The DNA Damage Response and Checkpoint Adaptation in Saccharomyces cerevisiae: Distinct Roles for the Replication Protein A2 (Rfa2) N-Terminus


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ABSTRACT

In response to DNA damage, two general but fundamental processes occur in the cell: (1) a DNA lesion is recognized and repaired, and (2) concomitantly, the cell halts the cell cycle to provide a window of opportunity for repair to occur. An essential factor for a proper DNA damage response is the heterotrimeric protein complex Replication Protein A (RPA). Of particular interest is hyper-phosphorylation of the 32-kDa subunit, called RPA2, on its serine/threonine-rich N-terminus following DNA damage in human cells. The unstructured N-terminus is often referred to as the phosphorylation domain and is conserved amongst eukaryotic RPA2 subunits, including Rfa2 in \textit{Saccharomyces cerevisiae}. An aspartic acid/alanine-scanning and genetic interaction approach was utilized to delineate the importance of this domain in budding yeast. It was determined that the Rfa2 N-terminus is important for a proper DNA damage response in yeast, although its phosphorylation is not required. Subregions of the Rfa2 N-terminus important for the DNA damage response were also identified. Finally, an Rfa2 N-terminal hyper-phosphorylation-mimetic mutant behaves similarly to another Rfa1 mutant (\textit{rfa1-t11}) with respect to genetic interactions, DNA damage sensitivity, and checkpoint adaptation. Our data indicate that post-translational modification of the Rfa2 N-terminus is not required for cells to deal with “repairable” DNA damage; however, post-translational modification of this domain might influence whether cells proceed into M-phase in the continued presence of unrepaired DNA lesions as a “last-resort” mechanism for cell survival.
INTRODUCTION

Cells encounter environmental stress on a continual basis and have evolved mechanisms to monitor the integrity of the genome and prevent temporary DNA lesions from becoming permanent DNA mutations. A central factor in genome monitoring is the protein complex Replication Protein A (RPA). The canonical RPA complex is composed of three subunits named RPA1, RPA2, and RPA3, also often referred to by their apparent molecular weights as RPA70, RPA32, and RPA14, respectively (Wold 1997; Iftode et al. 1999; Fanning et al. 2006; Zou et al. 2006; Oakley and Patrick 2010). Originally identified as a protein complex essential for in vitro SV40 DNA replication (Wold and Kelly 1988; Wold et al. 1989; Weinberg et al. 1990), this complex is also essential for DNA repair/recombination (Longhese et al. 1994; Firmenich et al. 1995; Sung 1997; Umez et al. 1998) and has roles in cell cycle regulation (Longhese et al. 1996; Lee et al. 1998; Anantha et al. 2008; Anantha and Borowiec 2009). This is consistent with the major biochemical function of RPA, which is high-affinity binding to single-stranded DNA (ssDNA), an intermediate of replication, repair/recombination, and substrate for checkpoint activation (Smith et al. 2010; Flynn and Zou 2010; Mimitou and Symington 2011; Ashton et al. 2013).

In addition to acting as a “sensor” of DNA damage through its ability to bind to ssDNA, RPA is also post-translationally modified in response to DNA damage. Identified post-translational modifications of RPA include acetylation (Choudhary et al. 2009), sumoylation (Burgess et al. 2007; Dou et al. 2010), and phosphorylation (Din et al. 1990; Dutta et al. 1991; Liu et al. 1995, 2005, 2012; Henrickson et al. 1996; Brush et al. 1996; Brush and Kelly 2000; Kim and Brill 2003; Vassin et al. 2004; Olson et al. 2006; Anantha et al. 2007, 2008; Lee et al. 2010; Shi et al. 2010; Wang et al. 2013). Most studies of RPA post-translational modifications have focused on hyper-phosphorylation of the 40 amino acid (aa) N-terminal region of human RPA2 in response to DNA damage. The use of “extensive” phospho-mutants (i.e., those where all serines/threonines in the region are changed to aspartic acids to mimic phosphorylation or alanines to prevent phosphorylation) indicates that mimicking a hyper-phosphorylated state results in the inability to detect RPA2 foci at replication centers in otherwise unstressed human cells (Vassin et al. 2004). This suggests that in response to DNA damage, phosphorylated human RPA is recruited away from replication centers to perform functions in DNA repair. Mutagenesis studies have also indicated that phosphorylation
of the human RPA2 N-terminus (NT) is important for halting the cell cycle during replicative stress (Olson et al. 2006), for progression into mitosis (Oakley et al. 2003; Anantha et al. 2008; Anantha and Borowiec 2009), and for differential protein interactions with some DNA damage response proteins (Oakley et al. 2003, 2009; Patrick et al. 2005; Wu et al. 2005).

Within the human RPA2 NT are nine serine/threonine (S/T) residues that are targets for phosphorylation (Iftode et al. 1999; Anantha et al. 2007; Liu et al. 2012). The combination of various RPA2 phospho-mutants and the generation of phospho-specific human RPA2 antibodies have advanced this area of research by allowing for the examination of phosphorylation at each individual target residue. The sites in the human RPA2 NT appear to be differentially phosphorylated in response to various types of DNA damage (Liu et al. 2012), likely due to different checkpoint kinases (e.g., ATR, ATM, and DNA-PK) having different preferential targets within the RPA2 NT (Brush et al. 1996; Olson et al. 2006; Cruet-Hennequart et al. 2008; Vassin et al. 2009; Liaw et al. 2011; Liu et al. 2012). Also, sequential phosphorylation of the human RPA2 NT has been reported, indicating a dependence on phosphorylation of one site to promote phosphorylation of another (Anantha et al. 2007; Liu et al. 2012). Although it is clear that many sites are differentially phosphorylated, the mechanism(s) by which post-translational modification of each site contributes to human RPA function in response to DNA damage remains undefined.

Recent examination of phosphorylation of Replication Factor A (RFA; yeast RPA) in the pathogenic yeast Candida albicans demonstrated that Rfa2 phosphorylation occurs both during the cell cycle and in response to DNA damage (Wang et al. 2013; Gao et al. 2014), similar to findings in Saccharomyces cerevisiae (Din et al. 1990; Brush et al. 1996; Bartrand et al. 2004). Dephosphorylation of C. albicans Rfa2 requires the Pph3-Psy2 phosphatase complex (Wang et al. 2013; Gao et al. 2014), and the PP2AC and PP4C phosphatases are necessary to dephosphorylate human RPA2 during the DNA damage response (Feng et al. 2009; Lee et al. 2010). Mass spectrometry analysis of proteins isolated from unstressed C. albicans pph3Δ mutant cells revealed five potential targets of phosphorylation in Rfa2, none of which were located within the first 40 amino acids. Upon treatment of Candida cells with hydroxyurea (HU), it was determined that T11, S18, S29, and S30 in the Rfa2 NT are targets of phosphorylation by the yeast checkpoint kinase and ATR homolog, Mec1 (Wang et al. 2013; Gao et al. 2014).

In the budding yeast S. cerevisiae, post-translational modifications of Replication Factor A have been
observed in response to DNA damage. Similar to human RPA1, yeast Rfa1 and Rfa2 are sumoylated in response to treatment of cells with methyl methanesulfonate (MMS) (Burgess et al. 2007; Cremona et al. 2012; Psakhie and Jentsch 2012). Phosphorylation of yeast Rfa1 at serine 178 (S178) and Rfa2 at serine 122 (S122) by Mec1 has also been observed in response to chemically-induced DNA damage during mitosis (Brush et al. 1996, 2001; Brush and Kelly 2000; Bartrand et al. 2004). Furthermore, Rfa2-S122 is phosphorylated in response to programmed double-strand break (DSB) formation during meiosis (Brush et al. 2001; Bartrand et al. 2006). Yeast Rfa2 can also be phosphorylated at serine 27 (S27) by the meiosis-specific kinase Ime2 (Clifford et al. 2004, 2005), and it has been suggested that other unidentified residues in the N-terminus are also post-translationally modified during meiosis (Clifford et al. 2004). Rad53-dependent phosphorylation of the Saccharomyces Rfa2 NT has been observed in mitotically growing cells; however, this phosphorylation is only observed in a set1Δ mutant. Global mass-spectrometry analyses thus far have confirmed phosphorylation of Rfa1-S178 and Rfa2-S122 and have revealed other phosphorylation target sites (Rfa1-S160; Rfa2-T38, S115, S116, Y120, S189; Rfa3-S34; www.phosphogrid.org; Smolka et al. 2007; Albuquerque et al. 2008; Holt et al. 2009; Gnad et al. 2009; Helbig et al. 2010; Stark et al. 2010; Soulard et al. 2010), although the biological significance of each has yet to be determined.

