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Multiple start codons and phosphorylation result in discrete Rad52 protein species

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ABSTRACT
The sequence of the Saccharomyces cerevisiae RAD52 gene contains five potential translation start sites and protein-blot analysis typically detects multiple Rad52 species with different electrophoretic mobilities. Here we define the gene products encoded by RAD52. We show that the multiple Rad52 protein species are due to promiscuous choice of start codons as well as post-translational modification. Specifically, Rad52 is phosphorylated both in a cell cycle-independent and in a cell cycle-dependent manner. Furthermore, phosphorylation is dependent on the presence of the Rad52 C terminus, but not dependent on its interaction with Rad51. We also show that the Rad52 protein can be translated from the last three start sites and expression from any one of them is sufficient for spontaneous recombination and the repair of gamma-ray-induced double-strand breaks.

INTRODUCTION
Saccharomyces cerevisiae RAD52 was initially isolated in a genetic screen for mutants that were sensitive to radiation and to agents known to cause DNA double-strand breaks (DSBs) (1,2). Further analysis showed that rad52 mutant strains display a pleiotropic phenotype, including defects in DNA DSB repair, reduced mitotic and meiotic recombination rates, deficient mating-type switching, elevated mutation rates, increased chromosome loss and low spore viability (3–8). The importance of RAD52 is underscored by its conservation through evolution in species ranging from yeast to humans (9–14).

Although the sequence of S.cerevisiae RAD52 has been known for more than 20 years (15), the precise gene product(s) have not been defined. This is due to the presence of five potential translation start sites in the RAD52 open reading frame (ORF). Previously, analysis by S1 nuclease digestion of the RAD52-encoded mRNA has shown that a major transcript starts 10 nt downstream of the second ATG triplet in the ORF (15). In accordance with this, most biochemical analyses of Rad52 have employed protein expressed from the third AUG triplet, leaving open the possibility that important aspects of the protein have been overlooked. It is possible that endogenous expression of Rad52 is more complex, as has been shown for other genes with multiple start codons. For example, the SUC2 invertase gene in yeast contains multiple ATG codons, and initiation at the first start site yields a glycosylated, secreted invertase protein. However, when translation initiates from a downstream AUG, the result is an unglycosylated invertase protein that remains in the cell (16).

The ribosomal ‘scanning’ model (17–20) proposes a mechanism by which eukaryotic ribosomes select the translation initiation site. Briefly, the 40S ribosomal subunit binds near the free 5' end of an mRNA and migrates through the non-coding region scanning for a translational start site. In yeast and higher eukaryotes, 95% of translation initiates at the AUG triplet near the 5' end (21,22). However, some eukaryotic transcripts have more complex arrangements and the sequence surrounding the AUG codon can either enhance or inhibit initiation of translation at that site. Hence, if the first AUG triplet encountered occurs in a suboptimal
sequence recognition context, some 40S subunits will bypass this triplet and initiate translation at a downstream start site by a process termed ‘leaky scanning’ (23–27). Three features near the start codon influence leaky scanning. First, multiple studies have analyzed mRNA sequences and the context surrounding the AUG triplet in many yeast genes to determine whether a consensus sequence exists (22,28,29). From these studies, only the preference for a purine at position −3 is consistent. This preference has been confirmed by mutational analysis of the 5′ upstream region of the CYC7 gene fused to the coding region of lacZ (27). In that study, the preferred nucleotide at position −3 was A=G>C>T, with relative protein translational levels 100:94:69:54 (27). In the case of the S. cerevisiae RAD52 gene, the nucleotide at the −3 position for the five ATG codons (from 5′ to 3′) is C, C, T, A and G, respectively.

Second, the length of the 5′ mRNA leader sequence also influences leaky scanning (30,31). In yeast, the majority of leader sequences (70%) range from 20 to 60 nt, which is sufficiently long to support initiation of translation (22). Inspection of the RAD52-encoded mRNA by S1 nuclease digestion (15) shows that a major transcript starts 10 nt downstream of the second ATG triplet, thus allowing for a minimum leader sequence of 47 nt upstream of the remaining ATGs.

