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Mol. Cell. Biol. **1992, 12(9):3939. DOI: 10.1128/MCB.12.9.3939.**

MOLECULAR AND CELLULAR BIOLOGY, Sept. 1992, p. 3939–3947
0270-7306/92/093939-09$02.00/0

Vol. 12, No. 9

PRP38 Encodes a Yeast Protein Required for Pre-mRNA Splicing and Maintenance of Stable U6 Small Nuclear RNA Levels

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Received 7 April 1992/Returned for modification 14 May 1992/Accepted 17 June 1992

An essential pre-mRNA splicing factor, the product of the *PRP38* gene, has been genetically identified in a screen of temperature-sensitive mutants of *Saccharomyces cerevisiae*. Shifting temperature-sensitive *prp38* cultures from 23 to 37°C prevents the first cleavage-ligation event in the excision of introns from mRNA precursors. In vitro splicing inactivation and complementation studies suggest that the *PRP38*-encoded factor functions, at least in part, after stable splicing complex formation. The *PRP38* locus contains a 726-bp open reading frame coding for an acidic 28-kDa polypeptide (PRP38). While PRP38 lacks obvious structural similarity to previously defined splicing factors, heat inactivation of PRP38, PRP19, or any of the known U6 (or U4/U6) small nuclear ribonucleoprotein-associating proteins (i.e., PRP3, PRP4, PRP6, and PRP24) leads to a common, unexpected consequence: intracellular U6 small nuclear RNA (snRNA) levels decrease as splicing activity is lost. Curiously, U4 snRNA, normally extensively base paired with U6 snRNA, persists in the virtual absence of U6 snRNA.

The excision of intervening sequences from eukaryotic pre-mRNA transcripts occurs in the nucleus on a large, complex structure termed the spliceosome (for recent reviews, see references 17, 18, and 40). Gene sequence comparisons and the analyses of naturally occurring and experimentally induced intron variants led to the identification of three short intron segments, the 5′ splice site, the branch point region, and the 3′ splice site, essential for splicing. These sequences function in part to guide the assembly of the spliceosome on newly synthesized pre-mRNA. Most conspicuous among the *trans*-acting factors associating with pre-mRNA are the U1, U2, U4/U6, and U5 small nuclear ribonucleoprotein (snRNP) particles. Each snRNP contains one or two small nuclear RNAs (snRNAs), a set of approximately eight common proteins (defined to date only in metazoa), and a variable number of snRNP-specific peptides (reviewed in references 30 and 61). The snRNP particles together with other splicing factors direct intron removal by a two-step mechanism comprising (i) cleavage at the 5′ splice site and ligation of the 5′-terminal nucleotide of the intron to an adenosine near the 3′ end on the intron and (ii) cleavage at the 3′ splice site and exon ligation.

The in vitro assembly of yeast (*Saccharomyces cerevisiae*) spliceosomes, like that of metazoa, occurs progressively. Assembly can be monitored by assaying the association of snRNP particles with exogenously added pre-mRNA (11, 37). Initially, and independently of ATP, U1 snRNP plus non-snRNP factors bind the pre-mRNA to form a commitment complex destined for the splicing pathway (reviewed in reference 38). Subsequently, in a step dependent upon ATP, U2 snRNP is added and a stable prespliceosome forms. U5 snRNP exists in dynamic association with the U4/U6 snRNP particle (5, 11, 29, 59); the three snRNAs appear to enter the spliceosome as part of a U4/U6/U5 tri-snRNP. Late in the assembly process, the U4/U6 intermolecular helices unwind and, under standard assay conditions, U4 snRNA dissociates from the spliceosome (11, 37). The catalytic events of splicing are believed to occur just subsequent to U4 dissociation and may involve direct participation of the exposed U6 snRNA (7, 15, 32). The excised intron product persists for some time associated with at least the U2, U5, and U6 snRNP particles, while spliced mRNA dissociates free of snRNPs. The details of snRNP-spliceosome dynamics, while integral to the splicing process, are poorly understood.

Unmasking the mechanism of spliceosome-mediated catalysis presents a considerable challenge. A necessary step toward this goal, the identification and characterization of individual splicing factors, is being successfully pursued in studies of *S. cerevisiae* by using genetic techniques (18, 40, 57). Two general experimental approaches have been used: (i) the screening of randomly mutagenized cells for mutants defective in precursor RNA processing (*prp* mutants) and (ii) the isolation of *trans*-acting suppressors of mutations in known splicing factors. At least 20 genes have been identified as temperature- or cold-sensitive strains that accumulate pre-mRNA, splicing intermediates, or intron products at restrictive temperatures. Immunological and genetic studies have established that a number of *PRP* genes encode snRNP polypeptides. PRP3, PRP4, PRP6, and PRP24 associate with the U6 or U4/U6 snRNP (1, 3, 5, 35, 47, 57a, 59); PRP8 and perhaps PRP28 bind the U5 snRNP (29, 52, 56). Other *PRP* products are spliceosome components (PRP11 [8] and PRP16 [45]) or are necessary for in vitro spliceosome assembly (PRP5 [13] and PRP9 [1]) or splicing (PRP2 [9, 27, 31], PRP18 [54], and PRP22 [12]) but have unknown snRNP association.