In this study, the function of the Saccharomyces Rfa2 NT in the DNA damage response was examined through a detailed genetic analysis of this region. It was determined that the Saccharomyces Rfa2 NT is necessary, yet its phosphorylation is not required for a proper DNA damage response. Although phosphorylation is not required, a constitutive phospho-mimetic form of Rfa2 resulted in sensitivity to DNA damage. Genetic interaction analyses indicate that the basis for this sensitivity is different from the Rfa2 mutant lacking this domain. Utilizing multiple mutant forms of yeast Rfa2, specific subregions of the Rfa2 NT important for the damage response were identified. Finally, although Rfa2 phospho-mutants do not obviously affect initiation of checkpoint function, the phospho-mimetic form of Rfa2 displayed genetic interactions and a checkpoint adaptation phenotype (i.e., release from the G2/M checkpoint in the presence of unrepaired DNA damage) similar to that observed for rfa1-t11 mutant cells.
MATERIALS AND METHODS

Strains and plasmids

Yeast strains and plasmids used in this study are described in Tables S1 and S2, respectively. The yeast strains RMY122-A (MATa leu2-3,112 trp1-1 can1-100 ura3-1 his3-11,15 rad5-G535R rfa1Δ::TRP1 rfa2Δ::TRP1) and RMY122-mre11Δ were used to measure viability after plasmid shuffle and after DNA damage treatment and are derivatives of W303 (MANIAR et al. 1997; kindly provided by Steve Brill). These strains also contain a centromeric vector, pJM132 (pRS416 derivative), which includes the wild-type RFA1, RFA2, and RFA3 genes expressed from their native promoters. All strains used for adaptation studies are derivatives of JKM179 (LEE et al. 1998; kindly provided by Jim Haber).

To generate a yeast shuttle vector containing wild-type RFA1 and its native promoter, pJM132 was digested with BamHI and HindIII, and this 2.6 kilobase pair (kbp) fragment was cloned into pRS313 (SIKORSKI and HIETER 1989) to generate pRS313-RFA1. The vector pKU2-rfa1-t11 (UMEZU et al. 1998), containing the rfa1-t11 (K45E) mutation, was digested with AgeI and HindIII, and this 2.0 kbp fragment was cloned into pRS313-RFA1 to generate pRS313-rfa1-t11.

A yeast shuttle vector containing wild-type RFA2 and its native promoter was generated as follows. RFA2 cDNA was removed from pGDB-C3-RFA2 by cleaving with EcoRI and HindIII (partial digest), and this 0.9 kbp fragment was cloned into the low copy centromeric vector pRS315 (SIKORSKI and HIETER 1989) to generate pRS315-rfa2-Δpromoter (note this plasmid contains a serine instead of a threonine at residue 3 of Rfa2). To amplify the native RFA2 promoter, PCR was performed on pJM218 (MANIAR et al. 1997) using primers –PR-R1 and –PR-Ncol. The resulting fragment was digested with SacII and Ncol and cloned into pRS315-RFA2-Δpromoter to generate pRS315-RFA2.

N-terminal phospho-mutant forms of the RFA2 gene were generated as follows. The plasmid pGDB-C3-rfa2-Dx was constructed by annealing five overlapping complementary primers (AspA-E; Table S3), followed by insertion of this fragment into pGDB-C3-RFA2 partially digested with EcoRI-Hpal. The partially digested 0.9 kbp EcoRI-HindIII fragment from pGDB-C3-RFA2 was then cloned into pRS315 to generate pRS315-rfa2-Dx-Δpromoter. The native RFA2 promoter was amplified as described previously, digested with SacII and Ncol, and cloned into pRS315-rfa2-Dx-Δpromoter to generate pRS315-rfa2-Dx. To generate
pGDB-C3-rfa2-Ax, five overlapping complementary primers (Ala-A; Table S3) were annealed followed by
insertion into the Ncol and Hpal sites of pGDB-C3-rfa2-Dx. Again, the 0.9 kbp EcoRI-HindIII fragment
produced by partial digestion of this plasmid was cloned into pRS315 to produce
pRS315-rfa2-Ax-Δpromoter. The PCR fragment containing the native RFA2 promoter was digested with
BamHI and Ncol and inserted into pRS315-rfa2-Ax-Δpromoter to generate pRS315-rfa2-Ax. Deletion of the
N-terminus of RFA2 was achieved by PCR amplification of RFA2 cDNA from pJM218 with a primer in which
the codon for amino acid 39 was replaced with a start codon contained within an Ncol site. The resulting
PCR product was digested with Ncol and HindIII and ligated into pRS315-rfa2-Dx to generate
pRS315-rfa2-ΔNx.

Yeast integrating plasmids were also generated for each of the rfa2 N-terminal mutant forms. Briefly,
the 1.2 kbp BamHI-HindIII fragment from pRS315-rfa2-Dx and pRS315-rfa2-Ax were each cloned into
pRS306 to generate pRS306-rfa2-Dx and pRS306-rfa2-Ax, respectively. These plasmids were then digested
with EcoRI to target integration into JKM179, and two-step gene replacement was performed to generate
rfa2-Dx or rfa2-Ax mutant strains. Double mutant derivatives of JKM179 were generated by crossing
isogenic strains, followed by sporulation and microdissection.

The construction of all individual and multi-mutant plasmids was performed using pAW7 as the original
DNA template. Briefly, in vitro site-directed mutagenesis using Phusion DNA Polymerase (New England
BioLabs) and the corresponding mutagenic primer listed in Table S3 was performed. Following DpnI
digestion, the mutagenesis reaction was transformed into bacterial cells. Plasmid DNA was isolated from
resulting colonies and each mutation was verified by restriction digestion and sequencing.

Assessing the viability and recovery of rfa2 N-terminal mutants by plasmid shuffle

Centromeric plasmids containing various forms of RFA1 (pRS313 derivative; HIS3) and RFA2 (pRS315
derivative; LEU2) were co-transformed into RMY122-A or RMY122-mre11Δ cells. Transformants were
selected on synthetic complete (0.5% ammonium sulfate, 0.17% yeast nitrogen base without amino acids)
media containing 2% dextrose and lacking histidine, leucine, and uracil (SD-His-Leu-Ura), resulting in cells
that contained three plasmids. Cells were grown in media (SD-His-Leu) selecting for the co-transformed
vectors containing RFA1 and RFA2 alleles. If the allelic forms of RFA1 or RFA2 support growth, the pJM132
vector can be lost, and these cells can be recovered on media containing 0.8 µg/mL 5-fluoroorotic acid (5-FOA). If the allelic forms of RFA1 and/or RFA2 cannot support growth, no 5-FOA-resistant cells can be recovered. Finally, if there were synthetic growth defects due to the allelic forms of RFA1 and/or RFA2, reduced loss of pJM132 (and a reduced number of 5-FOA-resistant cells) or slower growth of colonies on 5-FOA media is observed.

To assess the viability of RFA1 and/or RFA2 allele mutants, cells containing all three plasmids were grown in SD-His-Leu media overnight (16-24 hr) at 30°C at 220 RPM. The next day, cells were counted and diluted to an initial concentration of 1x10^6 cells/mL. Ten-fold serial dilutions were made, and 5 µL of cells from the initial concentration and serial dilutions were spotted onto SD-His-Leu and 5-FOA plates, and 50 µL of the initial dilution were also spread onto 5-FOA plates. Growth was compared on the 5-FOA plates and quantitated. From the 5-FOA spread plates, we recovered mutant strains that were used in further studies.

**Measuring growth rates of mutant strains**

Yeast cells were grown overnight at 30°C in 25-50 mL YPD (1% yeast extract, 2% peptone, 2% dextrose). The absorbance at 600 nm was measured to ensure cells were in exponential phase (OD_{600} < 2). Cells were then diluted to OD_{600} = 0.1 in 50 mL YPD, measured to verify the initial concentration (OD_{600}), and grown at 30°C. After 6-8 hr, the final concentration (OD_{600}) was measured. Growth rate (g; min/gen) was then calculated using the equation:

\[ g = t / (\ln(C_f/C_i)/\ln(2)) \]

where \( t \) = time of growth, \( C_f \) = final concentration of cells, and \( C_i \) = initial concentration of cells. Measurements were taken for at least three independent cultures.

**DNA damage spot assays**

Mutant strains that were viable were recovered as described above. These mutant strains were subjected to DNA damaging agents as follows. Wild-type or mutant cells were grown in liquid YPD overnight (16-24 hr) at 30°C at 220 RPM. The next day, cell concentrations were determined, and an initial dilution of cells to 2.4x10^5 cells/mL was made. Three-fold serial dilutions were performed, and 5 µL from
the initial dilution and serial dilutions were spotted onto the following plates: YPD, YPD+0.012-0.03% methyl methanesulfonate (MMS), YPD+0.2-25 µg/mL camptothecin (CPT), YPD+40-360 mM hydroxyurea (HU), YPD+0.2-25 µg/mL phleomycin (PHL), and SD-His-Leu. Plates were incubated for 2-4 days at 30°C, and growth differences between the mutant and wild-type cells were documented.