Finally, experimental data from mammalian systems suggest that a stable stem–loop structure 12–15 nt downstream of a start codon can cause the scanning ribosome to pause with its AUG-recognition center right over the initiator codon, providing more time for the recognition of this start site (32). In the S. cerevisiae RAD52-encoded mRNA, a potential stem–loop structure is located downstream of the fifth start codon. This hairpin may influence the preference of the ribosome for the start codons differently as the distance separating the stem–loop structure from the third, fourth and fifth start codons is 33, 21 and 15 nt, respectively.

Size determination of the Rad52 protein by gel-electrophoresis followed by immunoblot analysis typically detects multiple protein species. The existence of different Rad52 species suggests a promiscuous start codon choice. In addition, some of the multiple protein species could also result from post-translational modification and/or degradation. Here we show that yeast RAD52-encoded mRNA produces Rad52 expressed from three different start sites and that DNA DSB repair is supported by the three protein species. In addition, Rad52 is phosphorylated both in a cell cycle-independent and cell cycle-dependent manner and these modifications require the presence of the Rad52 C terminus. Finally, maintenance of wild-type Rad52 protein levels is important for efficient repair of some types of DNA damage.

**MATERIALS AND METHODS**

**Genetic methods, yeast strains, site-directed mutagenesis and plasmids**

Media were prepared as described previously and contains twice the amount of leucine (60 mg/l) and the yeast strains were manipulated using standard genetic techniques (33). All strains used in this study are RAD5 derivatives of W303 and are listed in Table 1 (34,35). The sequences of the oligonucleotides used to introduce the specific mutations in RAD52 are listed in Table 2.

The pRS414-RAD52 CEN vectors containing single start codon mutants were made by site-directed mutagenesis, as described previously (36). The rad52 point mutations were integrated into the RAD52 genomic locus using a cloning-free PCR-based allele replacement method (37). Individual rad52 point mutations were PCR amplified from the corresponding pRS414-RAD52 CEN vector in 100 μl reactions. For both triple rad52 mutant strains (E24Stop M38A M40A and E24Stop M34A M38A), the changes were introduced by three sets of PCRs. The first PCR generates overlapping fragments containing different mutations. In the second PCR, the two overlapping fragments were fused. Fragments containing the N-terminal and C-terminal two-thirds of the Kluyveromyces lactis URA3 gene were amplified. The final PCR fuses the K. lactis URA3 fragments to the RAD52 fragments. The products were gel purified and co-transformed into wild-type yeast strain W1588-4C to create the single rad52 mutants
The first six oligonucleotide primers were described previously (36, 37).

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adapt-a</td>
<td>5'-CATCCTGCTACCTGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>Adapt-b</td>
<td>5'-CATGGCAATTCCGGGATGATTCGTTCTGAGTAAGATCG-3'</td>
</tr>
<tr>
<td>ARad52</td>
<td>5'-AATTCAGGGCCACACCGACGATGCTGTTGTCG-3'</td>
</tr>
<tr>
<td>BRad52</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>3'-int</td>
<td>5'-CTTGAGCTTTGCTGACTGATGAGC-3'</td>
</tr>
<tr>
<td>5'-int</td>
<td>5'-CCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>AdapB-M40A38A</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>M38A34A</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>M34AM18A</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>A-4Ala</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>Bwd2AAla</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>Fwd2AAla</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>R52Bwd2353-B</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>ARad52</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>Adapt-a</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>M34AM38A</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>M38A34A</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>M34AM18A</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>A-4Ala</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>Bwd2AAla</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>Fwd2AAla</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
<tr>
<td>R52Bwd2353-B</td>
<td>5'-GATCCCCGGGGAATTCGATGATGTTCTGTGTT-3'</td>
</tr>
</tbody>
</table>

The first six oligonucleotide primers were described previously (36, 37).

or into J795 (E24Stop) to create the triple rad52 mutations. Transformants were selected on SC-Ura and ‘pop-out’ recombinants that excised the K.lactis URA3 marker were selected on SC-5-fluoro-orotic acid medium. All rad52 point mutations were designed to generate a restriction nuclease polymorphism and were further confirmed by DNA sequencing.

pRS423-RAD52, a 2 μ vector based on pRS423 (38) carrying the entire RAD52-containing SalI fragment (15) was used to make the pRS423-M34A plasmid. Briefly, pRS423-RAD52 was linearized with restriction enzyme Agel and transformed into the J789 yeast strain to gap-repair the chromosomal rad52-M34A mutation onto the plasmid. The rad52 point mutation alters a restriction enzyme site and was confirmed by PCR and restriction enzyme analysis.