In this study, we report the identification and characterization of a novel yeast splicing factor, PRP38. In vitro, inactivation of a temperature-sensitive PRP38 derivative (*ts* PRP38) inhibits 5′ splice site cleavage but does not perceptibly impede spliceosome assembly. In vivo, inactivation of *ts* PRP38 blocks splicing and promotes a marked decrease in the cellular content of U6 snRNA. We show that *ts* alleles encoding each of the previously defined U6 and U4/U6 proteins as well as the relatively uncharacterized PRP19 splicing factor likewise elicit temperature-dependent de-

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TABLE 1. Yeast strains

Strain	Genotype
MGD353 46D	*MATα ura3-52 leu2-3,112 his3 cyh*^{r}
MGD353 13D	*MATa ura3-52 ade2 leu2-3,112 arg4 trp1-289*
MGD407	*MATα/a ura3-52 leu2-3,112*
ts192	*MATα prp38-1 ura3-52 leu2-3,112 his3 cyh*^{r}
ts146	*MATα prp4 ura3-52 leu2-3,112 his3 cyh*^{r}
ts368	*MATa prp2-1 ade1 ade2 ura1 tyr1 his7 lys2 gal1*
ts125	*MATa prp3-1 ade1 ade2 ura1 tyr1 his7 lys2 gal1*
ts339	*MATa prp4-1 ade1 ade2 ura1 tyr1 his7 lys2 gal1*
ts108	*MATa prp5-1 ade1 ade2 ura1 tyr1 his7 lys2 gal1*
ts166	*MATa prp6-1 ade1 ade2 ura1 tyr1 his7 lys2 gal1*
ts226	*MATa prp7-2 ade1 ade2 ura1 tyr1 his7 lys2 gal1*
ts219	*MATa prp8-1 ade1 ade2 ura1 tyr1 his7 lys2 gal1*
ts257	*MATa prp9-1 ade1 ade2 ura1 tyr1 his7 lys2 gal1*
JM650	*MATa prp11-1 leu2-3,112 his7 tyr1 lys2*
ts514	*MATa prp16-2 ade2-101 his3 200 ura3-52 tyr1*
ts365	*MATa prp17 ade2-101 his3 200 ura3-52 lys2-801*
ts503	*MATa prp18 ade2-101 his3 200 ura3-52 lys2-801*
ts87c	*MATa prp19 ade2-101 his3 200 ura3-52 lys2-801 leu2*
ts319	*MATa prp20 ade2-101 his3 200 ura3-52 tyr1*
ts47	*MATa prp21 ade2-101 his3 200 ura3-52 tyr1*
ts107	*MATa prp22 ade2-101 his3 200 ura3-52 tyr1*
ts344	*MATa prp24 ade2-101 his3 200 ura3-52 lys2-801*
ts397	*MATa prp25 ade2-101 his3 200 ura3-52 lys2-801*

creases in U6 snRNA abundance. In light of this observation, we propose that snRNA instability is a hallmark of mutations that perturb snRNP structure. Our data suggest that *PRP19* and the newly defined *PRP38* gene encode proteins that interact (directly or indirectly) with at least one of the U6 snRNA-containing snRNP complexes required for pre-mRNA splicing.

MATERIALS AND METHODS

Yeast strains. Genotypes of the strains used are shown in Table 1. Strains MGD353 46D and 13D were obtained from B. Seraphin and M. Rosbash. *prp2-11* and *prp17-27* strains were provided by J. Woolford and J. Abelson, respectively.

Genetic studies. (i) Mutagenesis of yeast strains and selection for temperature sensitivity. A stationary-phase culture of MGD353 46D was mutagenized to 10% survival in phosphate buffer containing ethyl methanesulfonate as previously described (49). The mutagenesis was quenched with 5% sodium thiosulfate, and the cultures were immediately frozen in aliquots at −80°C. Cells from the mutagenized culture were grown under nonselective conditions (23°C, YEPD broth) for one to two generations (3 h) before plating on a master plate of YEPD agar (23°C). Temperature-sensitive mutants were identified as colonies from replica transfers that failed to grow at the restrictive temperature (37°C).

Complementation analysis, sporulation, and tetrad dissection were performed by standard techniques (49). Diploids were selected by scoring for nutritional markers (see above), and complementation of the splicing defect was assayed by monitoring the growth of diploid strains on YEPD media at 23 and 37°C. Asci were digested for 30 min in 0.5 mg of Zymolyase 100T (ICN) per ml–1 M sorbitol–0.1 mM EDTA and dissected on YEPD agarose.

(ii) Isolation of *PRP38*. Competent *ts192* cells were transformed by the lithium acetate procedure of Ito et al. (20) as previously modified (49) with 10 μg of a yeast DNA library on the centromeric plasmid vector YCp50 (39). The yeast cells were plated on complete medium lacking uracil for 24 h at room temperature (to allow expression of the plasmid-encoded genes) and then shifted to 37°C to identify transformants with complementing DNA segments. Plasmids were recovered from these cultures, amplified in *Escherichia coli*, and reintroduced into *ts192* and other mutant *prp* cultures to demonstrate plasmid-dependent, gene-specific complementation.

Linkage of the cloned 5.0-kbp *Pvu*II fragment with *PRP38* was established by inserting the fragment into the *Hin*dIII- and *Eco*RI-cleaved, Klenow enzyme-blunted (43) sites of the *URA3*-containing integrating vector YIp21 (16). This DNA was then cleaved with *Hin*dIII and targeted to its corresponding chromosomal location in *ts192* cells by transformation. The fidelity of the integration event was confirmed by Southern blot. Several yeast transformants were mated with MGD353 13D, the diploids were sporulated, and the segregation pattern of the temperature-sensitive and splicing phenotypes was monitored.

Disruption of the *PRP38* open reading frame was accomplished by inserting the 2.2-kb *Sal*I-*Xho*I *LEU2* fragment (6) into the *Kpn*I site of an *Xba*I-*Pst*I *PRP38* subclone on plasmid pTZ19R (U.S. Biochemical [USB]). Both the vector and insert DNAs were rendered blunt ended by using mung bean nuclease as instructed by the manufacturer (USB) prior to joining with T4 DNA ligase. The *LEU2*-disrupted *PRP38* gene was excised with *Hin*dIII and *Pst*I and used to transform diploid yeast strain MGD407. Leu$^+$ transformants were screened for the presence of the correct insertion event by Southern analysis.

DNA and RNA manipulations. DNA sequencing was performed by the dideoxy-chain termination method (44) with Sequenase DNA polymerase (USB). Single-stranded DNA templates were prepared from the pTZ18 and pTZ19 plasmid vector series as instructed by the manufacturer (USB). Both strands of *PRP38* were sequenced by using subclones derived from the available restriction sites (*Hin*dIII, *Kpn*I, and *Pst*I), using synthetic DNA oligonucleotides. M13 reverse and −40 DNA sequencing primers were purchased from USB; all other oligonucleotides used for DNA sequencing and mutagenesis (24) were prepared by the University of Kentucky DNA synthesis facility. The sequences (5′ to 3′) of the *PRP38*-specific sequencing primers were as follows: (i) TTTTGTGATATCAATAACGA, (ii) TACTGCCACTGAA ATATA, (iii) GGACTACAATGGCTGTCAATG, (iv) CCTA AGAAGATCGGGTCAAA, and (v) TGAAGTTAATCGAA ATCAGA. The mutagenesis oligonucleotide [GTTATAG GAG(T/C)(G/A)AGCAAAG(T/C)(G/A)GTCTACTTG] was also used for sequence analysis.