**Immunoblotting**

For protein analysis, wild-type and mutant cells were grown in liquid YPD media overnight (12-16 hr) to a concentration of ~1x10^7 cells/mL. The next day, cells were subcultured into fresh media to a concentration of ~2.5x10^6 cells/mL and grown for two generations. The cell cultures were split into two cultures, and MMS was added to one of the cultures to a final concentration of 0.03%. The cultures with/without MMS were grown at 30°C for an additional 3 hr. For protein extraction, ~3x10^7 cells were collected and treated as described by Kushnirov (2000). The samples were incubated at 100°C for 3 min, centrifuged at 21,000 x g for 1 min, and the indicated amounts of the supernatant were loaded onto SDS-PAGE gels (described below).

To detect Rad53 activation (i.e., phosphorylation), we loaded 10 µL (out of 100 µL) of sample onto a 6% SDS-polyacrylamide (37.5:1 mono:bis) mini gel. Following electrophoresis and transfer to 0.4 um nitrocellulose, the blot was blocked with 10% skim milk in TBS-T for 1-2 hr, followed by primary antibody incubation with rabbit polyclonal anti-Rad53 (Abcam) at a 1:6,000 dilution in 10% skim milk for 16-20 hr. After multiple washes with TBS-T, the blot was incubated with goat anti-rabbit IgG-HRP secondary antibody (Abcam) at a 1:40,000 dilution in 10% skim milk for 2 hr. The blot was washed multiple times and developed using the ECL2 Western Blotting Substrate (Thermo Scientific). Signal on the blot was detected using either myECL Imager (Thermo Scientific) or a Storm 865 (GE Healthcare).

To detect Rfa2, and its post-translational modification, 10 µL of extract was loaded onto a 8% polyacrylamide (29:1 mono:bis) gel with or without 25-50 µM Phos-Tag (Kinoshita et al. 2006). The gel was transferred, and the blot was blocked as previously described. The blot was incubated with rabbit polyclonal anti-Rfa2 (kindly provided by Steve Brill) at a 1:20,000 dilution in 10% skim milk for 16-20 hr. Secondary antibody incubation, washes, and developing of the blot were as described previously for Rad53. Detection of Rfa1, and its post-translational modification, was as described for Rfa2, except that 0.5 µL (out
of 100 μL) protein extract was used, and the primary antibody used was rabbit anti-Rfa1 (kindly provided by Steve Brill) at a 1:40,000 dilution in 10% skim milk for 16-20 hr. All secondary antibody incubations, washes, and developing of the blot were as described for Rad53.

**Measuring checkpoint adaptation**

The yeast strain JKM179, containing a deletion of both HML and HMR, was used to measure the ability of cells to override G2/M arrest in the presence of DNA damage (i.e., adaptation) as described previously (Lee et al. 1998). Two-step gene replacement was used to introduce allelic forms of RFA1 and/or RFA2, as described in the strains and plasmids section. The cells were grown overnight in YPR (1% yeast extract, 2% peptone, 2% raffinose) media and single unbudded G1 cells were micro-dissected onto synthetic complete plates containing 2% galactose and all required amino acids (SG-Com). At 0, 8, and 24 hr, each dissected cell was examined for progression through the cell cycle as evidenced by the appearance of multiple cells (i.e., cell division). Additionally, RFA1 and RFA2 mutant alleles were combined with other gene deletion mutations (i.e., yku70Δ) and examined for cell division.

To measure Rad53 phosphorylation, JKM179 derivatives were grown overnight in YPD to exponential phase. These cells were then transferred to YPR and grown 12-16 hr to exponential phase (~1x10^7 cells/mL). Galactose was added to a final concentration of 2% to induce HO endonuclease expression, and cells were collected at various times after galactose addition. Protein was isolated using the method of Pellicioli et al. (2001). Forty micrograms of each protein sample was separated on a 7.5% (37.5:1) SDS-polyacrylamide gel, and Rad53 immunoblotting was performed as described above.
RESULTS

Yeast RFA double mutants lacking both characterized Mec1 target sites do not display sensitivity to DNA damaging agents

The two major *Saccharomyces* RFA phosphorylation target sites (Rfa1-S178 and Rfa2-S122) lie in the Rfa1 linker region just upstream of DNA binding domain A (DBD-A) and in the Rfa2 loop 3-4 region (Brush et al. 1996; Brush and Kelly 2000; Figure 1A). Upon DNA damage, both sites (which are present as SQ motifs) are phosphorylated by the checkpoint kinase Mec1. Previous studies reported no obvious DNA damage sensitivity when either site was mutated individually (Brush et al. 1996; Brush and Kelly 2000; Mallory et al. 2003), and in meiosis, the only detectable effect is on crossover vs. noncrossover frequency when Rfa2-S122 was mutated (Bartrand et al. 2006). Potential redundancy of these two Mec1 target sites had not been examined.

Using a genetic approach, aspartic acid (*i.e.*, phospho-mimetic) or alanine (*i.e.*, non-phosphorylatable) forms of yeast Rfa1-S178 and Rfa2-S122 were generated. All possible mutant combinations were recovered by plasmid shuffle, indicating that mutation of either or both sites does not affect cell viability. When exposed to the DNA damaging agents hydroxyurea (HU), methyl methanesulfonate (MMS), or camptothecin (CPT) at concentrations that cause severe lethality in an rfa1-t11 mutant, both single mutants in either phospho-mutant form did not display damage sensitivity (Figure 1B). To rule out the possibility of redundancy (*i.e.*, phosphorylation at one site substituting for lack of phosphorylation at the other), we examined every possible double mutant combination. None of the mutant combinations displayed sensitivity to DNA damaging agents (Figure 1C). This indicates that although both sites are known targets for checkpoint kinase (Mec1) phosphorylation in response to damage, neither of these sites is important for the DNA damage response.

*rfa2* “extensive” mutants are viable and display sensitivity to DNA damaging agents

The human RPA2 NT is phosphorylated in response to DNA damage. An amino acid sequence alignment of the *S. cerevisiae* Rfa2 (NP_014087.1) and the human RPA2 (NP_002937.1) N-termini revealed two prominent features (Figure 2A). First, the budding yeast Rfa2 NT is S/T-rich, similar to the human RPA2 NT.
Figure 1 DNA damage assay of known phosphorylation site mutants.

[A] Schematic of RFA complex and individual subunits. The DNA binding domains (DBDs) of the RFA subunits are shown (F, A, B, and C in Rfa1; D in Rfa2; E in Rfa3), along with linker regions (designated by thick lines connecting DBDs and other regions), the putative C-terminal winged-helix domain (W) of Rfa2, and the putative N-terminal phosphorylation domain (P) of Rfa2. Mec1 damage-dependent target sites are denoted by a lightning symbol, with the target residue (e.g., S) and residue number (e.g., 178) denoted.

[B] DNA damage assays of rfa2-S122 and rfa1-S178 mutants. Alanine (A) or aspartic acid (D) mutant forms were examined in this study. Cells were grown overnight, sonicated, counted, and diluted to 2.4x10^5 cells/mL. Three-fold serial dilutions were made, and 5 µL of each dilution were spotted onto YPD (unstressed) or YPD containing 80 mM hydroxyurea (HU), 0.024% methyl methanesulfonate (MMS), or 1 µg/mL camptothecin (CPT). Plates were incubated for 2-4 days at 30°C. The rfa1-t11 strain was used as a control for DNA damage sensitivity.

[C] DNA damage assays of rfa2-S122 and rfa1-S178 double mutants. Damage assays were performed as described in Figure 1B.
Figure 2  Phenotypic analysis of rfa2 “extensive” (rfa2x) mutants.

[A] Alignment of RPA2 N-terminal regions (first 38 aa) from S. cerevisiae (ScRfa2; NP_014087.1) and H. sapiens (HsRPA2; NP_002937.1). Alignments were performed using T-Coffee (suitable for small alignments) with default settings. Highlighted residues indicate putative phosphorylation sites in S. cerevisiae Rfa2 and known phosphorylation sites in H. sapiens RPA2.

[B] Schematic of rfa2 extensive mutants used in this study. Designations for domains are as described in Figure 1A. Serine/threonine amino acid (aa) residues and positions are denoted. Extensive rfa2 N-terminal mutants (denoted by the subscript x) are shown as serine/threonine (S/T) residues mutated to aspartic acids (D) to mimic hyper-phosphorylation or to alanines (A) to generate a non-phosphorylatable N-terminus. The extensive deletion (∆N) mutant (denoted by the subscript x) removes amino acids 3-37. The rfa1-t11 allele used is shown above DBD-F in Rfa1, and its amino acid change (lysine→glutamic acid; K45E) is denoted in parentheses.

