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Repair and Homologous Recombination

PRINCIPAL INVESTIGATOR: Ms. Mariela Jaskelioff  
Doctor Craig Peterson

CONTRACTING ORGANIZATION: University of Massachusetts  
Medical School  
Worcester, Massachusetts 01655

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**Principal Investigator:** Jaskelioff, Mariela

**Organization:** University of Massachusetts Medical School

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Annual Report (April 1, 2002 - March 31, 2003)

**Title:** Role of Chromatin Remodeling by RAD54 in DNA Damage Repair and Homologous Recombination

## **INTRODUCTION**

Chromosomal double-strand breaks (DSBs) can arise from cellular DNA metabolism and from exogenous DNA-damaging agents. Efficient repair of these DSBs is critical for genome stability. Rad54, a member of the SWI2/SNF2 family, is involved in the homology recombination (HR) DNA repair pathway. Rad54 has been shown to physically associate with Rad51, a eukaryotic recombinase that in mammals interacts with tumor suppressors BRCA1 and BRCA2.

Homologous recombination (HR) can repair DSBs using the intact sister chromatid as a template, resulting in the accurate reversal of the damage. In organisms ranging from yeast to human, HR is mediated by the RAD52 epistasis group of proteins (Rad50, Rad51, Rad52, Rad54, Rad55, Rad57, Rad59, Mre11, Xrs2). Mutations in this group result in pleiotropic defects in DNA damage repair, including extreme sensitivity to IR and other DSB-inducing agents. DSBs are first processed into long single-stranded DNA regions by specialized exonucleases. Then, Rad51 polymerizes onto these overhangs to form a nucleoprotein filament that searches for the homologous duplex DNA. After the search has been successfully completed, DNA strand-exchange generates a joint molecule between the homologous damaged and undamaged DNA molecules. The missing

information is restored via DNA synthesis. Finally, resolution of crossed DNA strands by a resolvase yields two intact duplex DNAs (Kanaar, 1998).

RAD54, a member of the SWI2/SNF2 family of proteins has been shown to physically interact with RAD51, and to significantly increase the *in vitro* strand-exchange reaction (Petukhova, 1998). Its relevance in the HR repair pathway is underlined by the fact that mutations in RAD54 (Matsuda, 1999) and a RAD54 homologue, RAD54B (Hiramoto, 1999), have been found in human primary lymphoma and colon cancers. Moreover, RAD54 (Gonzalez, 1999) and RAD54B (Rasio, 1997) have been correlated with breast carcinomas in a loss of heterozygosity analysis.

The purpose of this project is to characterize the role of RAD54 in the HR pathway. We have shown that RAD54, like other SWI/SNF family members, is an ATP-dependent chromatin remodeling enzyme. We have also shown that RAD54 is able to introduce superhelical torsion on double-stranded DNA, and that nucleosomal DNA is the preferred substrate. These findings support the theory that RAD54 functions during homology-driven DNA repair by allowing the homology search to occur in chromatin-embedded regions of the genome.

The goals we set for this project are: (1) purification and identification of native RAD54 complexes; (2) study of RAD54's functional interactions with other DNA repair proteins, and (3) characterization of the *in vivo* chromatin remodeling activity of RAD54.

**BODY**

We have addressed the possibility that RAD54 resides *in vivo* in a complex with other proteins involved in HR, by tagging the endogenous yeast Rad54 protein with a Tandem Affinity Purification (TAP) tag and purifying it. The TAP tag was fused to the C-terminus of Rad54p, and the resulting fused protein presented a level of activity comparable to that of the untagged protein in a functional complementation test. The TAP-Rad54 protein was purified from both methyl methanesulfonate (MMS)-treated and untreated cells. Even though the preliminary data showed that a number of polypeptides co-purified with Rad54p, we found that Rad54p does not form a stable complex with the principal proteins of the HR pathway, Rad51p and Rad52p. Even after exposing the cells to the MMS, Rad54p, Rad51p and Rad52p did not coincide in the purification fractions, as assayed by Western Blots. Our results were confirmed by Roland Kanaar's group, as they reported that the proteins in the RAD52 group have extremely different nuclear dynamics, arguing that they do not reside in a stable complex (Essers, 2002). Moreover, work from our own group has shown that the different members of the RAD52 group of proteins arrive at a DNA damage site at different times after a DSB has been induced (Wolner, 2003).

We have also investigated the mechanism of action of Rad54p, and established that Rad54p is a DNA tracking enzyme, that introduces superhelical torsion on the donor partner in the central HR reaction, thus altering the chromatin structure and facilitating the strand invasion and exchange reactions promoted by Rad51p on chromatin substrates. We reached these conclusions after studying the activity of purified yeast Rad54p in a number of functional *in vitro* assays, designed to measure ATPase activity, chromatin remodeling, joint

molecule (D-loop) formation, superhelical torsion generation, triplex displacement, and DNA length dependence. Detailed descriptions of these assays and the results obtained can be found in the Appendix.

Other groups reported similar results (Alexiadis, 2002; Alexeev, 2003). Nevertheless, we are the only group to date to have published data that sheds light on the details of the mechanism used by Rad54p to perform its *in vivo* function (see Appendix).

The ability of Rad54p to disrupt the repressive structure of chromatin is consistent with the fact that Rad54p is required for the homologous recombination DNA repair pathway when the donor sequence is embedded in chromatin. Particularly, Rad54's ability to alter the DNA-histone interactions allow the recombinase Rad51p to carry out the central step in the HR pathway, namely the recombination reaction *per se*, in a chromatin context.

Our findings suggest that this is achieved through a DNA translocation mechanism. The translocation dynamics generate topological changes in the DNA double helix, which are propagated over the surface of the nucleosomes, thus disrupting the myriad of weak interactions (H bonds, salt links) that secure the nucleosomal structure and preclude the binding of other proteins to DNA.

The future efforts in this project will be directed at designing a more specific functional assay for Rad54p, and the study of the chromatin remodeling activity of Rad54p in a cellular context.

**KEY RESEARCH ACCOMPLISHMENTS**

- We have obtained data suggesting that the homologous recombination proteins do not reside in a stable complex, even after extensive DNA damage.
- We have established that Rad54p has the ability to remodel the structure of chromatin, and that this activity allows the homologous recombination process to take place on chromatin substrates.
- Our results indicate that Rad54p uses a DNA translocation mechanism to affect the chromatin structure of the homologous recombination substrate.

