (UV). To determine if the IR sensitive mutants discussed above also confer UV-sensitivity, we obtained UV survival curves for at least one strain carrying each mutant. Results are shown in Figure 10, which includes a wild-type strain and a highly UV-sensitive rad14null excision repair mutant as controls. It can be seen that none of the nine other mutants confer high UV sensitivity, and all except possibly the mdm20Δ and nat3Δ strains fall within or very close to the wild-type range. In the case of nat3Δ and mdm20Δ, we also studied meiotic tetrads from heterozygous diploids to test for segregation of a UV-sensitive phenotype. On UV-irradiated replica plates, we could not observe any clear segregation for a sensitivity phenotype among spore-clones from five and 13 complete tetrads segregating for mdm20Δ and nat3Δ respectively. The weaker growth of the mutant spore clones tended to complicate the interpretation, but we inferred that the difference in sensitivity between wild-type and mutant spore-clones was at most minor.

**GENERAL DISCUSSION**

We have documented here an IR-sensitive phenotype for haploid and homozygous diploid yeast mutants involving deletions of the DOT1, SPT7, SPT20, HFI1, MDM20, NAT3, VID21(EAF1) and DCC1 genes. We have found at most a
borderline X-ray sensitivity in mutants deleted for another gene, \textit{GCN5}. In each case except \textit{GCN5}, we have demonstrated that IR-sensitivity co-segregates with the deletion allele in meiotic tetrads. To confirm that a deletion mutation confers IR-sensitivity, we consider it essential to obtain quantitative survival data and also to demonstrate that the phenotype is conferred by the deletion itself. With this in mind, we confirmed that the \textit{nat3A}, \textit{vid21A} and \textit{dcc1A} mutations do confer IR sensitivity, following a previous report (\textit{Bennett et al.} 2001) that identified strains containing these deletions as sensitive in qualitative tests. Strains reported as sensitive that carried deletions in \textit{htl1A} or \textit{def1A/vid31A} (\textit{Bennett et al.} 2001) gave very poor spore viability in our crosses of the \textit{MAT\alpha} haploids to wild-type. We did not confirm that sensitivity is conferred by the deletion rather than another change such as altered ploidy, although both factors could have contributed to the sensitive phenotype. Apart from these mutants, we focused our initial screen on 357 mutants based on other criteria described earlier. Finally, we screened deletions involving three additional genes because their products formed complexes with the product of the \textit{SPT20} gene whose deletion we identified as IR-sensitive.

The results reported here complement the earlier identification of the \textit{RAD61} gene, which resulted from information from the pool assay (\textit{Birrell et al.} 2001; \textit{Game et
al. 2003) and has recently been reported to show a defect in sister-chromatid cohesion (Warren et al. 2004). We are continuing to characterize both the rad61 deletion and the mutants reported on here in terms of epistasis relationships and phenotypes involving mutation and recombination. No inferences can be drawn about the overall frequency of genes involved in IR-sensitivity from this work, because we used non-random criteria in choosing the initial set to study.

We find that none of the mutants reported on here confers substantial cross-sensitivity to UV radiation. This may argue against a significant role in post-replication repair (PRR) for these mutants. While not all known PRR mutants are significantly radiation sensitive, those that do confer IR sensitivity, such as rad6null, rad18null and rad5null, usually also confer substantial UV-sensitivity. In contrast, mutants in recombinational repair usually confer only minor UV-sensitivity (see Game, 1983).

We searched the online datasets at the Saccharomyces Genome Database to determine if the wild-type genes whose mutants we studied are induced by radiation. We found no evidence in the literature for a strong and consistent induction of any of these genes by IR. This is not necessarily surprising in view of reports that there is a poor correlation between Saccharomyces genes that are
induced by toxic agents and genes responsible for resisting those agents (Begley et al. 2002; Birrell et al. 2002).