[C] DNA damage assay of the rfa2 extensive mutants. The assay was performed exactly as described in Figure 1B. Sensitivities to increasing concentrations of phleomycin (PHL) and camptothecin (CPT) are shown. Sensitivities to hydroxyurea (HU) and methyl methanesulfonate (MMS) are shown in Figure S1.
Second, although there are no SQ motifs in the yeast Rfa2 NT, the number and position of S/T residues are similar to the human RPA2 NT. Phosphorylation of the yeast Rfa2 NT has only been identified in a set1Δ mutant during mitosis (SCHRAMKE et al. 2001) or by the meiosis-specific kinase Ime2 at serine 27 during meiosis (CLIFFORD et al. 2004). Rad53-dependent phosphorylation of the Rfa2 NT in a set1Δ mutant or deletion of the Rfa2 NT (rfa2-∆40) suppresses the MMS sensitivity of mec3Δ cells and results in increased expression of DNA repair genes (SCHRAMKE et al. 2001). Deletion of the yeast Rfa2 NT also results in shortening of telomeres (SCHRAMKE et al. 2004). To examine the potential physiological role of the yeast Rfa2 NT in response to DNA damage and outside of the context of a set1Δ or mec3Δ background, we generated yeast rfa2 phospho-mutant alleles, similar to those used in many human RPA2 studies (Figure 2B).

Introduction of any Rfa2 N-terminal mutation by plasmid shuffle resulted in the formation of viable cells (Figure S1A), as indicated by growth on 5-fluoroorotic acid (5-FOA). To determine if rfa2 phospho-mutants displayed general growth defects, the growth rate of each mutant was determined. Both the rfa2-Dx mutant (henceforth, the subscript x indicates extensive mutation of all N-terminal serines/threonines; D indicates mutation to aspartic acids) and the rfa2-∆Nx mutant (∆Nx indicates deletion of N-terminal amino acids 3-37; similar to rfa2-∆40 in SCHRAMKE et al. 2001, 2004) display reduced growth when the mutant form is expressed as the only copy of RFA2 from either from a plasmid (Table 1; RMY122-A background) or from its native chromosomal location (Table 1; JKM179 background). The reduced growth rate in the rfa2-∆Nx mutant is consistent with the delayed replication observed for rfa2-∆40 (SCHRAMKE et al. 2001). The rfa2-Ax mutant (Ax indicates alanines substituted for all N-terminal serines/threonines) grew similarly to wild-type (WT) cells in either background (Table 1). This suggests that an Rfa2 NT that is either lacking or constitutively mimics phosphorylation (i.e., negatively charged) results in a slight-to-modest growth defect, whereas a non-phosphorylatable Rfa2 NT mutant results in cells that grow as well as WT cells.

rfa2 mutants were examined for sensitivity to chemical DNA damaging agents (e.g., MMS, CPT, HU, or PHL), and although each of these chemicals induces DNA damage through a different mechanism, the results were similar for each treatment. The rfa2-Ax mutant showed nearly indistinguishable growth compared to WT RFA2-containing cells on all DNA damage-inducing media (Figure 2C; S1B) – slight differences were only observed at concentrations of agents that were at least 5- to 25-fold higher than
Table 1  Growth characteristics of rfa2, mutants

<table>
<thead>
<tr>
<th>RFA2 Allele</th>
<th>Strain Background</th>
<th>Growth Rate (min/gen)</th>
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<tr>
<td>WT</td>
<td>RMY122-A</td>
<td>105.6 ± 11.9</td>
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<tr>
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<td>161.9 ± 16.6</td>
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<td>105.6 ± 10.9</td>
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<td>rfa2-Dx</td>
<td>JKM179</td>
<td>131.3 ± 13.9</td>
</tr>
<tr>
<td>rfa2-Ax</td>
<td>JKM179</td>
<td>108.7 ± 13.7</td>
</tr>
<tr>
<td>rfa2-ΔNx</td>
<td>JKM179</td>
<td>144.2 ± 22.1</td>
</tr>
</tbody>
</table>

*In the strain RMY122-A, the WT or mutant rfa2 allele is expressed from its native promoter on a low-copy centromeric vector. In the JKM179 background, the WT or mutant rfa2 allele was integrated into its normal chromosomal location via two-step gene replacement.*
commonly used concentrations. The $rfa2-D_x$ and $rfa2-\Delta N_x$ mutants were sensitive to all DNA damaging agents tested (Figure 2C; S1B; S2).

**DNA damage sensitivity is only observed when multiple serine/threonine residues in the Rfa2 N-terminus are mutated**

It is clear that $rfa2$ extensive N-terminal mutants in which all of the S/T residues are mutated or deleted display damage-sensitive phenotypes. To determine which specific residue(s) might be important for the DNA damage response, we employed a mutagenesis strategy in which single residues (individual mutants) or clusters of residues were mutated (multi-mutants). Shuffling-in of any $rfa2-A_i$ or $rfa2-D_i$ (subscript $i$ denotes an individual amino acid change) mutant plasmids resulted in no discernible growth phenotypes on 5-fluoroorotic acid (5-FOA), indicating that each individual mutant allele was able to complement the chromosomal $rfa2\Delta$ with respect to supporting normal cell growth in unstressed conditions (Figure S3A; S4A). The ability to tolerate DNA damage was then examined. Although the $rfa2-D_x$ mutant displayed a damage-sensitive phenotype, $rfa2-D_i$ mutants were indistinguishable from WT RFA2 cells with respect to growth on media containing DNA damaging agents (Figure S3B). In addition, each of the $rfa2-A_i$ mutants showed resistance to DNA damaging agents similar to WT cells (Figure S4B), which was not unexpected given the lack of a DNA damage phenotype for the $rfa2-A_x$ mutant. Taken together, these results indicate that no single putative phosphorylation target site is responsible for the damage sensitivity observed for the extensive $rfa2$ mutants.

The above data suggest that if N-terminal residues are physiologically important and potential targets for low-level Rfa2 phosphorylation, there might be a requirement for modification of multiple residues (i.e., a critical mass of phosphorylation) to affect RFA’s role in the DNA damage response. This might also explain why single mutations have little effect, as other potential sites would remain in these mutants. To address this possibility, the Rfa2 NT was divided into three subregions, and clusters of 3-4 serine/threonine residues were mutated to mimic phosphorylation or to be non-phosphorylatable (Figure 3A; Table 2). These clusters are not only “geographically” partitioned, but also represent corresponding subregions of the human RPA2 NT with respect to order of phosphorylation identified by Anantha et al. (2007) and Liu et al. (2012). These multi-mutant alleles were also further combined to generate mutations of 6-7 residues within the
Figure 3 Phenotypic analysis of rfa2 “multi” (rfa2<sub>m</sub>) mutants.

[A] Schematic depicting rfa2 multi-mutants examined and the locations of the amino acid substitutions. Brackets indicate the clusters of serine/threonine (S/T) residues mutated to either asparagines (D) or alanines (A).

[B] DNA damage assays for rfa2-A<sub>m</sub> mutants. rfa2-A<sub>m</sub> mutants were recovered by plasmid shuffle (Figure S2A) and assayed for sensitivity to DNA damage as described in Figure 1B.

[C] DNA damage assays for rfa2-D<sub>m</sub> mutants. rfa2-D<sub>m</sub> mutants (Figure S2B) that could be recovered by plasmid shuffle were assayed for DNA damage sensitivity as described in Figure 1B. rfa2-D<sub>m1</sub> (not shown) was recovered and did not display a damage phenotype.
Table 2  Rfa2 N-terminal regions, multi-mutant alleles examined, serine/threonine residues mutated, and their putative analogous residues in human RPA2

<table>
<thead>
<tr>
<th>Rfa2 N-terminal Region</th>
<th>Allele&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Rfa2 Residues Changed/Removed</th>
<th>Putative Analogous Human RPA2 Residues</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (aa 3-14)</td>
<td>rfa2-D&lt;sub&gt;m1&lt;/sub&gt;, A&lt;sub&gt;m1&lt;/sub&gt;, or ΔN&lt;sub&gt;1&lt;/sub&gt;</td>
<td>T3, S11-12, T14</td>
<td>S4, S8, S11-13</td>
</tr>
<tr>
<td>2 (aa 21-27)</td>
<td>rfa2-D&lt;sub&gt;m2&lt;/sub&gt;, A&lt;sub&gt;m2&lt;/sub&gt;, or ΔN&lt;sub&gt;2&lt;/sub&gt;</td>
<td>S21, S23, S27</td>
<td>T21, S23, S29</td>
</tr>
<tr>
<td>3 (aa 30-40)</td>
<td>rfa2-D&lt;sub&gt;m3&lt;/sub&gt;, A&lt;sub&gt;m3&lt;/sub&gt;, or ΔN&lt;sub&gt;3&lt;/sub&gt;</td>
<td>S30, T32, T34</td>
<td>S33</td>
</tr>
</tbody>
</table>

<sup>a</sup> Multi-mutant allelic forms were also combined to form multi-mutants in which 6-7 serine/threonine (S/T) residues were mutated (e.g., <i>rfa2-D<sub>m1+m2</sub></i> designates a form where both regions 1 and 2 were mutated to aspartic acids (D)).
N-terminal region. All combinations of \textit{rfa2-A}$_m$ or \textit{rfa2-D}$_m$ multi-mutants supported cell growth in the absence of the original plasmid (Figure S5), and none of the alanine multi-mutants demonstrated a damage-sensitive phenotype (Figure 3B). DNA damage-sensitivity was observed for one aspartic acid multi-mutant (\textit{rfa2-D}$_{m1+m3}$; Figure 3C), suggesting that mimicking constitutive phosphorylation of S/T residues in subregions 1 and 3 is responsible for some of the damage sensitivity observed for \textit{rfa2-D}$_x$.