• **REPORTABLE OUTCOMES**

**Publications:**

**Jaskelioff M, Van Komen S, Krebs JE, Sung P, Peterson CL.**

Rad54p is a chromatin remodeling enzyme required for heteroduplex DNA joint formation with chromatin.

J Biol Chem. 2003 Mar 14; 278(11):9212-8.

**Presentations:**

**Jaskelioff M, Van Komen S, Sung P, and Peterson CL.**

The DNA repair protein Rad54 is an ATP-dependent Chromatin Remodeling Enzyme.

2002 Yeast Genetics and Molecular Biology Meeting. July 30-August 4, 2002. Madison, Wisconsin.

**Posters:**

**Jaskelioff M, Van Komen S, Sung P, and Peterson CL.**

Rad54p is a chromatin remodeling enzyme required for heteroduplex DNA joint formation with chromatin.

The Enzymology of Chromatin and Transcription Keystone Symposium. March 10-16, 2003. Santa Fe, New Mexico.

**Jaskelioff M, Van Komen S, Sung P, and Peterson CL.**

Chromatin remodeling during DNA repair and homologous recombination.

Sixth Annual Buffalo DNA Replication & Repair Symposium. June 14-15, 2002. Buffalo, New York.

**CONCLUSIONS**

The research described above supports the hypothesis that the homologous recombination protein Rad54 is a chromatin remodeling enzyme and that its function *in vivo* involves the alteration of the chromatin structure at the chromosomal site that serves as a donor for the recombination reaction. Our results suggest that this is a consequence of Rad54p translocating along the DNA and introducing topological changes in the double helix, which are translated into the transient disruption of the DNA-histone interactions. Our findings are consistent with the current literature in the fields of DNA repair and chromatin remodeling.

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## Rad54p Is a Chromatin Remodeling Enzyme Required for Heteroduplex DNA Joint Formation with Chromatin\*

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Mariela Jaskelioff<sup>‡§¶</sup>, Stephen Van Komen<sup>§||\*\*</sup>, Jocelyn E. Krebs<sup>‡ ††</sup>, Patrick Sung<sup>||</sup>,  
and Craig L. Peterson<sup>‡§§</sup>

From the <sup>‡</sup>Interdisciplinary Graduate Program and Program in Molecular Medicine, University of Massachusetts Medical School, Worcester, Massachusetts 01605, and <sup>||</sup>Department of Molecular Medicine and Institute of Biotechnology, University of Texas Health Science Center at San Antonio, San Antonio, Texas 78245-3207

In eukaryotic cells, the repair of DNA double-strand breaks by homologous recombination requires a RecA-like recombinase, Rad51p, and a Swi2p/Snf2p-like ATPase, Rad54p. Here we find that yeast Rad51p and Rad54p support robust homologous pairing between single-stranded DNA and a chromatin donor. In contrast, bacterial RecA is incapable of catalyzing homologous pairing with a chromatin donor. We also show that Rad54p possesses many of the biochemical properties of *bona fide* ATP-dependent chromatin-remodeling enzymes, such as  $\gamma$ SWI/SNF. Rad54p can enhance the accessibility of DNA within nucleosomal arrays, but it does not seem to disrupt nucleosome positioning. Taken together, our results indicate that Rad54p is a chromatin-remodeling enzyme that promotes homologous DNA pairing events within the context of chromatin.

Chromosomal DNA double-strand breaks (DSBs)<sup>1</sup> arise through exposure of cells to harmful environmental agents such as ionizing radiation or mutagenic chemicals (radiomimetics, alkylating agents, etc.). DSBs can also be caused by endogenously produced oxygen radicals, by errors in DNA replication, or as obligatory intermediates during programmed cellular processes, such as meiosis or V(D)J recombination (1–3). Cell survival and maintenance of genome integrity depend on efficient repair of DSBs, because unrepaired or misrepaired DSBs may lead to mutations, gene translocations, gross chromosomal rearrangements, or cellular lethality.

Several pathways for repairing DSBs have evolved and are highly conserved throughout eukaryotes. Homologous recombination (HR) is a major pathway of DSB repair in all eukaryotes and has a distinct advantage over other mechanisms in that it

is mostly error-free. In organisms ranging from yeast to human, HR is mediated by members of the *RAD52* epistasis group (*RAD50*, *RAD51*, *RAD52*, *RAD54*, *RAD55*, *RAD57*, *RAD59*, *MRE11*, and *XRS2*). Accordingly, mutations in any one of these genes result in sensitivity to ionizing radiation and other DSB-inducing agents (2). The importance of the HR pathway in maintaining genome integrity is underscored by the fact that mutations in each one of its critical factors have been correlated with chromosomal instability-related ailments, including ataxia telangiectasia-like disease, Nijmegen breakage syndrome, Li Fraumeni syndrome, as well as various forms of cancer (4).

*In vivo* and *in vitro* studies have suggested the following sequence of molecular events that lead to the recombinational repair of a DSB. First, the 5' ends of DNA that flank the break are resected by an exonuclease to create ssDNA tails (5). Next, Rad51p polymerizes onto these DNA tails to form a nucleoprotein filament that has the capability to search for a homologous duplex DNA molecule. After DNA homology has been located, the Rad51-ssDNA nucleoprotein filament catalyzes the formation of a heteroduplex DNA joint with the homolog. The process of DNA homology search and DNA joint molecule formation is called "homologous DNA pairing and strand exchange." Subsequent steps entail DNA synthesis to replace the missing information followed by resolution of DNA intermediates to yield two intact duplex DNA molecules (6).

The homologous DNA pairing activity of Rad51p is enhanced by Rad54p (7). Rad54p is a member of the Swi2p/Snf2p protein family (8) that has DNA-stimulated ATPase activity and physically interacts with Rad51p (7, 9, 10). Because of its relatedness to the Swi2p/Snf2p family of ATPases, Rad54p may have chromatin remodeling activities in addition to its established role in facilitating Rad51p-mediated homologous pairing reactions. In this study we show that Rad51p and Rad54p mediate robust D-loop formation with a chromatin donor, whereas the bacterial recombinase, RecA, can only function with naked DNA. Furthermore, we find that the ATPase activity of Rad54p is essential for D-loop formation on chromatin and that Rad54p can use the free energy from ATP hydrolysis to enhance the accessibility of nucleosomal DNA. Experiments are also presented to suggest that chromatin remodeling by Rad54p and yeast SWI/SNF involves DNA translocation.