Total yeast RNA was isolated from mechanically disrupted cell lysates according to previously published procedures (36) and fractionated on a 5% polyacrylamide–8 M urea gel or on a 1% agarose–formaldehyde gel. snRNA probes were prepared by random priming DNA fragments containing the following snRNA genes: U1 (polymerase chain reaction fragment of coding nucleotides 1 to 569 of *SNR19*) (23, 51); U2 (*Cla*I fragment of *LSR1*) (2); U4 (*Eco*RI-*Eco*RV fragment of *SNR14*) (50), U5, (*Hpa*I-*Nco*I fragment of *SNR7*) (34), and U6 (*Taq*I fragment of *SNR6*) (7). Plasmid SPRP51A (41) was labeled as an intron-plus-exon DNA probe. Autoradiograms were quantified by using a LKB 2400 gel scanner.

In vitro splicing. Yeast whole cell lysates were prepared according to the method of Lin et al. (28). In vitro splicing reactions were assembled, and the results were analyzed as described previously (37), using ~1 ng of *RP51a*-derived pT7Δ2 RNA (42).

Heat inactivation of the temperature-sensitive extracts was performed by incubating 4 μl of extract in dialysis buffer (28) for 20 min at 34°C. Control reaction mixtures were assembled and incubated at 23°C. Micrococcal nuclease (MN) digestions (10) and *N*-ethylmaleimide (NEM) treatment (22) were performed as previously described, using MGD353 46D whole cell extracts. Complementation studies were performed by mixing ~40 μg (protein) of MN-, NEM-, or heat-treated (10 min, 50°C) MGD353 46D extract with an equal amount of heat-inactivated *ts192* extract prior to addition of pre-mRNA. All splicing reactions were performed at 23°C.

Nucleotide sequence accession number. The *PRP38* DNA sequence has been deposited in the GenBank data base and assigned accession number M95921.

RESULTS

Identification of a conditional lethal splicing mutant. The *ts192* mutant was isolated from a bank of yeast mutants temperature sensitive for growth and for the correct processing of *RP51a* pre-mRNA. When assayed at 23°C, the *ts192* and wild-type strains exhibited comparable growth characteristics and *RP51a* RNA profiles (Fig. 1A and B). In contrast, at 37°C, the *ts192* cells selectively stopped growing, *RP51a* mRNA levels dropped, and an *RP51a* RNA form of lesser electrophoretic mobility accumulated. This new RNA species comigrated with *RP51a* pre-mRNA isolated from a *prp2* splicing mutant under the same conditions. Primer extension analysis of RNA from *ts192* cells transformed with the well-characterized *RP51a-lacZ* fusion gene *HZ18Δ2* (36) confirmed that the novel *RP51a* RNA accumulating at 37°C is unspliced precursor (Fig. 1C). The extent of the change in RNA pattern varied somewhat between experiments (compare Fig. 1B and C) but was consistently observed and limited to polymerase II genes having introns. Transcripts from the intron-containing *RP51a*, *ACT1*, *CYH2*, and *RPS10* genes each displayed the characteristic shift in electrophoretic mobility associated with increased pre-mRNA levels, while no changes were noted for the intronless *CYC1*, *ADE3*, and 5S rRNA transcripts (data not shown). Thus, at the restrictive temperature, *ts192* cells are specifically inhibited in the conversion of pre-mRNA into splicing intermediates and products.

The *ts192* strain defines a new gene, *PRP38*. The simplest explanation of the conditional lethal phenotype of *ts192* cells is that growth arrest at 37°C is a direct consequence of the defect in pre-mRNA splicing. Consistent with this interpretation, the temperature-sensitive growth and splicing deficiencies meiotically cosegregated in eight dissected asci (data not shown). Furthermore, a single cloned DNA segment simultaneously relieved both defects when introduced by transformation (Fig. 1A and data not shown). Complementation analysis performed between the *ts192* mutant and the previously defined splicing mutants (*prp2-11* and *prp17-24*) demonstrated that the *ts192* defect resides in a distinct chromosomal locus which we have named *PRP38*.

***PRP38* encodes a yeast splicing factor.** The *PRP38* gene product may influence pre-mRNA splicing directly by controlling the assembly or function of the spliceosome or indirectly by regulating the expression of other splicing factors, e.g., by modulating the transcription or translation of genes encoding components of the splicing apparatus. Proof that several *PRP* genes act directly by encoding bona fide splicing factors was provided, in part, by the demonstration that cell extracts prepared from mutant cultures