**Genetic interactions with another RPA subunit mutant or with a DSB repair mutant reveal differences in \textit{rfa2} damage-sensitive mutants**

Synthetic genetic interactions and epistasis studies are useful for identifying factors that act in the same pathway and/or the same complex. To identify the importance of the Rfa2 NT in a complex or pathway, we assayed for synthetic genetic interactions between \textit{rfa2} N-terminal mutants and either \textit{rfa1-t11} or \textit{mre11}A, both of which individually lead to DNA damage-sensitive phenotypes. Mre11 is a subunit of the yeast MRX complex (MRN in human cells) necessary for DSB repair and checkpoint function (Williams et al. 2007; Ijima et al. 2008; Rupnik et al. 2010). Synthetic genetic interaction between \textit{rfa2} N-terminal alleles and \textit{mre11}A was examined, because human RPA2 and Mre11 physically interact with one another, and this interaction appears to be regulated by the N-terminal state of human RPA2 and the N-terminus of RPA1 (Oakley et al. 2009). Synthetic genetic interaction with \textit{rfa1-t11} allele was examined, because it lies in a gene that encodes a different subunit within the same complex as Rfa2.

Genetic interactions between \textit{rfa1-t11} and \textit{rfa2} extensive mutants were examined by plasmid shuffle. Both the \textit{rfa1-t11 rfa2-D}$_x$ and \textit{rfa1-t11 rfa2-A}$_x$ double mutants were viable. However, the \textit{rfa1-t11 rfa2-ΔN}$_x$ double mutant displayed synthetically lethality, as only a few 5-FOA resistant microcolonies were observed for this mutant (Figure 4B), which were unable to be propagated any further. Thus, although both \textit{rfa2-D}$_x$ and \textit{rfa2-ΔN}$_x$ single mutants display damage-sensitive phenotypes, they display differential genetic interactions with \textit{rfa1-t11}.

Partial deletions of the Rfa2 NT were constructed to identify which mutated subregion(s) was responsible for the DNA damage-sensitive and/or \textit{rfa1-t11} synthetic lethal phenotypes. Similar to the multi-mutants, we divided the putative phosphorylation sites into three clusters (subregions) and deleted each subregion (Figure 4A). Deletion of any cluster of putative sites did not affect the ability to shuffle out
Figure 4  Genetic interactions with rfa1-t11.

[A] Schematic of rfa2 subregion deletion mutants examined.

[B] Spot assay measuring genetic interaction between rfa2 mutants and rfa1-t11 by plasmid shuffle. RMY122-A strains containing pJM132 were co-transformed with plasmids containing either RFA1 or rfa1-t11 and rfa2 mutant alleles. Transformants were selected for on SD-His-Leu-Ura plates and “shuffling out” of pJM132 (i.e., the ability of a particular mutant to support viability) was detected as growth on 5-FOA.

[C] Examining which subregion of the Rfa2 N-terminus is responsible for the DNA damage phenotypes of rfa2-ΔNx strains. Damage assays for rfa2-ΔN1, rfa2-ΔN2, or rfa2-ΔN3 strains were performed as described in Figure 1B.

[D] Examining genetic interactions between rfa2-ΔN subregion mutants and rfa1-t11. Since rfa2-ΔNx displays damage sensitivities and synthetic lethality with rfa1-t11, we examined rfa2-ΔN1, rfa2-ΔN2, or rfa2-ΔN3 subregion mutants in combination with rfa1-t11. Cells were examined as in Figure 4B.

[E] Growth assay of rfa1-t11 rfa2-ΔNx subregion double mutants recovered from plasmid shuffle. Cells were grown overnight, sonicated, counted, diluted to 2.4x10⁵ cells/mL, and serial diluted as three-fold dilutions. The serial dilutions were spotted and examined as described in Figure 1B (damage assays are not shown, as rfa1-t11 cells have a severe sensitivity that appears to be epistatic to any rfa2 extensive mutant form).
the WT RFA2 plasmid (Figure 4B); however, DNA damage assays revealed that rfa2-ΔN3 displayed a moderate damage-sensitive phenotype, indicating that this subregion (or perhaps this cluster of S/T residues) is important in the damage response (Figure 4C). Double mutants of these partial deletion alleles and rfa1-t11 revealed that all of the double mutants are viable, although both rfa1-t11 rfa2-ΔN3 and rfa1-t11 rfa2-ΔN3 display synthetic sickness, as indicated by less efficient loss of the WT RFA2-containing plasmid (Figure 4D) and by reduced growth of the recovered mutant on YPD under unstressed conditions (Figure 4E). Damage-sensitivity effects could not be determined in mutants containing rfa1-t11, as this mutation already leads to very severe damage-dependent phenotypes. It is of interest to note that rfa2-ΔN3 and rfa2-ΔN3 remove the same subregions that, when mutated to aspartic acids in the rfa2-Dm1+m3 mutant lead to a damage-sensitive phenotype (see results above and Figure 3C), suggesting that these subregions of the Rfa2 NT are important for Rfa2 function.

Although RPA and Mre11 physically interact, it has been previously demonstrated that yeast rfa1-DAmP (Decreased Abundance of mRNA Perturbation) mre11Δ or rfa2-DAmP mre11Δ double mutants display a synthetic lethality phenotype (Collins et al. 2007), suggesting that yeast RFA and Mre11 have synergistic, yet independent functions. It was possible that if the Rfa2 NT were important for function in the DNA damage response, that mutation of this domain alone might account for this synthetic genetic interaction observed previously. Each of the rfa2 N-terminal extensive mutants or rfa1-t11 was introduced into an isogenic mre11Δ strain, and viability was assessed via the plasmid shuffle assay. Three interesting results were observed. First, the rfa1-t11 mre11Δ double mutant was synthetically lethal under unstressed conditions (Figure 5A). It was known previously that a human RPA1-t11 mutation disrupts interaction with Mre11 (Oakley et al. 2009); however, it is clear that the synthetic lethality observed for the rfa1-t11 mre11Δ double mutant in yeast is not due to lack of interaction (i.e., any interaction would already be disrupted by virtue of the absence of Mre11). The data are consistent with a role for RFA independent from its interaction with Mre11. Second, the rfa2-Dx mre11Δ double mutant is synthetically lethal (Figure 5A), similar to that of an rfa1-t11 mre11Δ double mutant. This would suggest that rfa2-Dx and rfa1-t11 mutants might have a fundamentally similar defect in function. Third, the rfa2-ΔNx mre11Δ double mutant is viable (Figure 5A), unlike the rfa1-t11 mre11Δ or rfa2-Dx mre11Δ double mutants. This would again suggest that the defect in function in rfa2-ΔNx cells is different from that of rfa2-Dx or rfa1-t11.
[A] 
Replica plating to measure genetic interaction between rfa1 or rfa2 mutants and mre11Δ by plasmid shuffle.
RMY122::mre11Δ strains containing pJM132 were co-transformed with plasmids containing various allele combinations of RFA1 and RFA2. Transformants were selected for on SD•His•Leu•Ura plates and picked to a SD•His•Leu•Ura master plate (four independent colonies for each shuffle). “Shuffling out” of pJM132 was examined by replica plating the master plate onto SD•Com (synthetic complete with amino acids supplemented) and 5-FOA plates, and the plates were incubated at 30°C for 2-4 days. Growth on 5-FOA indicates that the combination of mutant RFA1 and/or RFA2 alleles supports cell viability.

[B] 
Examining which aspartic acid mutations in the Rfa2 N-terminus are responsible for the phenotype of rfa2-Dx strains. Since rfa2-Dx displays damage sensitivities and synthetic lethality with mre11Δ, we examined rfa2-Dmx mutations (where the multi-mutant form is indicated by the subregion of the Rfa2 N-terminus as shown in Figure 3A) in combination with mre11Δ. Cells were examined as in Figure 4B.