### EXPERIMENTAL PROCEDURES

**DNA**—All DNA manipulations were carried out using standard methods (11). Oligonucleotides were obtained from Operon Technologies (Alameda, CA). Plasmid pXG540 and T4 Endonuclease VII used in the cruciform extrusion experiments were a kind gift of Dr. T. Owen-Hughes.

The oligonucleotide used for triplex formation was TFO (triplex-forming oligonucleotide) (5'-TTCTTTTCTTTCTTTCTTTCTTT-3'). To

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§ Both authors contributed equally to this work.

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†† Current Address: Dept. of Biological Sciences, University of Alaska, 3211 Providence Dr., Anchorage, AK 99508.

§§ To whom correspondence should be addressed. Tel.: 508-856-5858; Fax: 508-856-5011; E-mail: Craig.Peterson@umassmed.edu.

<sup>1</sup> The abbreviations used are: DSB, double-strand break; HR, homologous recombination; ssDNA, single-stranded DNA; dsDNA, double-stranded DNA; TFO, triplex-forming oligonucleotide; DTT, dithiothreitol; BSA, bovine serum albumin; ATP $\gamma$ S, adenosine 5'-O-(thiotriphosphate); AMP-PNP, adenosine 5'-( $\beta$ , $\gamma$ -imino)triphosphate; Mnase, micrococcal nuclease.

generate pMJ5, the annealed oligonucleotides TFOB5 (5'-TCGAGAA-GAAAAGAAAGAAAGAAAC-3') and TFOB3 (5'-TCGAGT TTC'TT-TCTTCTTTCTTTCTTCT-3') were ligated to the product of a *Xho*I digestion carried out on pCL7c (12). This yielded a pBluescript SKII (-) plasmid containing 5 head-to-tail repeats of the 208-bp *Lytechinus variegatus* 5S rDNA nucleosome positioning element flanked by a TFO-binding site. The DNA template (208–11) for reconstituting nucleosomal arrays for the ATPase, remodeling, and Mnase assays consists of a *Not*I-*Hind*III fragment derived from pCL7b (12), containing 11 head-to-tail repeats of a 5S rRNA gene from *L. variegatus*, each one possessing a nucleosome positioning sequence. The sixth nucleosome is tagged by a unique *Sal*I restriction site.

**Reagent Preparation**—Recombinant yeast Rad51p, Rad54p, rad54K341Ap, and rad54K341Rp were overexpressed in yeast and purified as previously described (7). SWI/SNF purification was as described (13). Histone octamers were purified from chicken erythrocytes as described by Hansen *et al.* (14). Octamer concentrations were determined by measurements of  $A_{230}$  (15). Nucleosomal array DNA templates (pXG540, pMJ5, or 208–11) were labeled by the Klenow polymerase fill-in reaction using [ $\alpha$ - $^{32}$ P]dCTP (3000  $\mu$ Ci/mmol, Amersham Biosciences). Nucleosomal arrays were reconstituted by salt dialysis as previously described (13), and the nucleosome saturation was determined to be 60–80% by digestion analysis.

**D-loop Reactions**—Oligonucleotide D1 (90-mer) used in the D-loop experiments has the sequence: 5'-AAATCAATCTAAAGTATATATGAGTAAACCTGGTCTGACAGTACCAATGCTTAATCAAGTGGACCATATCTCAGCGATCTGTCTATTT-3', being complementary to positions 1932–2022 of pBluescript SK(-) replicative form I DNA. Oligonucleotide D1 was 5' end-labeled with  $^{32}$ P using [ $\gamma$ - $^{32}$ P]dATP and polynucleotide kinase, as described (7). Buffer R (35 mM Tris-HCl, pH 7.4, 2.0 mM ATP, 2.5 mM MgCl<sub>2</sub>, 30 mM KCl, 1 mM DTT, and an ATP-regenerating system consisting of 20 mM creatine phosphate and 30  $\mu$ g/ml creatine kinase) was used for the reactions; all of the incubation steps were carried out at 30 °C. Rad51 (0.8  $\mu$ M) and Rad54 (120 nM) were incubated with radiolabeled oligonucleotide D1 (2.4  $\mu$ M nucleotides) for 5 min to assemble the presynaptic filament, which was then mixed with naked pBluescript replicative form I DNA (38  $\mu$ M base pairs) or the same DNA assembled into chromatin (38  $\mu$ M base pairs). Chromatin assembly was monitored by following topological changes as well as measuring the degree of occlusion of a unique *Eco*RI restriction site close to the D1 sequence. Substrates were estimated to be ~80% saturated with nucleosomes. The reactions containing RecA protein (0.8  $\mu$ M) were assembled in the same manner, except that they were supplemented with an additional 12.5 mM MgCl<sub>2</sub> at the time of incorporation of the duplex substrates. At the indicated times, 4- $\mu$ l portions of the reactions were withdrawn and mixed with an equal volume of 1% SDS containing 1 mg/ml proteinase K. After incubation at 37 °C for 5 min, the deproteinized samples were run in 1% agarose gels in TAE buffer (40 mM Tris-HCl, pH 7.4, 0.5 mM EDTA) at 4 °C. The gels were dried, and the radiolabeled DNA species were visualized and quantified by PhosphorImager analysis (Personal Molecular Imager FX, Bio-Rad).