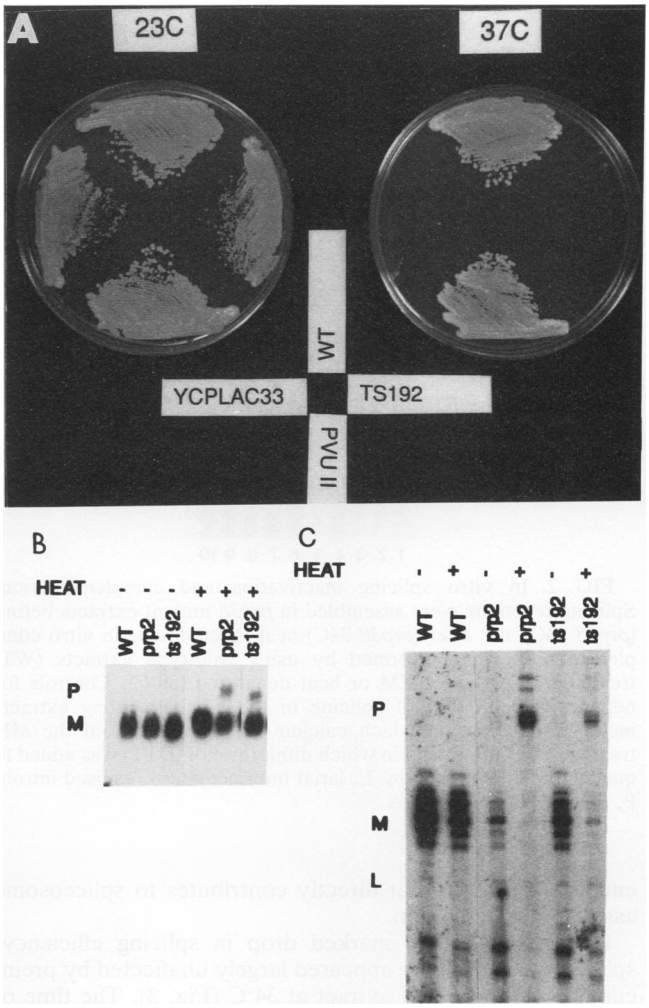

FIG. 1. (A) Colony size of wild-type strain MGD353 46D (WT), mutant *ts192* (temperature sensitive for growth and pre-mRNA splicing), and a *ts192* strain transformed with the plasmid vector YCplac33 (16) or YCplac33 containing a complementing yeast DNA fragment (*Pvu*II). (B) Northern blot of RNA isolated from wild-type (WT), *ts192*, and *prp2* cultures probed with the intron-containing *RP51a* gene. (C) Primer extension analysis using exon II primer RB1 (53) of *RP51a*. P, pre-mRNA; M, mRNA; L, lariat intermediate. HEAT refers to cultures continuously grown at 23°C (−) or shifted to 37°C for 2 h prior to harvesting (+).

were temperature sensitive for splicing (31). Relative to extracts prepared from the parental strain, *prp38* extracts are sensitive to heat inactivation (Fig. 2 and 3A); a 20-min incubation of the *prp38* extract at 34°C reduced splicing to less than 30% of that achieved for wild-type extracts (Fig. 3A, lanes 7 to 9 and 10 to 12) or the untreated mutant extract (Fig. 2, lanes 1 and 2; Fig. 3A, lanes 4 to 6 and 10 to 12). Splicing activity was recovered, albeit incompletely, if the heat-inactivated mutant extract was complemented with an MN-treated wild-type extract (Fig. 2, lane 4) but not if the complementing activity was heat inactivated at 50°C (Fig. 2, lane 6) or was pretreated with NEM (Fig. 2, lane 9). Similar success in reconstituting the heat-inactivated *prp38* extract was achieved by using a heat-inactivated *prp2* or *prp16* extract (data not shown). These data suggest that *PRP38*

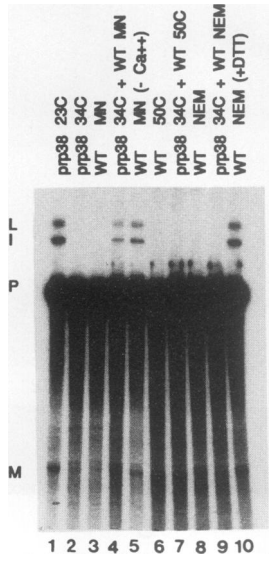

FIG. 2. In vitro splicing inactivation and complementation. Splicing reactions were assembled in *prp38* mutant extracts before (*prp38* 23C) and after (*prp38* 34C) heat inactivation. In vitro complementation was performed by using wild-type extracts (WT) treated with MN or NEM or heat denatured (50°C). Controls for nonspecific inhibition of splicing in the complementing extracts included reactions in which calcium was omitted from the MN treatment (−Ca++) and in which dithiothreitol (DTT) was added to quench the NEM reaction. L, lariat intermediate; I, excised intron; P, pre-mRNA; M, mRNA.

encodes a protein that directly contributes to spliceosome assembly or activation.

In contrast to the marked drop in splicing efficiency, spliceosome assembly appeared largely unaffected by preincubation of the *prp38* extract at 34°C (Fig. 3). The time of appearance and relative amounts of the prespliceosome (complex III) and the complex I intermediate were comparable in the heat-treated and control samples. Although not

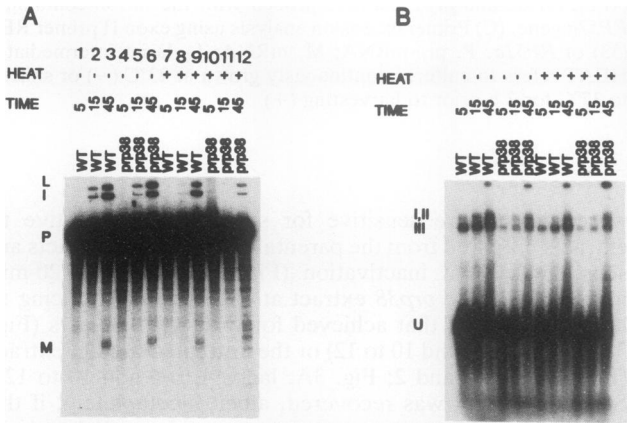

FIG. 3. Time course of splicing. Extracts prepared from the wild-type (WT) and *prp38* mutant strains were assayed for splicing products (A) and spliceosome complexes (B). Extracts were preincubated at 23°C (HEAT−) or 34°C (HEAT+) for 20 min prior to assay. TIME indicates length of incubation in minutes. L, lariat intermediate; I, excised intron; P, pre-mRNA; M, mRNA; I, II, and III, splicing complexes as defined by Pikielny et al. (37).