[C] 
Spotting of serial dilutions of rfa2-Dm mre11Δ cells recovered by plasmid shuffle. Cells were grown overnight, sonicated, counted, diluted to 2.4x10^5 cells/mL, and serial diluted as three-fold dilutions. Five microliters of each dilution were spotted onto YPD (damage assays are not shown, as mre11Δ cells have a severe sensitivity that appears to be epistatic to any rfa2 extensive mutant form).
Since \( \text{rfa2-D}_x \) showed a genetic interaction with \( \text{mre11}\Delta \), \( \text{rfa2} \) multi-mutants were utilized in an attempt to identify the subregion(s) contributing to the synthetic lethality observed in Figure 5A. \( \text{mre11}\Delta \text{rfa2-D}_m \) double mutant combinations were generated and assessed for viability. Interestingly, \( \text{mre11}\Delta \text{rfa2-D}_{m1+m3} \) was synthetically lethal, similar to the \( \text{mre11}\Delta \text{rfa2-D}_x \) mutant (Figure 5B). This suggests that S21, S23, and S27 do not contribute to the genetic interaction observed for the \( \text{mre11}\Delta \text{rfa2-D}_x \) mutant. This is also consistent with the \( \text{rfa2-D}_{m1+m3} \) mutant displaying the most severe damage-sensitive phenotype (Figure 3C). Finally, the double mutants \( \text{mre11}\Delta \text{rfa2-D}_{m2+m3} \) and \( \text{mre11}\Delta \text{rfa2-D}_{m3} \) show similar synthetic sickness (Figure 5B,C). Both of these double mutants have subregion 3 mutated to aspartic acids, identifying this subregion as contributing to synthetic sickness (\( \text{i.e.} \), slow growth or inviability) in an \( \text{mre11}\Delta \) strain, when in a constitutively phospho-mimetic state.

**Protein phosphorylation and checkpoint initiation occurs in \( \text{rfa2} \) N-terminal mutants in response to DNA damage**

While Rfa2 is phosphorylated on S122 by Mec1 in response to DNA damage (Bartrand et al. 2006; Brush et al. 1996; Mallory et al. 2003), it has not been directly demonstrated that phosphorylation occurs in mitotically damaged cells in the N-terminal region of yeast Rfa2 (in a \( \text{SET1} \) strain). This is in stark contrast to human RPA2, where upon DNA damage, the N-terminus is hyper-phosphorylated on multiple residues by ATR, ATM, and DNA-PK, displaying obvious shifts in mobility by SDS-PAGE (Liu et al. 2012). To determine whether the Rfa2 NT is also phosphorylated in response to DNA damage, we examined asynchronous exponentially-growing cells that were either unstressed or treated with MMS, leading to replicative stress and DNA breaks. In gels containing 50 \( \mu \text{M} \) Phos-Tag (Kinoshita et al. 2006), a distinct phospho-species was observed for all \( \text{rfa2} \) extensive mutants in both exponentially-growing and damaged cells (Figure 6A), similar to that observed previously (Schramke et al. 2001). The most important feature to note is that the shifted Rfa2 phospho-species was present in all \( \text{rfa2} \) extensive mutant cells examined, including the \( \text{rfa2-A}_x \) mutant lacking all S/T residues in the N-terminus, indicating that the Rfa2 NT is not a predominant target for phosphorylation.

Interestingly, we were able to observe a distinct phospho-species using 25 \( \mu \text{M} \) Phos-Tag technology for the \( \text{rfa2-D}_x \) and \( \text{rfa2-\Delta N}_x \) mutants. This Rfa2 species was also observed in a 50 \( \mu \text{M} \) Phos-Tag gel as a more
Figure 6  Phosphorylation phenotypes of rfa2 extensive mutants.

[A] Phosphorylation of Rfa2 before and after DNA damage. Cells were grown to ~1x10⁷ cells/mL, split into two cultures, and one of the cultures was treated with 0.03% MMS for 3 hr. Following treatment, ~2x10⁷ cells were collected, lysed, and one-tenth of each protein extract (equivalent to ~2x10⁶ cells) was resolved in 8% polyacrylamide (29:1 mono:bis) gel in the absence or presence of Phos-Tag (PT; amount in µM is indicated to left of each blot) in the gel. RFA1 and RFA2 alleles present and type of damage treatment is denoted above each blot. Following transfer, Rfa2 protein species were detected with rabbit polyclonal antibody to Rfa2. Symbols: dash = unphosphorylated species; arrowhead = phosphorylated/slower mobility species; rightmost symbols represent Rfa2 species from the rfa2-ΔNx strain. In gels where no Phos-Tag was added, phosphorylated/changed species were difficult to resolve. Also, note two diffuse shifted Rfa2 species from the rfa2-ΔNx strain, consistent with the shift observed for 25 mM PT.

[B] Detection of Rad53 and Rfa1 proteins and post-translational modifications. For Rad53, one-tenth of the protein extract was separated in a 6% polyacrylamide (37.5:1 mono:bis) gel. For Rfa1, one-twentieth of each protein extract (equivalent to ~1x10⁶ cells) was resolved in a 6% polyacrylamide (29:1 mono:bis) gel in the absence or presence of Phos-Tag in the gel. Proteins were detected with rabbit polyclonal antibodies to Rad53 and Rfa1, respectively. Designations are as in Figure 6A.
diffuse and slightly higher-shifted species identified from rfa2-Dx mutant cells following DNA damage, consistent with the 25 μM Phos-Tag result. This species was not present in WT, rfa1-t11, or rfa2-Ax cells. It is worth noting that this phospho-species was only observed in rfa2 extensive mutants that are DNA damage-sensitive, and the species was DNA damage-specific (Figure 6A). It has not been determined if this phospho-species is the same in rfa2-Dx and rfa2-ΔNx cells, nor if this phosphorylation is causative of or simply correlative with DNA damage sensitivity. Post-translational modification of Rfa1 is unaffected in all of the rfa2 extensive mutant cells both before and after DNA damage (Figure 6B). Although the intensity of the Rfa2 protein signal in rfa2-ΔNx cells was consistently reduced, it was unclear if this is due to instability of Rfa2 protein, epitope masking, or a reduction in available epitope due to the missing N-terminus. Consistent with the latter possibilities, the level of Rfa1 protein detected is similar in all mutants (Figure 6B). Since human RPA1 stability is dependent on RPA2 (HARING et al. 2010), one would predict that if yeast Rfa2 were reduced, a similar reduction in Rfa1 might also occur. However, this was not observed.

One mechanism by which a mutant could display DNA damage sensitivity is through the inability to activate, maintain, or recover properly from a checkpoint. Since human RPA2 is phosphorylated by checkpoint kinases in response to DNA damage, we surmised that the damage sensitivity observed in rfa2 mutant yeast strains might be due to misregulation of checkpoint function. We examined G2/M checkpoint activation in rfa2 mutants by measuring the phosphorylation of yeast Rad53 (homolog of human Chk2). Rad53 lies downstream of yeast RFA in the checkpoint pathway and becomes phosphorylated (activated) in response to DNA damage (LEE et al. 2000; PELLCICOLI and FOIANI 2005; HARRISON and HABER 2006; BRANZEI and FOIANI 2006). Rad53 is phosphorylated not only in WT cells, but also in all of the rfa2 extensive mutants when cells are treated with MMS (Figure 6B) or when a single DSB is induced (Figure 7B). This indicates that the modification or loss of the Rfa2 NT has no observable effect on Rad53 activation and suggests that checkpoint establishment after DNA stress is unaffected.

**Checkpoint adaptation in rfa2 extensive mutant strains**

Checkpoint adaptation is the ability of a cell to override G2/M checkpoint arrest and proceed through the cell cycle even in the presence of unrepaired DNA damage, and it has been suggested that this is a mechanism by which cells might survive, even when damage persists (GALGOCZY and TOCZYSKI 2001).
Figure 7  Checkpoint adaptation phenotypes of rfa2 extensive mutants.

[A] Adaptation phenotypes in rfa2-Dx and rfa2-Ax mutant cells at 0, 8, and 24 hr after HO break induction. Microdissection was used to identify and separate early S-phase cells onto 5G-Com plates, which led to expression of HO endonuclease. After 0, 8, and 24 hr, cells were examined microscopically and quantitated for number of cells observed for each colony.

[B] Quantitation and microscopic representation of adaptation after 24 hr post HO break induction. Microscopic representation (top), and multiple independent experiments (N>8 for all strains) were quantitated (bottom) to determine the percentage of colonies with >2 cells.

[C] Rad53 phosphorylation in rfa2 extensive mutants. Expression of HO endonuclease was induced in exponentially-growing cells by the addition of 2% galactose to the media. Cells were collected at various time points following galactose addition, and 40 ug of whole cell extracts were probed with anti-Rad53 antibody. Slower migrating species indicate phosphorylated Rad53 (as described in Pellicoli et al. 2001).