Of the 9 mutants we report on here perhaps the most interesting is the dot1 deletion, which specifically eliminates the methylation of the lysine-79 residue in the core of the histone H3 protein (Ng et al. 2002; Feng et al. 2002; Van Leeuwen et al. 2002). Histone H3 mutants in which this target lysine is replaced by other amino-acids show nearly equivalent IR-sensitivity (see Figure 1). This provides strong evidence that this methylation, which cannot occur on the substituted amino acids, is responsible for the role of the highly conserved DOT1 gene in IR-resistance. It further links histone modification to DNA repair, and provides an opportunity to use epistasis analysis and additional characterization to identify the repair pathways involved.

In addition to histone H3 lysine-79 methylation, we have shown that five genes involved in histone acetylation and transcriptional regulation (HAT) complexes play some role in IR-resistance. Four of these, SPT7, SPT20, HFI1 and GCN5, encode components of the SAGA protein complex, while VID21/EAF1 encodes a protein in the separate NuA4 HAT complex. Given the milder phenotype in gcn5Δ compared to the other HAT mutants, it is plausible that the IR sensitivity seen in
these different HAT complex mutants could be mediated indirectly by effects on transcriptional activation, which could influence the activity levels of other repair genes, rather than via histone acetylation *per se*. This is also possible in the case of the *dot1null* mutant, but perhaps less likely given the greater degree of IR-sensitivity and the known role of *DOT1* in the control of gene silencing and chromatin structure. Two other genes amongst the nine, *NAT3* and *MDM20*, are also involved in acetylation, although there are multiple target protein(s) for the NatB acetylase that they encode (POLEVODA and SHERMAN 2003). In contrast, it seems probable that the deletion of *DCC1* leads to X-ray sensitivity through disruption of sister-chromatid cohesion, since the gene product has a known function in ensuring this process (MAYER et al. 2001), and it is known that mutants affected in sister-chromatid cohesion can be sensitive to radiation and compromised in recombinational repair (reviewed by STRUNNIKOV and JESSBERGER 1999).

The diverse roles of the genes studied here confirm that much remains to be learned about recovery from IR damage. None of them has a product that is known to interact directly with DNA. Genes whose products modify other proteins that themselves may interact with DNA are emerging as a significant class of all those involved in IR-recovery. Such genes include the well-known *RAD5*, *RAD6*,


and \textit{RAD18} loci \cite{Hoege2002, Stelter2003} as well as some of those more recently identified. Since some protein-modifying enzymes such as the Nat3 complex have multiple targets, knowledge of their enzymatic function does not necessarily clarify their role in repair, or even which repair mode they are involved in. However, double-mutant analysis can take advantage of the many \textit{Saccharomyces} genes already associated with identified repair pathways. This should determine which if any of the currently known pathways require the functions recently identified as relevant.

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### TABLE 1.

Spore viability and available co-segregation data for nine deletion-mutant heterozygous diploids.

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Systematic name</th>
<th>% spore viability</th>
<th># tetrads obtained with 4 live spore-clones</th>
<th># tetrads showing 2+:2- co-segregation for geneticin resistance and IR-sensitivity.</th>
</tr>
</thead>
<tbody>
<tr>
<td>DOT1</td>
<td>YDR440W</td>
<td>95.8</td>
<td>21</td>
<td>21</td>
</tr>
<tr>
<td>SPT7*</td>
<td>YBR081C</td>
<td>97.9</td>
<td>22</td>
<td>22</td>
</tr>
<tr>
<td>SPT20</td>
<td>YOL148C</td>
<td>85.0</td>
<td>31</td>
<td>31</td>
</tr>
<tr>
<td>HFII (ADA1)</td>
<td>YPL254W</td>
<td>95.5</td>
<td>18</td>
<td>18</td>
</tr>
<tr>
<td>MDM20</td>
<td>YOL076W</td>
<td>97.5</td>
<td>17</td>
<td>17</td>
</tr>
<tr>
<td>NAT3</td>
<td>YPR131C</td>
<td>94.2</td>
<td>20</td>
<td>19**</td>
</tr>
<tr>
<td>VID21</td>
<td>YDR359C</td>
<td>98.4</td>
<td>15</td>
<td>15</td>
</tr>
<tr>
<td>DCC1</td>
<td>YCL016C</td>
<td>97.4</td>
<td>18</td>
<td>18</td>
</tr>
<tr>
<td>GCN5</td>
<td>YGR252W</td>
<td>90.6</td>
<td>31</td>
<td>See Text</td>
</tr>
<tr>
<td>HTL1</td>
<td>YCR020W-B</td>
<td>38.9</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>DEF1 (VID31)</td>
<td>YKL054C</td>
<td>40.3</td>
<td>2</td>
<td>0</td>
</tr>
</tbody>
</table>