### Analysis of sensitivity to gamma-irradiation

The sensitivity to gamma rays was analyzed as described previously (39) and quantitative survival curves were made by calculating ln(percent survival) for each dose. The slope (α) of the resulting straight line can be used to calculate an LD37 value [—ln(1/0.37)/ln(α)]. The LD37 value represents the dose in krad necessary to induce a mean of one lethal hit per cell and was used to quantitatively compare survival of different strains.

The effect of overexpressing the M34A mutant for gamma-irradiation survival was determined as follows. An M34A strain (J789) was transformed with 2 μ pRS423 (empty vector control), pRS423-RAD52 and pRS423-M34A. Wild-type (W1588-4C) was transformed with pRS423 as a control. Overnight cultures were plated on SC-His medium and survival after gamma-irradiation was measured.

**Spontaneous LEU2 heteroallelic recombination**

Mitotic interchromosomal recombination between the leu2-DcoRI and leu2Δ-BstEII heteroalleles was measured in diploid strains as described previously (39), except that the strains were pre-grown in liquid SC medium before plating. Plating efficiency and the number of recombinants were determined by plating an appropriate number of cells on SC and SC-Leu plates, respectively. For each strain, 5–9 independent trials were carried out and the corresponding recombination rates and their standard deviations were calculated according to the median of the described previously (40).

**Cell cycle synchronization, protein extraction and immunoblot analysis**

Yeast cultures were grown at 30°C to early/mid-log phase in YPD (pH 3.7). Cells were arrested in G1 phase by incubating in the presence of α-mating factor for 90 min (3.4 μg/ml; Sigma, St Louis, MO). Next, cells were released from the G1-arrest by washing in 1 vol four times and resuspending the cells in 1 vol of pre-warmed YPD (pH 5.6). An aliquot of 1.5 ml samples were taken at different time points after release from G1. For protein samples from unsynchronized cells, the cultures were grown at 30°C to early/mid-log phase in YPD before aliquots were taken. The cells were harvested by centrifugation and resuspended in 0.5 ml of 25% TCA. After centrifugation, the resulting pellets were washed twice with 90% acetone, resuspended in 1% SDS and an equal volume of glass beads added. The samples were vortexed 3 times for 30 s and incubated on ice for 1 min between each round of vortexing. An equal volume of loading buffer (60 mM Tris–HCl, pH 6.8, 25% glycerol, 2% SDS, 14.4 mM 2-mercaptoethanol, 0.1% bromophenol
Polyacrylamide, polyacrylamide/bis 37.5:1, 20 cm × 16 cm × 1 mm gels) and immunoblot analysis performed as described previously (41).

**Fluorescence-activated cell sorting**

Fluorescence-activated cell sorting (FACS) analysis was performed to determine DNA content of cells collected from cell cycle synchronization experiments. At each time point, a 1 ml sample was collected and fixed in 70% ethanol overnight at room temperature. Ethanol was removed and the cells were washed once with 50 mM sodium citrate. The pellet was resuspended in 50 mM sodium citrate and 0.25 mg/ml RNase A and incubated at 50°C for 1 h. Proteinase K was added to a final concentration of 1 mg/ml and incubated at 50°C for 1 h. An equal volume of 50 mM sodium citrate containing 8 µg/ml propidium iodide was added and the samples placed on a shaker in the dark at room temperature for 30 min. Samples were sonicated and then analyzed using a FACS Calibur (Becton Dickinson, Franklin Lakes, NJ).

**Phosphatase treatment**

Rad52 protein was isolated as described above, except that, after the acetone washes, the pellet was resuspended in NP-40 buffer (50 mM Tris–HCl, pH 8.0, 1% NP-40 and 150 mM NaCl). Immediately, before use, this buffer was supplemented with complete mini EDTA-free protease inhibitor cocktail (Roche, catalog no. 118361700). An equal volume of glass beads was added and the samples were vortexed 3 times for 30 s and incubated on ice for 1 min in between each vortexing. The samples were treated with λ-phosphatase (New England Biolabs) for 45 min at 30°C, an equal volume of loading buffer was added and they were boiled for 5 min before loading. Rad52 protein species were separated by SDS–PAGE and immunoblot analysis performed as described previously (41).