[D] The effect of rfa2 extensive mutations on Rad53 phosphorylation state in yku70Δ strains. Phosphorylation of Rad53 was examined as described in Figure 7C. yku70Δ and yku70Δ rfa1-t11 were previously examined in Pellicoli et al. (2001) and are controls for Rad53 phosphorylation in adaptation-deficient and adaptation-proficient strains, respectively.
initial phosphorylation of Rad53 is necessary to establish a checkpoint in yeast, and it should be noted that
*rfa1-t11* cells have initial Rad53 phosphorylation that is indistinguishable from WT cells in response to DNA
damage (Lee et al. 2000; Figure 6B). However, *rfa1-t11* promotes adaptation in normally
adaptation-deficient *yku70Δ* or *tid1Δ* mutants that is mediated through a reduction in phosphorylation of
Rad53 (Lee et al. 1998; Pelllicioli et al. 2001).

We have demonstrated in this study that *rfa1-t11* and *rfa2-Dx* mutants both displayed damage
sensitivity, and each displayed synthetic lethality when combined with *mre11Δ*. We addressed whether or
not *rfa2* N-terminal mutants affect adaptation. In the presence of a single, irreparable DSB at the *MAT*
locus, *rfa2-Dx* or *rfa2-Ax* mutant cells are capable of arresting at the G2/M checkpoint by 8 hr similar to WT
cells, as indicated microscopically as a cell with a single large-bud (Figure 7A) and by phosphorylation
(activation) of Rad53 (Figure 7C). However, only *rfa2-Dx* cells display an adaptation frequency that is nearly
indistinguishable from WT or *rfa1-t11* cells (Figure 7B). Furthermore, when *rfa2-Dx* was combined with
*yku70Δ* (normally adaptation-deficient), the cells now showed adaptation-proficiency, similar to that
reported previously for *rfa1-t11 yku70Δ* cells (Lee et al. 1998; Figure 7A,B). This is corroborated by the
observation that the majority of Rad53 is not phosphorylated by 18 hr after induction of a DSB (Figure 7D)
in these cells.

Interestingly, *rfa2-Ax* cells display reduced adaptation (Figure 7A,B) and a slightly later reduction in
phosphorylation of Rad53 after DNA damage (Figure 7C). Furthermore, the *rfa2-Ax yku70Δ* mutant is
adaptation-deficient, similar to the *yku70Δ* single mutant (Figure 7B). Supporting *rfa2-Ax yku70Δ*
adaptation deficiency is the inability of Rad53 to be dephosphorylated, even 18 hr after damage induction
(Figure 7D).
DISCUSSION

The N-terminal region of Rfa2 is important for proper cellular response to DNA damage

The results presented in this work demonstrate that the N-terminus of yeast Rfa2 is required for a proper DNA damage response. This is indicated by the fact that removal of this domain (rfa2-ΔNₜ) leads to DNA damage-sensitive phenotypes. However, phosphorylation of the yeast Rfa2 NT is not necessary for cells to respond to repairable DNA damage, since cells bearing a non-phosphorylatable form of this domain (rfa2-Δₜ) exhibit near wild-type growth and DNA damage-tolerance phenotypes.

Using western blotting and Phos-Tag technology, we were unable to detect major differences in yeast Rfa2 phosphorylation in the rfa2 NT mutants, except for an additional phospho-species in the damage-sensitive rfa2 mutants only. The additional modification observed must reside outside of the Rfa2 NT, as it is observed in the rfa2-ΔNₜ mutant. This indicates that the Saccharomyces Rfa2 NT is not the predominant region for damage-induced phosphorylation, but that the state of this domain can influence the damage response and/or additional modification of Rfa2 outside of the N-terminus. The lack of readily detectable damage-specific phosphorylation in the yeast Rfa2 NT is in stark contrast to the human RPA2 NT, but is completely consistent with the observation that rfa2-Δₜ mutant yeast cells are resistant to DNA damage.

It is worth noting that even in N-terminal mutants where DNA damage sensitivity was observed, post-translational modification of Rfa1 did not appear to be affected. Despite the apparent lack of major phosphorylation in the WT Rfa2 NT, we note that when individual residues on RFA (Rfa1-S178 and Rfa2-S122) previously identified to be phosphorylated by Mec1 are mutated to non-phosphorylatable forms (or phospho-mimetic forms), there was no observable DNA damage-sensitive phenotype. This indicates that Rfa1-S178 and Rfa2-S122 are neither redundant nor important for the damage response, or that any mutant phenotype is so subtle that it cannot be detected by the assays performed in this study. As our study was done in haploid strains growing mitotically, this does not preclude the importance of post-translational modification of these residues in meiosis, where a phenotype has been observed for Rfa2-S122 mutants (Bartrand et al. 2006). It is clear that the phenotypes observed for N-terminal mutants of yeast Rfa2 are far more severe than those for known phosphorylation target site mutants, suggesting
that similar to human RPA2, the N-terminal region is more important for the DNA damage response.

Subregions 1 and 3 are responsible for phenotypes observed in Rfa2 N-terminal mutants

All rfa2 individual site mutants showed robust growth and resistance to DNA damage, suggesting that perturbing one site in the Rfa2 NT is not enough to elicit a phenotype. Although we could not detect an obvious lack of phosphorylation in any of the rfa2 extensive mutants in response to DNA damage, we did observe that certain regions of the Rfa2 NT were more sensitive to alteration than others. Dividing the yeast Rfa2 NT into three subregions revealed that all of the growth defects, DNA damage defects, and genetic interactions we observed could be attributed to mutation of subregion 1 (aa 3-14) and/or subregion 3 (aa 30-40) of the N-terminus (Table 3). It is interesting to note that subregions 1 and 3 are analogous to subregions of human RPA2 (Table 3) that contain all but one (T21) of the primary DNA damage-specific targets of checkpoint kinases (Anantha et al. 2007; Liu et al. 2012). If low-level (currently undetectable) post-translational modification is occurring in the Rfa2 NT, we would suggest that it is potentially occurring in both of these subregions. Alternatively, these subregions are important and may have evolved in higher eukaryotes to be post-translationally modified during DNA damage for reasons that are not yet clear.

Genetic interactions suggest overlapping, yet different functions for the yeast Rfa1 and Rfa2 N-termini

Phosphorylation (or phospho-mimetic mutations) of the human RPA2 NT can have an effect in regulating protein interactions and/or DNA interactions that involve the N-terminus of RPA1 (DBD-F). Evidence that a phospho-mimetic RPA2 N-terminal peptide affects the NMR structure of purified RPA1 DBD-F in a fashion similar to that of ssDNA binding to RPA1 DBD-F suggests that this peptide competes with ssDNA for binding to DBD-F (Binz et al. 2003). Furthermore, it has been demonstrated that DBD-F is important for interaction of human RPA1 with human Mre11, and mutation of this domain (RPA1-t11) or a phospho-mimetic form of human RPA2 (RPA2-Dx) disrupts this interaction (Oakley et al. 2009).

Based on this idea, one might conjecture that a yeast rfa2-Dx mutant would behave similarly to an rfa1-t11 mutant. In this regard, both mutants grew more slowly, displayed damage sensitivities, were
Table 3  Qualitative summary of rfa2 N-terminal mutant phenotypes and genetic interactions

<table>
<thead>
<tr>
<th>RFA2 Allele</th>
<th>Mitotic Growth</th>
<th>Damage Resistance</th>
<th>Genetic Interaction</th>
<th>Adaptation</th>
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<tbody>
<tr>
<td>WT</td>
<td>+++</td>
<td>+++</td>
<td>NA</td>
<td>Proficient</td>
</tr>
<tr>
<td>rfa1-t11</td>
<td>+</td>
<td>0</td>
<td>NA</td>
<td>Proficient</td>
</tr>
<tr>
<td>rfa2-Dx</td>
<td>+++</td>
<td>++</td>
<td>None</td>
<td>Proficient</td>
</tr>
<tr>
<td>rfa2-Ax</td>
<td>+++</td>
<td>+++</td>
<td>None</td>
<td>Reduced</td>
</tr>
<tr>
<td>rfa2-ΔNx</td>
<td>+++</td>
<td>++</td>
<td>Lethality</td>
<td>ND</td>
</tr>
<tr>
<td>rfa2-Dm1-m3</td>
<td>+++</td>
<td>+++</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>rfa2-ΔN1</td>
<td>+++</td>
<td>+++</td>
<td>Sickness</td>
<td>ND</td>
</tr>
<tr>
<td>rfa2-ΔN3</td>
<td>+++</td>
<td>++</td>
<td>Sickness</td>
<td>ND</td>
</tr>
<tr>
<td>rfa2-Dm2-m3</td>
<td>+++</td>
<td>++</td>
<td>ND</td>
<td>Sickness</td>
</tr>
<tr>
<td>rfa2-Dm3</td>
<td>+++</td>
<td>+++</td>
<td>ND</td>
<td>Sickness</td>
</tr>
</tbody>
</table>

a NA = Not Available/Applicable; ND = Not Determined.
b Scale is ++++= best growth/most damage resistant, +++ = moderate growth/moderately damage resistant, + = slow growth/slightly damage resistant, 0 = no growth/not damage resistant.
synthetically lethal in combination with \textit{mre11}\textgreek{A}, and exhibited the ability to promote adaptation in a \textit{yku70}\textgreek{A} background. This is consistent with a model in which a phosphorylated RPA2 N-terminus affects the function of the RPA1 N-terminus (DBD-F), similar to if DBD-F were mutated. It has not been determined whether a phospho-mimetic human RPA2 affects the NMR structure of an RPA1-t11 (DBD-F) mutant. However, our results are consistent with this model in which hyper-phosphorylated yeast Rfa2 interacts with DBD-F of yeast Rfa1 to potentially disrupt protein/DNA interactions.