**ATPase Assay**—Recombinant yeast Rad54p (1 nM) was incubated at 30 °C or 37 °C with 5 nM of either naked 208–11 dsDNA or reconstituted nucleosomal arrays in the presence of 100  $\mu$ M ATP, 2.5  $\mu$ Ci [ $\gamma$ - $^{32}$ P]dATP (6000  $\mu$ Ci/mmol, Amersham Biosciences), 2.5% glycerol, 0.1% Tween 20, 20 mM Tris-HCl, pH 8.0, 200  $\mu$ M DTT, 5 mM MgCl<sub>2</sub>, 100  $\mu$ g/ml BSA. For the DNA length-dependence assays, 5 nM Rad54p, 5 nM Rad51p, or 10 nM SWI/SNF were used. Oligonucleotides (random N-mers ranging from 10–100 nucleotides in length) were PAGE-purified to ensure length homogeneity (Integrated DNA Technologies, Inc., Coralville, IA). Samples were taken after 2, 5, 15, and 30 min and resolved by TLC. The proportion of liberated  $^{32}$ P-pyrophosphate was determined using the Molecular Dynamics PhosphorImager and ImageQuant Software. ATPase assays were independently repeated 3 times, yielding very similar results.

**Cruciform Formation Assay**—Cruciform formation assays were performed as previously described (16). Briefly, 8 ng of *Ava*I-linearized pXG540 (either naked, N, or nucleosomal, C) were incubated with various concentrations of Rad54, Rad51, or rad54 K341A and 0.15 mg/ml EndoVII (except where noted), in the presence of 10 mM Hepes, pH 7.9, 50 mM NaCl, 3 mM MgCl<sub>2</sub>, 5% glycerol, 0.1 mM DTT, 1 mM ATP (except where noted), 3 mM phosphoenolpyruvate, and 20 units/ml pyruvate kinase for 30 min at 30 °C. The products were resolved in 1.2% agarose gels and visualized with Sybr Gold staining (Molecular Probes, Eugene, OR) followed by analysis with ImageQuant software.

**Chromatin-remodeling Reaction**—For the coupled SWI/SNF or Rad54-*Sal*I reactions, reconstituted 208–11 nucleosomal arrays (~1 nM final concentration) were preincubated at 37 °C for 20 min with

2.5 units/ $\mu$ l *Sal*I in a buffer containing (final concentrations) 50 mM NaCl, 5 mM MgCl<sub>2</sub>, 1 mM ATP, 3 mM phosphoenolpyruvate, 10 units/ml pyruvate kinase, 1 mM DTT, 10 mM Tris-HCl, pH 8.0, 100  $\mu$ g/ml BSA, and 3% glycerol. Nucleosomal arrays were ~80% saturated with nucleosomes. Buffer, 2 nM SWI/SNF complex, or various concentrations of recombinant Rad51p and Rad54p were added and samples were taken at the indicated time points, vigorously mixed for 10 s with 25  $\mu$ l TE and 50  $\mu$ l 1:1 solution of phenol/chloroform. The purified DNA fragments were resolved by electrophoresis in 1.2% agarose gels in the presence of 50  $\mu$ g/ml ethidium bromide. The gels were then dried on 3MM Whatman paper. The fraction of cut and uncut DNA was determined by PhosphorImager analysis using a Molecular Dynamics PhosphorImager and ImageQuant software. Experiments were repeated independently at least 3 times, which yielded very similar results.

**Micrococcal Nuclease Digestion**—15 nM reconstituted 208–11 nucleosomal arrays were incubated at 37 °C with 2 nM SWI/SNF, 100 nM Rad54p, or buffer, in the presence of 2 mM ATP, 5 mM NaCl, 2.5 mM Tris-HCl, pH 8.0, 0.25 mM MgCl<sub>2</sub>, 0.3 mM CaCl<sub>2</sub>, 3 mM phosphoenolpyruvate, 10 units/ml pyruvate kinase, 1 mM DTT, 10  $\mu$ g/ml BSA, 0.5% glycerol. After 20 min, 0.0005 units of Micrococcal Nuclease (Worthington) was added to the reaction, and aliquots were taken at the indicated time points and then treated for 20 min with 2  $\mu$ g/ $\mu$ l proteinase K and extracted twice with a 1:1 solution of phenol:chloroform. The resulting digestion products were resolved by electrophoresis in 2% agarose gels, run at 2.5 volts/cm for 12 h. The gels were fixed, dried, and analyzed using a Molecular Dynamics PhosphorImager and ImageQuant Software.

**Triple-helix Displacement Assay**—Triple-helix formation was performed as described (17). Briefly, equimolar concentrations (100 nM) of *Ssp*I-linearized pMJ5 and  $^{32}$ P-labeled TFO were mixed in buffer MM (25 mM MES, pH 5.5, 10 mM MgCl<sub>2</sub>) at 57 °C for 15 min and left to cool to room temperature overnight. The resulting triplex was either used directly or reconstituted into nucleosomal arrays. To introduce nicks into the DNA, pMJ5 was exposed to various concentrations of DNaseI (Promega, Madison, WI) for 2 min at 37 °C, the reactions were stopped with 5 mM EDTA, vigorously mixed for 10 s with a 1:1 solution of phenol/chloroform, ethanol-precipitated, and resuspended in water. The degree of nicking introduced by DNaseI treatment was assessed by electrophoretic analysis of native and heat-denatured samples (in the presence of 15% formamide) on denaturing 1.3% agarose gels, followed by Sybr Gold Stain (Molecular Probes, Eugene, OR).

The triplex-containing substrates (5 nM) were incubated at 30 °C with 5 nM recombinant Rad54 protein or SWI/SNF complex, in a buffer containing 35 mM Tris-HCl, pH 7.2, 3 mM MgCl<sub>2</sub>, 100  $\mu$ g/ml BSA, 50 mM KCl, 1 mM DTT, 3 mM phosphocreatine, 28  $\mu$ g/ml creatine phosphokinase, and where noted, 3 mM ATP. Samples were taken at the indicated time points, the reactions were quenched with GSMB buffer (15% (w/v) glucose, 3% (w/v) SDS, 250 mM 4-morpholinepropanesulfonic acid, pH 5.5, 0.4 mg/ml bromophenol blue), and analyzed in 1.2% agarose gels (40 mM Tris acetate, 5 mM sodium acetate, 1 mM MgCl<sub>2</sub>, pH 5.5) at 10 volts/cm for 1.5 h at 4 °C. Gels were fixed in 5% acetic acid, 50% methanol for 1 h, and dried. The proportion of bound and free TFO was determined using a Molecular Dynamics PhosphorImager and ImageQuant Software.