*The data for SPT7 are from a secondary cross using an spt7Δ spore-clone back-crossed to wild-type, see text.  
** In one tetrad, all four spores-clones were geneticin-resistant and X-ray sensitive. This could have arisen from a diploid cell that had become homozygous for the deletion. Two of these spore-clones appeared less IR-sensitive than the other two, for unknown reasons, but were clearly more sensitive than wild-type.
FIGURE LEGENDS

FIGURE 1. Survival versus X-ray dose for two haploid dot1 deletion strains and an hht2-K79Q mutant haploid. This mutant (from K. Struhl) is chromosomally deleted for both of the genes that encode histone H3 (HHT1 and HHT2) and both of the histone H4 genes (HHF1 and HHF2) that are linked to them. It carries a CEN plasmid bearing a wild-type HHF1 gene and a mutant allele of HHT2 (hht2-K79Q) encoding a glutamine substitution at the lysine-79 position. Controls shown are UCC1111, which carries wild-type HHT1 and HHF1 genes on a CEN plasmid to cover the chromosomally deleted copies; and standard wild-type, rad51Δ and rad5Δ haploids in the deletion library background.

FIGURE 2. Survival versus X-ray dose for two spt7 and two spt20 haploid deletion strains. A wild-type and a rad51Δ haploid are included for comparison.

FIGURE 3. Survival versus X-ray dose for two gcn5 and two hfi1 haploid deletion strains. A wild-type and a rad51Δ haploid are included for comparison.

FIGURE 4. Survival versus X-ray dose for two mdm20 and two nat3 haploid deletion strains. g1229-1D mdm20Δ is unable to grow at 37° and g1229-9B
mdm20Δ spore clone can grow at 37°, see text. A wild-type and a rad51Δ haploid are included for comparison.

FIGURE 5. Survival versus X-ray dose for nat3Δ and wild-type strains pre-grown at 25° and incubated at 25° or 37° after X-ray treatment. Survival data for a rad51null haploid pre-grown and incubated at 30° is included for comparison. An experiment (not shown) in which nat3Δ strains were pre-grown at 25° and incubated after X-rays at 30° gave survival curves equivalent to those shown in Figure 4

FIGURE 6. Survival versus X-ray dose for two haploid vid21 (ORF YDR359C) deletion strains. A wild-type and a rad51Δ haploid are included for comparison.

FIGURE 7. Survival versus X-ray dose for two haploid dcc1 deletion strains. A wild-type and a rad51Δ haploid are included for comparison.

FIGURE 8. Survival versus X-ray dose for diploids homozygous for dot1Δ, mdm20Δ, nat3Δ, vid21Δ, and dcc1Δ mutations. Survival data for a wild-type and a rad51null diploid are included for comparison.
FIGURE 9. Survival versus X-ray dose for diploids homozygous for \textit{gcn5}\Delta, \textit{hfi1}\Delta, \textit{spt7}\Delta \textit{and spt20}\Delta \textit{mutations}. Survival data for a wild-type and a \textit{rad51null} diploid are included for comparison.

FIGURE 10. Survival versus ultra-violet radiation dose for ten haploid deletion mutant strains compared with wild-type. A \textit{radl4null} mutant, defective in nucleotide excision repair, is included for comparison and shows the high sensitivity expected for such strains.
Figure 1
Figure 2
Figure 3
Figure 4
Figure 5
Figure 6
Figure 7
Figure 8
Figure 9
Figure 10