**Preparation of Rad52 extracts from E.coli**

*E. coli* strain M15 (pREP4) was transformed with pQE60-Rad52-His6 (42) and plated on Luria–Bertani broth containing 100 µg/ml ampicillin and 25 µg/ml kanamycin. An overnight culture was grown at 37°C, diluted 1:40 and grown for an additional 3 h. At this point, the expression of Rad52-HIS6 was induced by adding IPTG to a final concentration of 1 mM. After a 1 h induction, the cells were pelleted by centrifugation and the pellet was resuspended in 5 ml equilibration buffer (20 mM phosphate buffer, pH 8.0, 400 mM NaCl, 10% glycerol, 1 mM PMSF, 0.66 ml/ml lysozyme and 5% Triton X-100). The sample was sonicated (Ultrasonic W-385 Processor, Heat System-Ultrasonics, Inc.) five times for 1 min separated by a 2 min ice incubation and subsequently spun for 5 min at 18 000 r.c.f. Rad52-HIS6 protein was separated by SDS–PAGE and immunoblot analysis was performed as described above.

**Statistical analysis**

A t-test was used to determine the significance for gamma-ray survival differences.

## RESULTS

The first two potential start codons in *RAD52* are not used

Analysis of wild-type *S.cerevisiae* Rad52 reveals multiple protein species with different electrophoretic mobilities (42–45). In the resolution obtained in the present study, 3–4 Rad52 protein bands were typically detected for the wild-type strain. The apparent molecular weight of the three Rad52 protein bands in Figure 1A are ~54, 57 and 60 kDa. The different Rad52 species may represent the result of differential start codon usage and/or post-translational modifications. To investigate these possibilities, *RAD52* sequences obtained from three other species from the *Saccharomyces sensu stricto* group (*S.paradoxus, S.uvarum* and *S.monacensis* var. *pastorianus*) were inspected for the presence of multiple potential start codons. As shown in Figure 1B, the first, third, fourth and fifth *S.cerevisiae* ATG codons are present in the other three *Saccharomyces* species. However, in the three closely related species, the first start codon is not in-frame with the remaining *RAD52* ORFs due to single base-pair deletions and insertions within the first 70 nt. Furthermore, stop codons following the first ATG start site prevent the formation of a peptide of significant length in all three related species. Hence, in *S.paradoxus, S.uvarum* and *S.monacensis* Rad52 protein can only be translated from the ATGs that are equivalent to the third, fourth and fifth start codons in-frame with the previous ATG encountered are underlined. * denotes conserved nucleotides.
codons in \textit{S. cerevisiae}. These results suggest that Rad52 translation in \textit{S. cerevisiae} starts from the third, fourth and/or fifth start codons. To test this hypothesis, the glutamic acid codon at position 24 (between the second and third potential ATGs) was replaced with a stop codon. As expected, this mutant strain is as resistant to gamma-irradiation as the wild-type strain, and immunoblot analysis demonstrated that the mutation did not significantly change the Rad52 protein level (data not shown). In addition, the analysis detects multiple protein species with the same electrophoretic mobilities as those observed for wild-type Rad52 (data not shown).

**Rad52 protein contribution from the third start codon**

To test the possibility that the multiple Rad52 species detected by protein-blot analysis result from differential usage of the third, fourth and fifth start codon, various point mutations were created to analyze the contribution from the third start codon. First, three different types of mutations: a methionine-to-alanine substitution at amino acid 34 (M34A), a stop codon (E36Stop) and a frameshift mutation (FS3-4) were individually introduced to disrupt translation from the third start codon (Figure 2A). Strains that contain either of the two latter mutations produce short peptides (a 2 amino acid peptide and 28 amino acid frameshifted peptide, respectively) if translation is attempted from the third start codon. Hence, in these three mutant strains, Rad52 protein can only be expressed from the fourth and/or fifth start codons. To determine the sensitivity of these mutants to gamma-irradiation, survival curves were determined and LD37 values were calculated (see Materials and Methods). Comparison of the resulting LD37 values demonstrates that each mutant strain is ∼3-fold more sensitive to gamma-irradiation than the wild-type strain (Figure 2C and Table 3). In contrast, a rad52 null (rad52Δ) strain is 20-fold more sensitive than the wild-type strain.