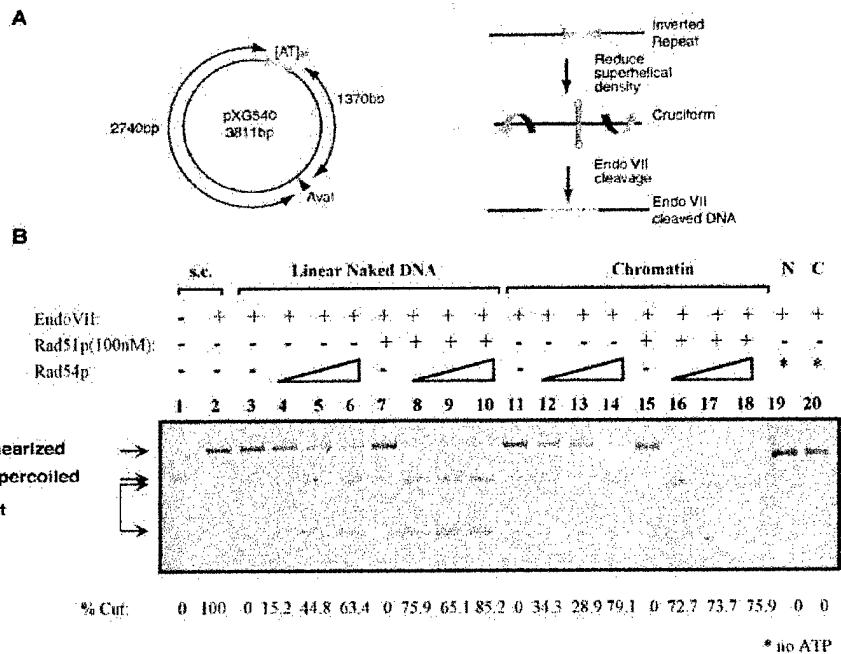
## RESULTS

**Rad51p and Rad54p Promote DNA Pairing with a Chromatin Donor**—Repair of a DSB by homologous recombination begins with the invasion of a double-stranded, homologous donor by a Rad51-ssDNA nucleoprotein filament, also referred to as the presynaptic filament. This strand invasion reaction is typically monitored *in vitro* by following the Rad51p-dependent formation of a D-loop between a radiolabeled oligonucleotide and a homologous double-stranded DNA donor (Fig. 1A). In this case, efficient D-loop formation also requires the ATPase activity of Rad54p. *In vivo*, however, the search for homology and strand invasion involves a homologous donor that is assembled into chromatin. Given that the Rad54p ATPase shows sequence relatedness to known chromatin remodeling enzymes, it was of considerable interest to examine the ability of Rad54p to promote Rad51p-dependent D-loop formation with a nucleosomal donor.

Fig. 1 shows the results of D-loop assays that use either a circular, naked DNA donor or this same circular DNA assembled into nucleosomes. Consistent with previous studies, the

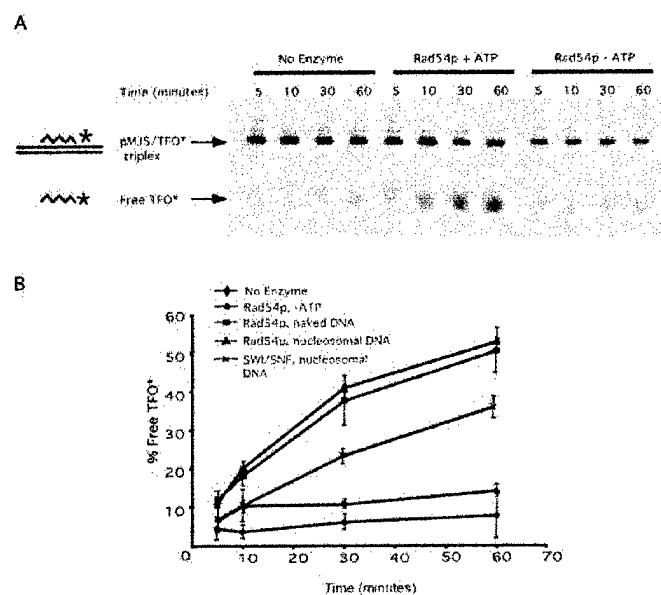


**FIG. 3. Rad54 generates superhelical torsion on nucleosomal DNA.** *A*, schematic illustration of the cruciform extrusion assay. A linearized plasmid (pXG540) containing an inverted repeat sequence is incubated with T4 Endonuclease VII, a highly selective junction resolving enzyme, and Rad54p, in the presence of ATP. Rad54p increases the local unconstrained superhelical density, resulting in the extrusion of a cruciform structure, which is recognized and cut by Endo VII. Adapted from Havas *et al.* (16). *B*, results of a typical cruciform formation assay. Supercoiled (*lanes 1, 2*), *Ava*I-linearized pXG540 DNA (*lanes 3–10, 19*), or nucleosomal pXG540 (*lanes 11–18, 20*) was incubated with 12.5, 25, or 50 nM Rad54p as indicated, in the presence or absence of 100 nM Rad51p. EndoVII was omitted in *lane 1*. ATP was omitted in *lanes 19* and *20*. The numbers below each lane (% cut) represent the percentage of pXG540 molecules cleaved by EndoVII. *s.c.*, supercoiled substrate; *C*, chromatin substrate; *N*, naked linear DNA substrate.



torsion leads to extrusion of a cruciform that is then recognized and cleaved by bacteriophage T4 endonuclease VII that has high specificity for this DNA structure (16). Consistent with previous studies (19), Rad54p action generates torsional stress on a linear, dsDNA substrate (*N*) which leads to cruciform extrusion (Fig. 3*B*, *lanes 4–6*). Importantly, Rad54p was able to generate torsional stress on the nucleosomal substrate (*C*) with comparable efficiency (*lanes 12–14*). The addition of 100 nM Rad51p greatly stimulated the ability of Rad54p to promote the formation of cruciform structures on both naked and nucleosomal substrates (compare *lanes 4* and *8*, and *12* and *16*, respectively). Also note the decreased levels of linear template in *lanes 16–18*). Importantly, Rad51p fails to support cruciform formation by itself (*lanes 7* and *15*). As expected, the generation of torsional stress required ATP (*lanes 19* and *20*). Furthermore, the ATP hydrolysis mutant variant rad54 K341A was inactive in these assays (data not shown). These data indicate that Rad54p, like other Swi2/Snf2 family members, uses the free energy from ATP hydrolysis to alter DNA topology and that nucleosomal arrays constitute excellent substrates for this activity.