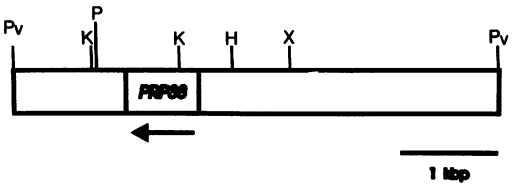

FIG. 4. Restriction map of the 5-kbp *prp38*-complementing DNA. The shaded box represents the coding portion of *PRP38*; the arrow underneath indicates the direction of transcription. Restriction sites: Pv, *Pvu*II; P, *Pst*I; K, *Kpn*I; H, *Hin*dIII; X, *Xba*I.

well resolved on this gel, a complex comigrating with mature spliceosome (complex II [37]) was detected in heat-treated *prp38* extracts (41a). We note, however, that the temperature-imposed splicing block was not absolute; limited splicing did occur in the heat-treated extracts. Furthermore, as the denatured (splicing-impaired) *ts* PRP38 protein remained present during the assembly reaction, residual (or partial) PRP38 activity may have contributed to the formation of the observed complexes. Nevertheless, these results suggest an essential function for PRP38 late in spliceosome assembly or directly during splicing.

Isolation of *PRP38*. The wild-type *PRP38* allele was isolated from a yeast DNA plasmid library (39) by in vivo complementation of the *ts192* growth defect. Three different complementing plasmids were obtained, each containing a 5.0-kb *Pvu*II fragment within a larger (15- to 20-kb) yeast DNA insert. This 5.0-kb fragment was subcloned from one isolate and found to complement the *ts192* growth defect (Fig. 1A and 4).

To demonstrate that the cloned DNA contained the wild-type allele of *PRP38* and not an extragenic suppressor, we mapped its chromosomal location relative to the *ts192* lesion. The 5.0-kb *Pvu*II fragment was subcloned into the *URA3*-containing integrating vector YIp21 (16) and targeted to its resident chromosomal location in *ts192* (*ura3*) cells (see Materials and Methods). Diploids were constructed by mating the resultant YIp21/*Pvu*II transformant with the splicing-competent strain MGD343 13D. In 10 dissected tetrads derived from this cross, the Ura^+ phenotype segregated 2:2 and no temperature-sensitive spores were found. Thus, the integrated cloned DNA was tightly linked to the *ts192* lesion and ostensibly contains wild-type *PRP38* DNA.

The *PRP38* gene was localized by additional complementation analysis to a DNA fragment containing an open reading frame of 726 bp, sufficient to encode a 242-amino-acid, 28-kDa protein (Fig. 5). The importance of this open reading frame was tested by site-directed mutagenesis. Two mutant alleles were created; in one, a base pair deletion was introduced at nucleotide position 846. This change creates a termination codon in the next position (amino acid Val-172→STOP). In the second mutant allele, the *LEU2* gene was inserted at a *Kpn*I site within codon 66. Both mutant constructs failed to complement the *ts prp38* lesion. Furthermore, when the *LEU2* insertion derivative was used to replace the wild-type allele in a gene substitution experiment (see Materials and Methods), no viable Leu^+ spore products were found in 15 dissected tetrads, thereby establishing *PRP38* as an essential yeast gene.

***PRP38* structure.** The DNA sequence of *PRP38* provides little clue as to its regulation or function. A putative TATA-box element is present 67 bp 5′ to the presumed site of *PRP38* translational initiation. The sequence context of this

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        10         20         30         40         50         60         70         80         90        100        110
GAAGCTTTAA AGAAGGTAGA TGAGTTGATT GCTTCCAAGA AGGGTTCGAA GTATGCCAAG AGAGTAGAAA AAATGAAAAA AAACCAAAGT ATAGGCTGGT TCTGAAGAAT
CTTCGAAATT TCTTCCATCT ACTCAACTAA CGAAGGTTCT TCCCAAGCTT CATACGGTTC TCTCATCTTT TTTACTTTTT TTTGGTTTCA TATCCGACCA AGACTTCTTA
       120        130        140        150        160        170        180        190        200        210        220
AAGAGAGAAG ATAACTATAG TTTAGAATAG TAAACCCTAT GTGTACTGTT TTATGTTTTT AATGTCTAAT CATGTAAATA ATTTTGTGAT ATCAATAACG AACGTTCTGA
TTCTCTCTTC TATTGATATC AAATCTTATC ATTTGGGATA CACATGACAA AATACAAAAA TTACAGATTA GTACATTTAT TAAAACACTA TAGTTATTGC TTGCAAGACT
       230        240        250        260        270        280        290        300        310        320        330
ACAAGAATTA TGATAAAAAA AAGTAAAATC TAAAGCCATT ACAACGCTAT ATTTTCAGTG GCAGTAAAAA CGCAAGAACA AAAACAAAAC GTGGGTAAAG AACAAGGACT
TGTTCTTAAT ACTATTTTTT TTCATTTTAG ATTTCGGTAA TGTTGCGATA TAAAAGTCAC CGTCATTTTT GCGTTCTTGT TTTTGTTTTG CACCCATTTC TTGTTCCTGA

        340        350        360        370        380        390        400        410        420
ACA ATG GCT GTC AAT GAA TTT CAA GTG GAG TCT AAC ATC TCT CCA AAA CAA CTG AAT AAC CAG TCA GTG TCA CTT GTT ATT CCT CGG TTG
TGT TAC CGA CAG TTA CTT AAA GTT CAC CTC AGA TTG TAG AGA GGT TTT GTT GAC TTA TTG GTC AGT CAC AGT GAA CAA TAA GGA GCC AAC
    Met Ala Val Asn Glu Phe Gln Val Glu Ser Asn Ile Ser Pro Lys Gln Leu Asn Asn Gln Ser Val Ser Leu Val Ile Pro Arg Leu

        430        440        450        460        470        480        490        500        510
ACA AGA GAT AAA ATT CAT AAT TCA ATG TAC TAT AAA GTA AAT CTA AGC AAC GAA TCT TTG AGA GGC AAT ACA ATG GTA GAG CTT TTG AAA
TGT TCT CTA TTT TAA GTA TTA AGT TAC ATG ATA TTT CAT TTA GAT TCG TTG CTT AGA AAC TCT CCG TTA TGT TAC CAT CTC GAA AAC TTT
Thr Arg Asp Lys Ile His Asn Ser Met Tyr Tyr Lys Val Asn Leu Ser Asn Glu Ser Leu Arg Gly Asn Thr Met Val Glu Leu Leu Lys