Second, to analyze whether expression from the third start codon is sufficient to repair DNA damage, a triple mutant strain, \textit{E24Stop M38A M40A}, was made. This

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**Figure 2.** Analysis of the third start codon. Note, \textit{RAD52}-mRNA initiates 10 nt downstream of start codon 2 (15). (A) Schematic diagram of M34A, E36Stop and FS3-4 mutant strains. M34A results from a methionine-to-alanine substitution at amino acid 34. E36Stop results from a stop codon inserted at amino acid 36. FS3-4 mutant results from a frameshift mutation inserted between the third and fourth ATGs. In FS3-4, translation initiated upstream of the fourth start codon results in truncation at amino acid 63. Hence in these mutant strains, Rad52 can only be expressed from the fourth and/or fifth start codons. (B) Schematic diagram of \textit{E24Stop M38A M40A} mutant having a stop codon at residue 24, and two methionine-to-alanine substitutions at amino acids 38 and 40. In this mutant, translation can only start at the third start codon. M, methionine residues indicating the position of the ATG codons. A, alanine residues substitute the methionine amino acids at the indicated positions. Residues in gray are not productive for translation start. (C) Survival curves of haploid strains after increasing doses of gamma-ray-induced DNA damage. Black diamond, \textit{RAD52}; open circle, \textit{rad52Δ} null; black circle, M34A; black square, FS3-4; inverted open triangle, E36Stop; and open diamond, \textit{E24Stop M38A M40A}. (D) Gamma-ray survival after overexpression of the \textit{RAD52} and M34A genes from 2\textit{μ} plasmids. Cells carrying 2\textit{μ} plasmids were grown and plated on SC-His medium. Open square, \textit{RAD52} transformed with pRS423 (empty vector); open triangle, M34A transformed with pRS423-M34A; inverted black triangle, M34A transformed with pRS423; and black triangle, M34A transformed with pRS423-rad52Δ.
Table 3. The effect of start codon mutants on gamma-ray sensitivity (LD37) and mitotic heteroallelic recombination rate

<table>
<thead>
<tr>
<th>Strain</th>
<th>Gamma-ray sensitivity (LD37)</th>
<th>Mitotic recombination rate ×10−6b</th>
</tr>
</thead>
<tbody>
<tr>
<td>RAD52</td>
<td>51.2 ± 2.9</td>
<td>1.2 ± 0.2</td>
</tr>
<tr>
<td>E24Stop</td>
<td>56.5 ± 3.6</td>
<td>1.7 ± 0.3</td>
</tr>
<tr>
<td>M38A</td>
<td>52.8 ± 5.7</td>
<td>1.1 ± 0.2</td>
</tr>
<tr>
<td>M40A</td>
<td>44.2 ± 1.6</td>
<td>0.5 ± 0.1</td>
</tr>
<tr>
<td>E24Stop M34A M38A</td>
<td>53.8 ± 8.9</td>
<td>1.0 ± 0.2</td>
</tr>
<tr>
<td>M34A</td>
<td>19.1 ± 1.0</td>
<td>0.4 ± 0.1</td>
</tr>
<tr>
<td>FS3-4</td>
<td>15.8 ± 0.1</td>
<td>0.8 ± 0.1</td>
</tr>
<tr>
<td>E36Stop</td>
<td>16.9 ± 0.4</td>
<td>2.0 ± 0.3</td>
</tr>
<tr>
<td>E24Stop M38A M40A</td>
<td>14.8 ± 0.1</td>
<td>0.6 ± 0.1</td>
</tr>
<tr>
<td>FS4-5</td>
<td>6.2 ± 0.1</td>
<td>0.02 ± 0.03</td>
</tr>
<tr>
<td>rad52::HIS5</td>
<td>2.6 ± 0.1</td>
<td>0.006 ± 0.003</td>
</tr>
<tr>
<td>Y66o SUP4-o</td>
<td>21.0 ± 1.7</td>
<td>0.3 ± 0.04</td>
</tr>
</tbody>
</table>

aLD37, the dose in krad necessary to induce a mean of one lethal hit per cell, as described in Materials and Methods.
bRecombination rate (events per cell per generation) is presented as the mean ± SD as described in Materials and Methods.

mutant strain has a stop codon at amino acid 24 and two methionine-to-alanine changes at amino acids 38 and 40; thus, Rad52 can only be produced from the third start codon, M34 (Figure 2B). The survival curves and LD37 values indicate that this strain is ~3-fold more sensitive to gamma-irradiation than the wild-type strain (Figure 2C and Table 3). In summary, translation from the third start codon is necessary, but not sufficient for full Rad52 activity (Figure 2C).