**Rad54p Can Disrupt a DNA Triple Helix**—How Rad54p introduces topological stress in nucleosomal DNA is unclear. Previously, we suggested that superhelical torsion might result from translocation of Rad54p along the DNA double helix (19). Recently, chromatin remodeling by the yeast RSC complex (which contains the Swi2/Snf2-related ATPase, Sth1p) has been shown to involve ATP-dependent DNA translocation (21). To further evaluate the ability of Rad54p to translocate on DNA, we used a DNA triple-helix-displacement assay that was originally developed to follow the translocation of a type I restriction endonuclease along DNA (17). The substrate used (see Fig. 4*A*) consists of a radioactively labeled oligonucleotide (TFO\*) bound via Hoogsteen hydrogen bonds to the major groove of a 2.5-kb linear dsDNA. Translocation of a protein along the DNA displaces the triplex, which can be detected as dissociation of the radioactive TFO\* from the DNA triplex. Fig. 4*B* shows typical levels of triplex displacement in the absence or presence of Rad54p or yeast SWI/SNF. Both Rad54p and ySWI/SNF were able to efficiently displace a preformed triplex from both naked (*squares*) and nucleosomal (*triangles*) substrates in an ATP-dependent manner. Similar results were



**FIG. 4. Rad54p action displaces a preformed triplex.** *A*, typical results obtained with naked triplex-containing substrate. The upper band corresponds to the duplex-bound TFO\*; the lower band corresponds to free TFO\*. Reactions contained 5 nM triplex substrate and 5 nM Rad54p. *B*, percentage of free TFO\* in four or more experiments were averaged and plotted as a function of time. Note that triplex displacement from the nucleosomal template occurs at equal efficiency to that of naked DNA.

obtained when the TFO\*-bound substrate contained single-strand nicks (data not shown), strongly suggesting that the displacement of the TFO\* reflects translocation of Rad54p and ySWI/SNF and that it is not due simply to the generation of torsional stress. Thus, yeast RSC (21), ySWI/SNF, and Rad54p (Fig. 4) all share the ability to use the free energy from ATP hydrolysis to disrupt triplex DNA.

**Rad54p Has ATPase Kinetics Diagnostic of a DNA-translocating Enzyme**—The "inch-worm" model for DNA translocation, originally envisioned (22) for DNA helicases and later modified by Velankar *et al.* (23), proposes that the translocating enzyme progresses along the contour of the DNA in steps of

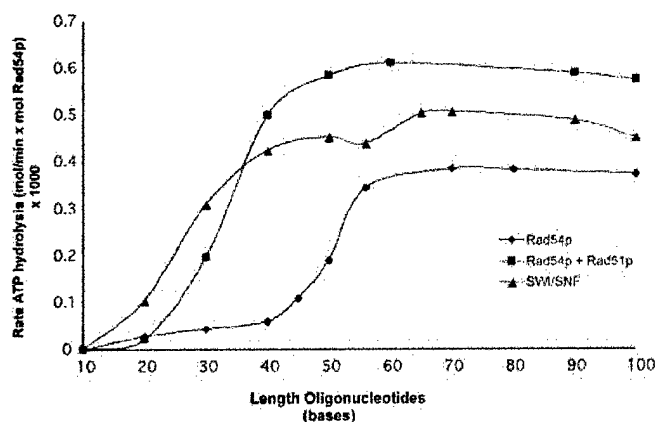


FIG. 5. Rad54 has ATPase kinetics typical of a unidirectional DNA translocating enzyme. The rate of ATP hydrolysis by 5 nM Rad54p (diamonds), 5 nM Rad54p + 5 nM Rad51p (squares), or 10 nM SWI/SNF (triangles) was measured in the presence of 50  $\mu$ M ssDNA (n-mers) oligonucleotides of different lengths. The average values from 3 independent experiments were plotted. Rates were determined from experiments with at least four time points.

a single base, and each step requires the hydrolysis of one ATP molecule. This model predicts that the rate of ATP hydrolysis of a unidirectional DNA translocating enzyme will depend on the length of the DNA (24).

To investigate whether Rad54p has ATPase properties characteristic of a unidirectional DNA translocating enzyme, the rate of ATP hydrolysis was measured in the presence of saturating amounts of single-stranded oligonucleotides ranging from 10 to 100 nucleotides in length (Fig. 5). For comparison, we also monitored the ATPase activity of yeast SWI/SNF (triangles). In the case of Rad54p, oligonucleotides shorter than 40 bases failed to stimulate the ATPase activity of Rad54p (diamonds), whereas oligonucleotides between 40 and 70 bases led to a stimulation of ATPase activity that was proportional to DNA length. For oligonucleotides longer than 70 bases, the ATPase activity no longer increased with the DNA length. When Rad51p was added to these reactions (squares), shorter oligonucleotides became more effective in promoting ATP hydrolysis, and the overall activity was enhanced. Likewise, the ATPase activity of ySWI/SNF (triangles) was also proportional to the DNA length, with a plateau reached at 60 bases.

These results are fully consistent with both Rad54p and ySWI/SNF coupling ATP hydrolysis to unidirectional translocation, in which the rate of DNA binding is slower than the rate of DNA translocation (21). In this case, no ATP hydrolysis is observed with very short substrates, presumably because a minimum DNA length is required for Rad54p or ySWI/SNF to bind and to translocate before reaching an end and releasing the DNA. When the substrate is ~30–40 nucleotides in length, Rad54p and ySWI/SNF readily bind the substrate, and more extended translocation events take place. The rate of ATP hydrolysis is fairly constant with DNA substrates longer than 60–70 nucleotides, reflecting the possibility that Rad54p and ySWI/SNF have little processivity, and thus they release their substrate after ~60–70 bases regardless of the total length of the DNA molecule. Although the triphasic kinetics of ATPase activity are consistent with a DNA-translocation mechanism, it remains a possibility that the longer single-stranded oligonucleotides exhibit more extended secondary structures that are either more proficient at binding Rad54p (or SWI/SNF) or stimulating its ATPase activity.