        520        530        540        550        560        570        580        590        600
GTT ATG ATT GGC GCA TTT GGT ACC ATA AAA GGT CAA AAT GGT CAT TTA CAC ATG ATG GTT CTC GGT GGC ATT GAG TTT AAA TGC ATC TTA
CAA TAC TAA CCG CGT AAA CCA TGG TAT TTT CCA GTT TTA CCA GTA AAT GTG TAC TAC CAA GAG CCA CCG TAA CTC AAA TTT ACG TAG AAT
Val Met Ile Gly Ala Phe Gly Thr Ile Lys Gly Gln Asn Gly His Leu His Met Met Val Leu Gly Gly Ile Glu Phe Lys Cys Ile Leu

        610        620        630        640        650        660        670        680        690
ATG AAG TTA ATC GAA ATC AGA CCG AAT TTC CAG CAG TTG AAC TTC TTA TTG AAT GTA AAA AAT GAG AAC GGT TTT GAC TCG AAA TAT ATT
TAC TTC AAT TAG CTT TAG TCT GGC TTA AAG GTC GTC AAC TTG AAG AAT AAC TTA CAT TTT TTA CTC TTG CCA AAA CTG AGC TTT ATA TAA
Met Lys Leu Ile Glu Ile Arg Pro Asn Phe Gln Gln Leu Asn Phe Leu Leu Asn Val Lys Asn Glu Asn Gly Phe Asp Ser Lys Tyr Ile

        700        710        720        730        740        750        760        770        780
ATT GCT TTG CTT CTG GTT TAT GCG CGG TTA CAG TAT TAT TAT TTG AAT GGC AAT AAC AAA AAC GAT GAT GAT GAA AAT GAT TTG ATA AAG
TAA CGA AAC GAA GAC CAA ATA CGC GCC AAT GTC ATA ATA ATA AAC TTA CCG TTA TTG TTT TTG CTA CTA CTA CTT TTA CTA AAC TAT TTC
Ile Ala Leu Leu Leu Val Tyr Ala Arg Leu Gln Tyr Tyr Tyr Leu Asn Gly Asn Asn Lys Asn Asp Asp Asp Glu Asn Asp Leu Ile Lys

        790        800        810        820        830        840        850        860        870
TTA TTT AAA GTA CAA TTA TAC AAA TAT TCA CAG CAT TAT TTC AAA CTA AAA AGT TTC CCA CTA CAA GTA GAC TGC TTT GCT CAC TCC TAT
AAT AAA TTT CAT GTT AAT ATG TTT ATA AGT GTC GTA ATA AAG TTT GAT TTT TCA AAG GGT GAT GTT CAT CTG ACG AAA CGA GTG AGG ATA
Leu Phe Lys Val Gln Leu Tyr Lys Tyr Ser Gln His Tyr Phe Lys Leu Lys Ser Phe Pro Leu Gln Val Asp Cys Phe Ala His Ser Tyr

        880        890        900        910        920        930        940        950        960
AAC GAA GAA CTT TGT ATA ATA CAC ATT GAT GAA TTA GTC GAT TGG TTG GCC ACA CAG GAC CAT ATC TGG GGT ATT CCA TTA GGG AAA TGT
TTG CTT CTT GAA ACA TAT TAT GTG TAA CTA CTT AAT CAG CTA ACC AAC CGG TGT GTC CTG GTA TAG ACC CCA TAA GGT AAT CCC TTT ACA
Asn Glu Glu Leu Cys Ile Ile His Ile Asp Glu Leu Val Asp Trp Leu Ala Thr Gln Asp His Ile Trp Gly Ile Pro Leu Gly Lys Cys

        970        980        990       1000       1010       1020       1030       1040       1050
CAA TGG AAT AAA ATA TAC AAC TCT GAT GAA GAG AGT AGT TCT AGC GAA AGC GAA AGT AAT GGT GAC AGT GAA GAT GAC AAC GAC ACC AGC
GTT ACC TTA TTT TAT ATG TTG AGA CTA CTT CTC TCA TCA AGA TCG CTT TCG CTT TCA TTA CCA CTG TCA CTT CTA CTG TTG CTG TGG TCG
Gln Trp Asn Lys Ile Tyr Asn Ser Asp Glu Glu Ser Ser Ser Ser Glu Ser Glu Ser Asn Gly Asp Ser Glu Asp Asp Asn Asp Thr Ser