Despite both being DNA damage-sensitive, it is clear that the defect(s) in \textit{rfa2-D}, mutants differs from the defect(s) in \textit{rfa2-}\textgreek{A}, mutants. The \textit{rfa2-}\textgreek{A}, mutant is intriguing, because it does not behave like an \textit{rfa2-}\textgreek{A}, mutant, even though neither of these Rfa2 proteins is phosphorylatable on their N-terminus. This clearly delineates between a requirement for the presence of the domain vs. a requirement for phosphorylation of the domain. Perhaps more intriguing is the fact that the \textit{rfa2-}\textgreek{A}, mutant does not display a genetic interaction with \textit{mre11}\textgreek{A}, but does display a genetic interaction with \textit{rfa1-t11}. This suggests that removal of the Rfa2 NT results in a cellular defect similar to when Mre11 is deleted. Furthermore, deletion of the Rfa2 NT confers a defect distinct from that observed in \textit{rfa1-t11} mutant cells that lack a functional DBD-F. It has been proposed that the human RPA2 N-terminus may function by regulating the function of the human RPA1 N-terminus (\textit{Binz et al.} 2003; \textit{Oakley et al.} 2009). These studies indicate that the Rfa2 N-terminus has a role beyond regulating the Rfa1 N-terminus, and it will be important to determine what that role(s) is.

\textbf{Transition from a “normal” damage response to adaptation may depend on the Rfa2 N-terminus}

In this study, a non-phosphorylatable N-terminal form of Rfa2 functions nearly indistinguishably from WT Rfa2 after DNA damage. Perhaps more importantly, the \textit{rfa2-D}, mutant is damage-sensitive. Therefore, it is curious that in response to DNA damage, human RPA2 is hyper-phosphorylated on its N-terminus. Differences between yeast Rfa2 and human RPA2 might simply be due to cellular complexity (\textit{e.g.}, human RPA interacts with proteins not found in yeast cells and might require additional modification to regulate these interactions). Alternatively, differences could be due to the experimental parameters of studies performed in human tissue culture vs. yeast. Whatever the case, it is clear that lack of phosphorylation in
the Rfa2 NT is tolerated quite well under commonly used DNA damage assay conditions in yeast.

What if the DNA lesion was such that it was either difficult to repair, or perhaps, irreparable? A feature shared between a cell that is permanently arrested vs. a cell that is inviable is that neither is “growing”. Checkpoint adaptation allows for the possibility of cell growth, with the potential for the lesion to be repaired later. Although genome stability appears to be compromised (i.e., increased spontaneous chromosome loss and break-induced repair (BIR)) in adaptation-proficient mutants, it has also been demonstrated that adaptation results in cells with higher resistance upon exposure to DNA damaging agents (e.g., X-irradiation) in diploid cells (GALGOCZY and TOCZYSKI 2001). It is clear that all of the rfa2 extensive mutants display initial phosphorylation of Rad53 indistinguishable from WT cells following MMS treatment or eight hours after an HO-induced DSB. This would suggest that a G2/M checkpoint establishment defect is not the explanation for the damage sensitivity observed for some rfa2 N-terminal mutants. However, we have observed that the rfa2-D Δ mutant promotes adaptation when combined with yku70Δ, similar to that observed for rfa1-t11. There is a precedent for checkpoint release in human cells, as it has been demonstrated that RPA2 N-terminal phosphorylation is necessary to exit M-phase and enter G1 phase in the presence of mitotic DNA damage (ANANTHA et al. 2008). We propose that the DNA damage sensitivity observed for rfa2-D Δ strains may indeed be due to the ability to promote premature adaptation, resulting in mitotic division despite the persistence of damaged DNA. If cells “adapt” during continued/prolonged treatment with genotoxic agents (i.e., spot assays on plates containing DNA damaging agents), the lack of arrest and coupled increase in genomic instability would presumably lead to additional DNA damage and/or chromosomal loss. Although tolerated in diploid cells (GALGOCZY and TOCZYSKI 2001), this would be quite detrimental to the haploid cells in our studies and would manifest as reduced colony growth in a damage assay. Our data corroborate the idea that adaptation is only beneficial to the cell when it has a diploid genome content to compensate for chromosomal loss or rearrangement.

It is worth noting that rfa2-A Δ mutants were indistinguishable from WT cells in almost every assay, except for adaptation. In fact, the rfa2-A Δ mutant displayed an adaptation-reduced phenotype, and only became fully adaptation-proficient when combined with an rfa1-t11 mutation. This suggests that the lack of serine/threonine residues and/or an inability to post-translationally modify these residues in the Rfa2 NT inhibits adaptation in otherwise WT cells (and especially in yku70Δ cells). Because these cells prolong
resistance to progression into M phase until DNA damage has been repaired, this is a plausible explanation for why they do not display DNA damage sensitivities using common DNA stressors. Despite being adaptation-deficient, rfa2-Ax cells grow indistinguishably from WT cells in the absence of stress, indicating that the inability to enter M phase is only reduced in the presence of unrepaired DNA and not during unstressed conditions.

We propose a model (Figure 8) in which the yeast Rfa2 NT plays a role in determining whether or not cells adapt. In this model, we propose that prolonged checkpoint arrest will lead to adaptation through “inactivation” of the yeast Rfa1 N-terminus (DBD-F; similar to that of the rfa1-t11 mutation) or modification of the yeast Rfa2 N-terminus (Figure 8; right side). Alternatively, an inability to disrupt Rfa1 DBD-F function or lack of modification of the Rfa2 NT in the presence of DNA damage helps to reinforce (i.e., maintain) the checkpoint until the damage is repaired, promoting proper checkpoint recovery (Figure 8; left side). Consistent with this, a non-phosphorylatable rfa2 NT mutant displays reduced adaptation. In cases where damage is repairable and adaptation would not be necessary, the rfa2 mutants that are non-phosphorylatable (rfa2-Ax and rfa2-ΔNx) display very different phenotypes, indicating that there is a difference between having a domain that cannot be phosphorylated on serine/threonine residues and not having the domain at all, as long as the damage is repairable and does not persist.

It is important to address the physiological importance of hyper-phosphorylation of RPA2 in response to DNA damage in human (and potentially many higher eukaryotic) cells. It is also important to understand how yeast accomplish proper DNA repair and cell cycle regulation without obvious post-translational modification of the Rfa2 NT. Why this domain is necessary in yeast, but post-translational modification is not, will be of importance in identifying the mechanism(s) of RFA function, not only in yeast, but perhaps in other eukaryotic organisms where phosphorylation of the RPA2 N-terminus is not necessary or does not occur in response to DNA damage.
In response to DNA damage, cells undergo recognition of the lesion and signaling to halt the cell cycle by establishing the G2/M checkpoint. The initiation of the checkpoint response occurs, regardless of the state of the N-terminus of either Rfa1 or Rfa2 (denoted as grey boxes to indicate each is either inactive or not present). The decision to override the checkpoint is affected by the state of the Rfa1 and/or Rfa2 N-termini. Cells with a functional Rfa1 DBD-F (denoted by a green box) or Rfa2 where the N-terminus is present and in a non-phosphorylated state (denoted by a blue box) appear to less readily adapt, suggesting a propensity to maintain checkpoint function until repair is complete followed by proper checkpoint recovery. If damage persists, the N-terminus of Rfa1 may be inactivated (denoted by a grey box with red circle-slash) and/or the Rfa2 N-terminus may become phosphorylated (denoted by multiple red circles). The Rfa2 N-terminus may not be phosphorylated or may be dephosphorylated when normal ("repairable") DNA damage is present; however, upon persistent ("irreparable") damage, modification of the Rfa2 N-terminus may occur to promote entry into M-phase as a "last-ditch effort" for cell survival.

Figure 8  Model for Rfa2 N-terminus function in checkpoint maintenance and adaptation.
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