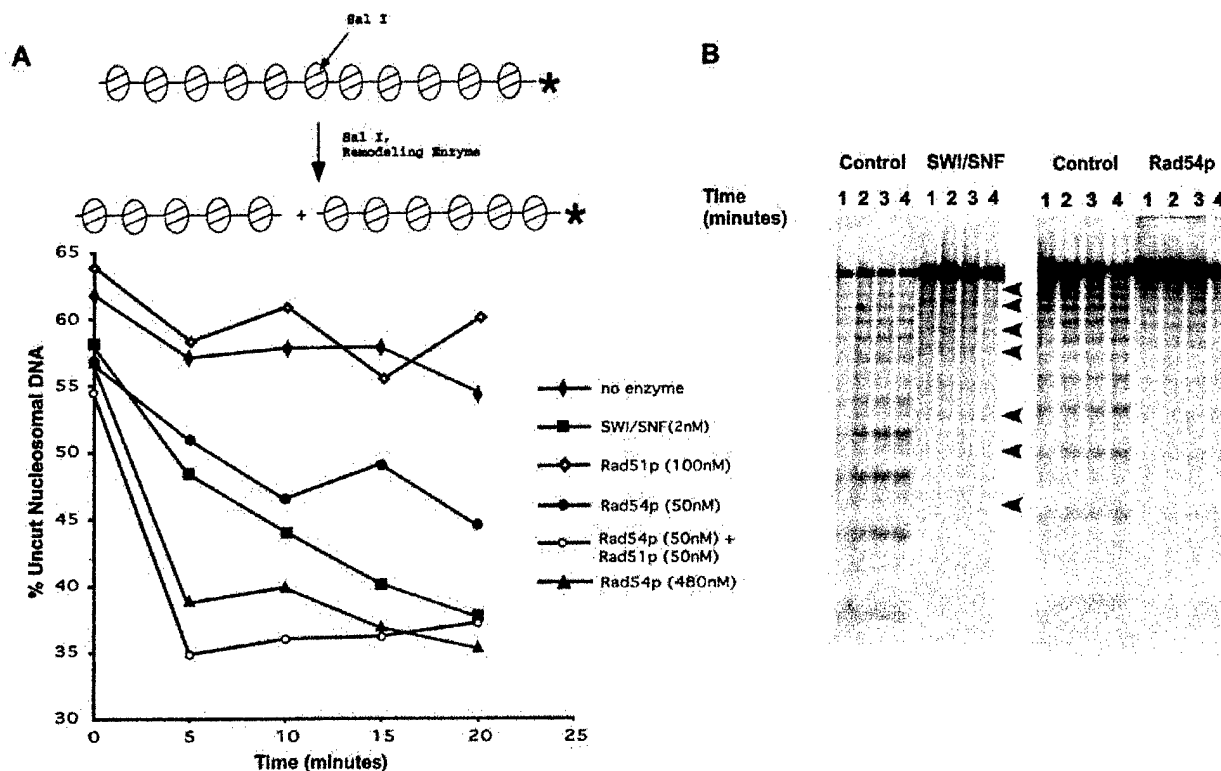
**Rad54 Is an ATP-dependent Chromatin Remodeling Enzyme**—Cairns and colleagues (21) proposed that short-range translocation events may be the key feature of chromatin remodeling enzymes, leading to a "pumping" of DNA across the

surface of the histone octamer, which then results in enhanced DNA accessibility and nucleosome movements. To investigate whether Rad54p might also enhance the accessibility of nucleosomal DNA, we used an assay in which nucleosome remodeling activity is coupled to restriction enzyme activity such that remodeling is revealed as an enhancement of restriction-enzyme cleavage rates (12). This assay uses a nucleosomal array substrate in which the central nucleosome of an 11-mer array contains a unique *Sall* site located at the predicted dyad axis of symmetry (see Fig. 6A). In the absence of a remodeling enzyme, the rate of *Sall* cleavage is very slow (Fig. 6A, solid diamonds), whereas addition of a remodeling enzyme, such as yeast SWI/SNF, leads to enhanced digestion (Fig. 6A, solid squares). When Rad54p was added to the remodeling reactions, *Sall* digestion was also dramatically enhanced (solid circles, triangles), although a higher concentration of this protein (50 nM) was required to achieve a rate of digestion comparable with that of reactions that contained yeast SWI/SNF (2 nM, squares). However, when Rad51p (50 nM) and Rad54p (50 nM) were both present in the reaction, much higher levels of remodeling were attained (open circles). Note that Rad51p has no intrinsic chromatin remodeling activity (open diamonds). The stimulation of the Rad54p chromatin remodeling activity by Rad51p is congruent with previous studies showing that Rad51p enhances the rate of ATP hydrolysis and DNA supercoiling by Rad54p (19, 25, see Fig. 3). Thus, the above data indicate that Rad54p is sufficient for chromatin remodeling activity but that the combination of Rad51p and Rad54p constitutes a more potent remodeling machine.

**Rad54p Does Not Induce Significant Nucleosome Mobilization**—A number of chromatin remodeling complexes that contain a Swi2/Snf2-related ATPase (ySWI/SNF, dCHRAC, dNURF, and xMi-2) can use the energy of ATP hydrolysis to move nucleosomes in cis (26–30). To investigate whether Rad54p can also catalyze nucleosome mobilization,  $^{32}$ P-end-labeled nucleosomal arrays were incubated with buffer, ySWI/SNF, or Rad54p, and nucleosome positions were mapped by micrococcal nuclease (Mnase) digestion (Fig. 6B). Mnase can only cleave DNA between nucleosomes, which leads to a periodic ladder of digestion products indicative of a positioned 11-mer nucleosomal array (Fig. 6B). Consistent with our previous studies, incubation with ySWI/SNF (2 nM) and ATP leads to a complete disruption of the Mnase digestion pattern, indicative of nucleosome sliding (Fig. 6B, left panel; also see Ref. 28). In contrast, addition of Rad54p (100 nM) and ATP had very little effect on the cleavage periodicity (Fig. 6B, right panel). Likewise, addition of both Rad51p and Rad54p (100 nM each) to these assays did not change the Mnase digestion profile (data not shown). Importantly, these experiments used concentrations of ySWI/SNF and Rad54p that yielded similar levels of chromatin remodeling in the restriction enzyme accessibility assay (Fig. 6A). Thus, although Rad54p can enhance the accessibility of nucleosomal DNA to restriction enzymes, this activity does not appear to reflect large scale rearrangement of nucleosome positions.