       1060       1070       1080       1090
AGC GAA TCA TAG A CCTCTTC TTGGCCTTTT ATTCGCTGGT GCACC
TCG CTT AGT ATC T GGAGAAG AACCGGAAAA TAAGCGACCA CGTGG
Ser Glu Ser End
```

FIG. 5. DNA and deduced protein sequences of *PRP38*. The putative TATA-box element and positions of the in vitro-generated single-base deletion and *LEU2* insertion are underlined. The four cysteines and the acidic serine-rich regions of the protein are italicized.

initiating codon, ACTACAATGGCT, is a suboptimal fit to the consensus sequence (A/T)A(A/C)A(A/C)AATGTC(U/C) of well-expressed yeast genes (19). No intron consensus elements are found within *PRP38*. A comparison of the *PRP38* DNA sequence with the GenBank data base revealed that base pairs 1 to 524 were previously reported 3′ of *YMR26* (21), a nuclear-encoded mitochondrial ribosomal protein gene located on chromosome VII or XV.

Consistent with the NEM sensitivity of the PRP38-complementing activity, four cysteines are present in PRP38 (amino acids 87, 174, 184, and 209). At least one of these cysteines is dispensable for function, as mutant alleles encoding variants in which cysteine 174 is changed to either a histidine or a tyrosine fully complement a *prp38* null mutation (20a). The most remarkable feature of PRP38 is its highly acidic, serine-rich C-terminal region; of the final 26 amino acids, 5 are aspartic acid, 6 are glutamic acid, and 11 are serine. This segment is responsible for the acidic character of PRP38; removing the terminal 26 amino acids increases the predicted pI from 5.0 to 8.1. The codon distribution of the C-terminal serines is typical of the protein as a whole and characteristic of poorly expressed genes; 8 of 11 are either AGT or AGC, very infrequent codons in yeast genes (48).

Inactivation of several *PRP* proteins alters the snRNA profile. The heat inactivation of PRP38 presumably perturbs its structure. Such a change might cause PRP38 or interacting components of the splicing apparatus to turn over at an accelerated rate. As a means of characterizing the splicing block imposed by *prp38* and other *prp* mutations, we determined whether heat inactivation of their respective proteins altered the normal intracellular snRNA profile.

Beyond a slight decrease in the yield of U6 snRNA from the *prp3* and *prp4* strains and a somewhat lower yield of U2 snRNA from our wild-type strain and its *prp4'* and *prp38* derivatives, no reproducible snRNA variation was observed at 23°C (Fig. 6A). In contrast, when *prp38*, *prp3*, *prp4*, *prp6*, *prp19*, and *prp24* cultures were shifted to 37°C for 4 h, U6 snRNA levels dropped to 5 to 30% of the wild-type level (Fig. 6B; for unknown reasons, *prp7* U6 snRNA levels were variable between experiments and in this example are exaggerated because of sample underloading). U6 snRNA reduction for this mutant set was observed in three separate experiments; similar observations for *prp4* strains have been noted independently by Abovich and Rosbash (1a). U4 snRNA levels did not change even in strains in which U6 loss was almost complete (e.g., *prp3* and *prp4*). The snRNA profiles of *prp25* and of the intron-accumulating strains *prp26* and *prp27* (55) were also assayed and found to be similar to that of the wild type (data not shown). No other temperature-dependent changes in snRNA abundance were noted except for a decrease in the level of U5L snRNA in the *prp8* strain.

The magnitude of U6 loss in the *prp* mutants did not correlate with the severity of the splicing defect. When the Northern (RNA) transfer filter used for snRNA analysis in Fig. 6B was probed with *RP51a*, virtually no processed *RP51a* mRNA was detectable in the *prp2* and *prp5* samples, indicating a severe splicing block (Fig. 6C), yet in these same cultures, U6 snRNA levels were comparable to that of the wild type. In contrast, the *prp19* block to splicing was incomplete (i.e., comparatively low pre-mRNA/mRNA ratio [36]), yet U6 levels decreased markedly. Therefore, U6 snRNA levels are sensitive to particular RNA processing blocks and not simply responding to the loss of splicing competence.

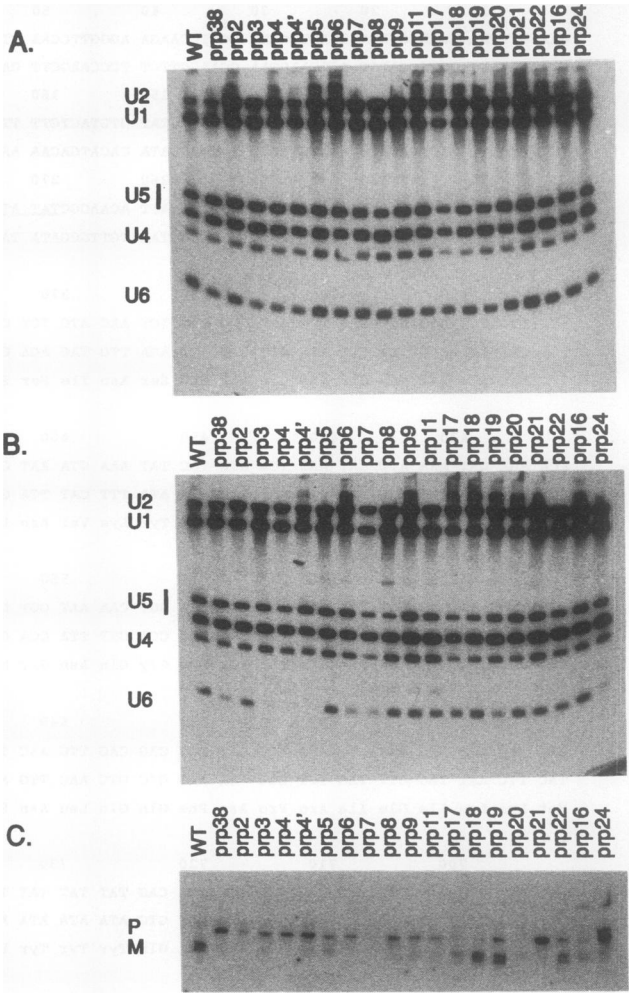

FIG. 6. snRNA and splicing profiles of *prp* strains. Total RNA was extracted from wild-type (WT) and *prp* mutant cultures growing at 23°C (A) or after a 4-h shift to 37°C (B and C) and resolved on a denaturing 5% polyacrylamide gel. The lane labeled *prp4'* contains RNA from a second *prp4* strain (*ts146*) isolated in course of this study. Northern transfers were probed with DNA containing U1, U2, U4, U5, and U6 snRNA genes (A and B) or the intron-containing *RP51a* gene (C). P, pre-mRNA; M, mRNA.

DISCUSSION

The eukaryotic pre-mRNA splicing apparatus consists of five snRNAs and a complex, poorly defined array of proteins (17, 18). This study shows that a 28-kDa acidic protein, PRP38, is an essential splicing factor and, like PRP3, PRP4, PRP6, PRP19, and PRP24, is necessary for both intron excision and the maintenance of normal U6 snRNA abundance.

In vivo, loss of *PRP38* function correlates with an increase in the pre-mRNA/mRNA ratio of intron-containing transcripts and a decrease in intracellular U6 snRNA. Time course studies indicate that U6 loss is a consequence, rather than a primary cause, of the initial *prp38* splicing block. Decreased splicing efficiency, as evidenced by a 5- to 10-fold increase in the pre-mRNA/mRNA ratio, is evident 1 to 2.0 h after a temperature shift. In contrast, U6 snRNA abundance remains virtually unchanged during this period (58a).

While the loss of PRP38 activity might lower U6 levels through either decreased synthesis or accelerated decay, we favor the latter interpretation for three reasons. First, the measured rate of U6 snRNA turnover is slower than that observed with the *prp38* strain. Blocking U6 synthesis by inactivating a temperature-sensitive polymerase III mutant results in only a minor decrease in U6 snRNA after 5 h (33).