The slightly increased gamma-ray sensitivity of the M34A, E36Stop, FS3-4 and E24Stop M38A M40A mutant strains may indicate that a combination of the different Rad52 protein species expressed from the third, fourth and fifth start codons are required for full DNA repair activity. Alternatively, the phenotype of these mutant strains may result from variations in Rad52 protein levels. To distinguish between these possibilities, the RAD52 and M34A alleles were overexpressed from 2μ plasmids (pRS423-RAD52 and pRS423-M34A, respectively) and survival curves after gamma-irradiation determined (Figure 2D). Overexpression of M34A or wild-type Rad52 in the M34A background results in gamma-ray survival curves that are not statistically different. The survival of these two strains is also not significantly different from a wild-type strain transformed with an empty vector (pRS423). However, these three strains are more resistant to gamma-irradiation than M34A itself transformed with the empty vector. Thus, the suppression of the gamma-ray sensitivity of M34A by its overexpression shows that the phenotype of M34A expressed from its endogenous promoter is likely due to reduced protein levels (see below).

Rad52 protein contribution from the fourth and fifth start codons

To determine the role of the fourth and fifth start codons, methionine-to-alanine substitutions were individually introduced into the cell (M38A and M40A, respectively) to prevent translation initiation from these two start codons (Figure 3A). None of these start codons is essential since both strains are as gamma-ray resistant as the wild-type strain (Figure 3B and Table 3).

Next, we constructed FS4-5 to obtain an independent estimate of the amount of protein initiated from start codon five in wild-type cells (Figure 3C). The frameshift mutation results in a dramatic increase in gamma-ray sensitivity, which could be due to either decreased Rad52 protein levels or a repair defect of this shorter protein (Figure 3D and Table 3; Figure 4, lane 8). To distinguish between these possibilities, a triple mutant was created that has a stop codon at amino acid 24 and two methionine-to-alanine codon changes at codons 34 and 38 (E24Stop M34A M38A) (Figure 3C). We find that the increased expression of Rad52 from the fifth start codon in this construct provides wild-type levels of Rad52 activity (Figure 3D and Table 3; Figure 4, lane 10). Taken together, these results indicate that the fifth start codon normally contributes a minor amount of Rad52 protein, which is, however, fully functional for DSB repair after gamma-irradiation.

The increased gamma-ray sensitivity of FS4-5 compared to E24Stop M34A M38A suggests that Rad52 protein levels are important for efficient repair of DSBs (Figure 3D and Figure 4, lanes 8 and 10). To address this issue, a strain was made that expresses decreased levels of wild-type Rad52 protein by combining a SUP4-o nonsense suppressor with a RAD52 ORF containing an ochre termination codon (Y66o). Since ochre suppression is not complete (46, 47), this strain expresses Rad52 at 25% of wild-type levels as determined by quantitative immunoblot analysis (data not shown). At this reduced protein level, we find that the resulting LD37 value is 2- to 3-fold lower than that of wild-type (Table 3), demonstrating that Rad52 becomes limiting for gamma-ray survival at reduced protein levels.

Spontaneous heteroallelic recombination is reduced in strains with decreased levels of Rad52

To investigate the possibility that distinct Rad52 species influence Rad52 functions differentially, spontaneous interchromosomal heteroallelic recombination was measured between two non-functional leu2 heteroalleles, leu2Δ-BstEI1 and leu2Δ-EcoRI (39) for all the rad52 mutants presented in this study. Using this assay, mitotic recombination was investigated in diploid cells homozygous for the RAD52 alleles presented above (Table 3). Compared to a wild-type strain, a rad52Δ strain has a 200-fold lower recombination rate. Among the different start codon mutants, FS4-5 shows the greatest decrease in the rate of spontaneous recombination, consistent with it having decreased protein levels and being the most sensitive to ionizing radiation. In addition, there is a 4-fold reduction in the rate of spontaneous recombination in Y66o SUP4-o strains compared to wild-type cells (Table 3). Thus, at reduced levels, Rad52 protein becomes limiting for spontaneous heteroallelic recombination.