#### DISCUSSION

In eukaryotes, chromatin presents an accessibility dilemma for all DNA-mediated processes, including gene transcription and DNA repair. Although much progress has been made on identifying the enzymes that remodel chromatin structure to facilitate transcription, less is known of how the DNA-repair machinery gains access to damaged DNA within chromatin (reviewed in Ref. 31). In particular, it has not been clear how the recombinational repair machinery can locate short regions of DNA homology when those DNA donor sequences are assembled into chromatin. Here we have shown that the yeast re-



**FIG. 6. Rad54 is an ATP-dependent chromatin remodeling enzyme.** *A*, various concentrations of recombinant Rad54p were tested for chromatin-remodeling activity in a coupled remodeling-restriction enzyme cleavage assay. The nucleosomal substrate was incubated with 50 nM (closed circles) or 480 nM Rad54p (triangles), 100 nM Rad51p (open diamonds), 50 nM Rad54p + 50 nM Rad51p (open circles), 2 nM ySWI/SNF (squares), or buffer (closed diamonds). *B*, 208–11 reconstituted nucleosomal arrays were incubated at 37 °C with 2 nM SWI/SNF, 100 nM Rad54p, or buffer (control lanes). Aliquots were treated with Mnase for the indicated times. The arrowheads in the left panel indicate the alternate banding pattern as a result of SWI/SNF-induced nucleosome movement.

combination proteins, Rad51p and Rad54p, are sufficient to promote heteroduplex DNA joint formation with chromatin. In contrast, the bacterial recombinase RecA is completely inactive with a chromatin donor. The unique capacity of the eukaryotic machinery to contend with chromatin likely reflects the chromatin-remodeling activity of Rad54p, in which the free energy from ATP hydrolysis enhances the accessibility of nucleosomal DNA. Strand invasion with chromatin may also require a specific interaction between Rad51p and Rad54p because the chromatin remodeling activity of Rad54p does not facilitate RecA-dependent D-loop formation with chromatin (Fig. 1D). Recently, Alexiadis and Kadonaga have reported that the *Drosophila* Rad51 and Rad54 proteins can also facilitate strand invasion with chromatin (35).

**How Does Rad54p Remodel Chromatin Structure?**—Several studies have shown that SWI/SNF-like chromatin remodeling enzymes can perform two separable reactions: 1) they can use the free energy from ATP hydrolysis to enhance the accessibility of nucleosomal DNA and 2) they can use this free energy to mobilize nucleosomes in cis (reviewed in Ref. 32). Recent work from Cairns and colleagues have suggested that both of these activities may be caused by ATP-dependent “pumping” of DNA into the nucleosome (21). In this model, small amounts of DNA translocation might lead to transient exposure of small “loops” of DNA on the surface of the histone octamer, whereas larger quantities of DNA “pumped” into the nucleosome would lead to changes in nucleosome positions. Our data support this model, as we find that both yeast SWI/SNF and Rad54p, like yeast RSC (21), can disrupt a DNA triplex in an ATP-dependent reaction, presumably by translocation of DNA along the surface of the enzyme or by translocation of the enzyme along the DNA. Furthermore, the ATPase activities of ySWI/SNF and Rad54p

are sensitive to DNA length, which is diagnostic of DNA-translocating enzymes (21).

Although ySWI/SNF and Rad54p can both enhance the accessibility of nucleosomal DNA, only ySWI/SNF appears to be proficient at changing nucleosome positioning. This result suggests that the precise mechanism of chromatin remodeling by Rad54p may be distinct from that of ySWI/SNF. For instance, Rad54p may only be able to pump small amounts of DNA across the histone octamer surface. Alternatively, Rad54p may translocate along DNA, rather than pumping DNA into the nucleosome. In this model, Rad54p may “pull” the Rad51-ssDNA nucleoprotein filament along the chromatin fiber, leading to changes in nucleosomal DNA topology and DNA accessibility. Such a DNA tracking mechanism might play a key role in facilitating both the search for homology as well as the strand invasion step.

**Multiple Roles for Rad54p during Homologous Recombination**—Our results suggest that Rad54p is an extremely versatile recombination protein that plays key roles in several steps of homologous recombination. Recently, we found that Rad54p is required for optimal recruitment of Rad51p to a double strand break *in vivo*, and likewise Rad54p can promote formation of the presynaptic filament *in vitro* by helping Rad51p contend with the inhibitory effects of the ssDNA-binding protein replication protein A.<sup>2</sup> Several studies over the past few years have also shown that the ATPase activity of Rad54p plays key roles subsequent to formation of the presynaptic filament. For instance, Rad54p is required for the Rad51p-nucleoprotein filament to form a heteroduplex joint DNA mol-

<sup>2</sup> B. Wolner, S. Van Komen, P. Sung, and C.L. Peterson, submitted for publication.

ecule, even when the homologous donor is naked DNA (Fig. 1A; see also Refs. 7, 18, 33). In this case, it has been proposed that Rad54p might use the free energy from ATP hydrolysis to translocate along DNA, which facilitates the homology search process. This DNA-translocation model is fully consistent with our findings that Rad54p can displace a DNA triplex and that the ATPase activity of Rad54p is proportional to DNA length. Rad54p also stimulates heteroduplex DNA extension of established joint molecules (34). Finally, we have shown that Rad54p is required for Rad51p-dependent heteroduplex joint molecule formation with a chromatin donor. In this case, our results suggest that the ATPase activity of Rad54p is used to translocate the enzyme along the nucleosomal fiber, generating superhelical torsion, which leads to enhanced nucleosomal DNA accessibility. It seems likely that this chromatin remodeling activity of Rad54p might also facilitate additional steps after heteroduplex joint formation. Future studies are now poised to reconstitute the complete homologous recombinational repair reaction that fully mimics each step in the repair of chromosomal DNA double strand breaks *in vivo*.

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