Second, multiple means of U6 destabilization clearly exist, as intracellular U6 snRNA levels drop in response to inactivation of any one of at least five other *PRP* gene products (PRP3, PRP4, PRP6, PRP19, and PRP24). With the possible exception of the untested PRP19, each of these proteins functions by binding a U6 snRNA-containing snRNP complex, that is, U6, U4/U6, or U4/U6/U5 (1, 3, 5, 35, 47, 59). Reported genetic or biochemical links between these products, e.g., suppression of a *prp4* mutation by overexpression of *PRP3* (25) or failure of heat-inactivated *prp3* and *prp4* extracts to complement one another (31), may relate to their joint contributions to U6 snRNA stability. Finally, it is clear from our in vitro studies that PRP38 functions, at least to support splicing, in the absence of appreciable transcription.

With extended incubation at the restrictive temperature, less U6 is recovered from *prp38* mutant cultures, decreasing to 20 to 30% of the wild-type level 4 h after the temperature shift. We interpret these data to indicate that the initial effect of the *prp38* lesion is to arrest splicing in a state that ultimately compromises the integrity of a U6-containing snRNP particle. The concordance of a rapid (<4 h) and extensive (>70%) reduction of U6 snRNA with strains bearing mutations in known U6 (or U4/U6)-associating proteins suggests a direct PRP38/U6 association. However, it is also possible that U6 snRNA is simply the most labile of the spliceosome-associated snRNAs and shows the greatest sensitivity to general spliceosomal or snRNP perturbation. Under different laboratory conditions (e.g., higher temperatures, longer periods of inactivation, and complete metabolic depletion), the removal of splicing factors other than those deemed sensitive in this study may result in U6 snRNA loss. Indeed, Brown and Beggs have observed U4 and U6 as well as U5 snRNA decreases in cells with diminished *PRP8* activity (7a). While it is not yet clear why we do not see this *prp8* effect on U4 or U6, their result is consistent with the general view that the removal or inactivation of an snRNP-specific polypeptide, that is PRP8/U5, can directly impact the stability of the associated snRNA and that U6 snRNA is sensitive to snRNP (presumably U4/U5/U6 tri-snRNP) perturbation.

In vitro, the *prp38* block to splicing appears to occur late in the maturation of the splicing complex or during the splicing reaction itself; spliceosome assembly progresses efficiently to the formation of a structure similar to the complete spliceosome, yet splicing progresses poorly. While we have not analyzed the snRNA content of these complexes, spliceosomes stalled after the dissociation of U4 snRNA might present particularly vulnerable targets for U6 snRNA degradation. U4 release by itself appears insufficient to promote U6 degradation, however, as splicing-defective *prp2* spliceosomes release U4 snRNA (60) and yet U6 is not especially unstable in cells bearing this mutation.

The intracellular U6 snRNA concentration is normally at least twofold greater than that of U4 snRNA (11, 50, 59). This bias is expected to drive the formation of U4/U6 snRNA hybrids, and indeed, relatively little free U4 snRNP is apparent in yeast cell extracts (11, 50). Nevertheless, as noted for heat-treated *prp3* and *prp4* cultures, U4 snRNA levels remain constant even in the virtual absence of U6 snRNA. The U4 snRNP liberated after U6 snRNA degradation may be similar to the U4 snRNP released during normal spliceosome maturation. Regardless, it is clear that U4 snRNA stability is not obligately linked to the presence of U6 snRNA.

PRP38 terminates in a very acidic, serine-rich segment. The carboxy terminus is apparently needed for protein stability or function, as a frameshift mutation designed to generate a truncated, two-thirds peptide fails to complement the *ts prp38* allele. Acidic regions are found in a variety of nuclear proteins (14), although the significance of such domains remains obscure. The yeast NSR1 protein (26) contains a serine-rich acidic domain similar to but more extensive than that found in PRP38 (Fig. 7). NSR1 is a 67-kDa nuclear protein, identified by virtue of its ability to bind nuclear localization sequences. Intriguingly, NSR1 also contains a pair of RNP consensus sequences, suggesting that it may function in the trafficking of RNPs. Whether mediated by the acidic serine-rich segment or not, nuclear localization and RNP association are characteristics likely to be shared between PRP38 and NSR1.

NSR1 (from amino acid 1)

MAKTTKVKGN KKEVKASKQA KEEKAKAVSS SSSESSSSSS SSSESESESE SESESSSSSS SSDSESSSSS SSDSESEAET KKEESKDSSS SSSDSSSDEE EEEEKEETKK EESKESSSSD SSSSSSSDSE SEKEESNDKK RKSEDAEEEE DEESS....amino acid 404.

PRP38 (from amino acid 211)

WNKIYNSDEE SSSSESESNG DSEDDNDTSS ES

FIG. 7. Comparison of the PRP38 and NSR1 serine-rich acidic domains (underlined).

Recent studies on snRNP structure have revealed remarkable complexity in the protein composition of the various U6-containing complexes (4; also see references in references 17, 18, and 46). Protein-protein interactions appear to mediate complex assembly and disassembly. For example, the human U4/U6/U5 snRNP contains five proteins, including a 27-kDa peptide similar in size to PRP38, required for the assembly of the U4/U6/U5 snRNP but not stably bound to either the U4/U6 or U5 snRNP (4). It remains to be seen whether PRP38 also participates in U4/U6/U5 snRNP biogenesis or, like the acidic peptides of the ribosome (reviewed in reference 58), associates with assembled structures to promote or regulate RNP function.

ACKNOWLEDGMENTS

This work was supported by PHS award R29 GM42476, ACS award IN 163, and BRSG award RR07114 to B.C.R.

We thank M. Rosbash and N. Abovich for helpful discussions during the course of this work, J. D. Beggs and J. L. Woolford for communicating results prior to publication, and the Abelson, Ares, Guthrie, Rosbash, and Woolford laboratories for providing various strains and DNA molecules. We acknowledge the many constructive comments of our colleagues at the University of Kentucky during the preparation of this report and appreciate their ongoing interest in this work.

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