Rad52 is phosphorylated in a cell cycle-independent and cell cycle-dependent manner

Some of the multiple Rad52 protein bands observed for the wild-type strain are accounted for by the promiscuous choice of start codons. For example, the 54 kDa protein band jointly represents Rad52 translated from the fourth and fifth start
Mutational analysis of the fourth and fifth start codons. (A) Schematic diagram of M38A and M40A mutants. M38A or M40A mutant strains result from methionine-to-alanine substitutions at amino acid 38 or 40, respectively. Residues in gray are not productive for translation start. (B) Survival curves of haploid strains after exposure to gamma-irradiation. Black diamond, RAD52; open circle, rad52 null; inverted black triangle, M38A; open triangle, M40A. (C) Schematic diagram of E24Stop M34A M38A and E24Stop M34A M38A mutants. The E24Stop M34A M38A mutant strain has a stop codon at residue 24 and two methionine-to-alanine substitutions at amino acids 34 and 38. In this triple mutant, translation can only start at the fifth start codon. The FS4-5 mutant results from a frameshift mutation inserted between the fourth and fifth ATGs. In FS4-5, translation initiated upstream of the fifth start codon results in truncation at amino acid 63. M, methionine residues indicating the position of the ATG codons. A, alanine residues substitute the methionine amino acids at the indicated positions. Residues in gray are not productive for translation start. (D) Survival curves of haploid strains after exposure to gamma-irradiation. Black diamond, RAD52; open circle, rad52 null; black circle, FS4-5; and open diamond, E24Stop M34A M38A.

Figure 3.Mutational analysis of the fourth and fifth start codons. (A) Schematic diagram of M38A and M40A mutants. M38A or M40A mutant strains result from methionine-to-alanine substitutions at amino acid 38 or 40, respectively. Residues in gray are not productive for translation start. (B) Survival curves of haploid strains after exposure to gamma-irradiation. Black diamond, RAD52; open circle, rad52 null; inverted black triangle, M38A; open triangle, M40A. (C) Schematic diagram of E24Stop M34A M38A and E24Stop M34A M38A mutants. The E24Stop M34A M38A mutant strain has a stop codon at residue 24 and two methionine-to-alanine substitutions at amino acids 34 and 38. In this triple mutant, translation can only start at the fifth start codon. The FS4-5 mutant results from a frameshift mutation inserted between the fourth and fifth ATGs. In FS4-5, translation initiated upstream of the fifth start codon results in truncation at amino acid 63. M, methionine residues indicating the position of the ATG codons. A, alanine residues substitute the methionine amino acids at the indicated positions. Residues in gray are not productive for translation start. (D) Survival curves of haploid strains after exposure to gamma-irradiation. Black diamond, RAD52; open circle, rad52 null; black circle, FS4-5; and open diamond, E24Stop M34A M38A.

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shown). In summary, these results demonstrate that Rad52 is phosphorylated at serine and/or threonine residues in both a cell cycle-independent and cell cycle-dependent manner.

Post-translational modification of Rad52 requires its C-terminus

A key function of the C-terminal domain of Rad52 involves its interaction with Rad51, since the gamma-ray sensitivity of a C-terminal RAD52 truncation, rad52-327Δ (327Δ), can be partially suppressed by overexpression of Rad51 (48,49). Surprisingly, only two Rad52 protein bands were observed in a 327Δ mutant strain at any point in the cell cycle (Figure 5D). These truncated bands likely correspond to the 54 and 57 kDa bands seen in wild-type cells. This result suggests that the C terminus of Rad52 is phosphorylated, or alternatively, that Rad52 phosphorylation requires sequences in the C terminus.

Since the Rad51 interaction domain resides in the C terminus, we tested whether this interaction is required...
for Rad52 phosphorylation by examining Rad52 protein from rad52-409-412Δ (409-412Δ), which has a four-amino acid deletion within the C-terminal domain of Rad52 that ablates its interaction with Rad51 (50). In the 409-412Δ strain, the protein band pattern is identical to wild-type. This result shows that the Rad52–Rad51 interaction is not required for phosphorylation (Figure 5E).

**DISCUSSION**

In this study, we analyzed the multiple start codons present in the *S. cerevisiae* RAD52 ORF by generating a series of mutations within its N-terminus. We conclude that translation of RAD52 is initiated from three start codons and each of the resulting protein species are competent in DNA repair and homologous recombination. According to the 'scanning' model (17–20), translation should initiate preferentially when the ribosome encounters the first AUG start site. In the case of *S. cerevisiae* RAD52, the mRNA transcript begins after the second ATG codon (15); therefore, the third ATG codon corresponds to the first translational start site that can be encountered. However, owing to the suboptimal context around the third start site (a T at the −3 position), ribosome slippage at this site likely results in protein expressed from the fourth ATG triplet, which has an optimal A at the −3 position. Alternatively, initiation at the fourth or fifth AUG could be due to shunting or internal ribosome entry [for a review see (51)]. Moreover, the small amount of Rad52 protein synthesized in the FS4-5 strain suggests that leaky scanning by the ribosomes occurs to bypass start codons three and four and initiate from the fifth (Figure 4, lane 8). By eliminating translation initiation from codons three and four (*E24Stop M34A M38A*), wild-type levels and leaky scanning by the ribosomes occurs to bypass start codons three and four and initiate from the fifth (Figure 4, lane 8). By eliminating translation initiation from codons three and four (*E24Stop M34A M38A*), wild-type levels and leaky scanning by the ribosomes occurs to bypass start codons three and four and initiate from the fifth (Figure 4, lane 8). By eliminating translation initiation from codons three and four (*E24Stop M34A M38A*), wild-type levels and leaky scanning by the ribosomes occurs to bypass start codons three and four and initiate from the fifth (Figure 4, lane 8).

Multiple Rad52 bands are observed where Rad52 can only be translated from either start site three or five (Figure 4, lanes 8–10). Although previous results indicated that protein mobilities of the multiple Rad52 species were not altered after treatment with calf intestinal alkaline phosphatase (45); in this study, we demonstrate that Rad52 protein is indeed phosphorylated and this modification occurs in a cell cycle-independent and cell cycle-dependent manner at serine and/or threonine residues. For example, wild-type cells that are synchronized and released from a G1 arrest exhibit multiple Rad52 bands that after dephosphorylation collapse to a doublet band corresponding to translational products starting from codon three and from codons four and five, which co-migrate (Figure 5C). In addition, both the cell cycle-independent and cell cycle-dependent phosphorylation events require the C-terminal domain of Rad52 (Figure 5D), suggesting that Rad52 is phosphorylated at the C terminus. Alternatively, Rad52 may be phosphorylated within the N-terminal domain but its modification requires the presence of the C-terminus. One of the known functions of the C-terminal domain is to interact with Rad51. However, the phosphorylation pattern is not altered by specifically disrupting the Rad52–Rad51 interaction (Figure 5E), suggesting that this interaction, per se, is not required for phosphorylation to occur. We, therefore, favor the notion that the C terminus contains phosphorylation targets that function to regulate the interaction between Rad52 and Rad51.

Figure 6 summarizes our interpretation of the pattern of electrophoretic mobilities of Rad52 protein. Unmodified Rad52 translated from the fourth and fifth start codons results in the 54 kDa protein band, which is an unresolved doublet, whereas unmodified Rad52 translated from the third start codon migrates more slowly at 57 kDa (Figure 6A). In G1-arrested wild-type cells, three Rad52 protein bands are detected and they are the result of a combination of unmodified Rad52 species together with a first phosphorylation event (Figure 6B). We suggest that the 57 kDa protein band is a combination of unmodified Rad52 expressed from the third start codon together with additional protein species corresponding to phosphorylated Rad52 translated from the fourth and fifth start codons (Figure 6B, 4* and 5*). Similarly, phosphorylation of Rad52 translated from the third start codon sequence rather than the first AUG of the *RAD52*-encoded mRNA.

**Figure 6.** Model to explain the multiple Rad52 protein species. (A) *RAD52*-encoded mRNA allows protein translation from the third and, by leaky scanning, also from the fourth and fifth start codons (3, 4 and 5, respectively). (B) First phosphorylation: cell cycle-independent. Rad52 species from (A) (3, 4 and 5) are modified resulting in slower migrating protein species (3*, 4* and 5*, respectively). (C) Second phosphorylation: cell cycle-dependent. During S phase, some of 3*, 4* and 5* are modified into 3**, 4** and 5**, respectively. Approximate molecular weights (kDa) corresponding to the observed mobility are indicated.
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