Identification of ebs1, lsm6 and nup159 as suppressors of spt10 effects at ADH2 in Saccharomyces cerevisiae suggests post-transcriptional defects affect mRNA synthesis

Bradley Anderson, Carrie Ann May, Clyde L. Denis*

Department of Molecular, Cellular, and Biomedical Sciences, University of New Hampshire, Durham, NH, USA
Email: *eldenis@unh.edu

Received 11 January 2012; revised 27 April 2012; accepted 14 May 2012

ABSTRACT

Suppression of the effects of an spt10 mutation on ADH2 expression is a phenotype shared by a small number of genes whose protein products are either components of the CCR4-NOT complex required for mRNA deenylation and degradation (CCR4, CAF1, NOT4) or have been shown to interact with the complex (DBF2, SBR9, SBR10). In this work, we conducted a screen for additional suppressors of spt10 at ADH2 to identify new factors related to CCR4 function. In addition to reisolating ccr4 and caf1 alleles, three previously unidentified suppressors of spt10 were obtained: ebs1, lsm6, and nup159. These three genes are known or presumed to affect mRNA export or degradation. Mutations in EBS1, LSM6 and NUP-159 not only suppressed spt10-induced ADH2 expression but also, like ccr4 and caf1 defects, reduced the ability of ADH2 to derepress. None of these defects affected the expression of CCR4-NOT complex components or the formation of the CCR4-NOT complex. The reduced ADH2 expression was also not the result of increased degradation of ADH2 mRNA, as the lsm6 and nup159 alleles, like that of a ccr4 deletion, actually slowed ADH2 degradation. Our results indicate that alterations in factors that slow mRNA degradation or affect mRNA transport may also interfere with the synthesis of mRNA and suggest an integration of such events in gene expression.

Keywords: CCR4-NOT Complex; Transcription; mRNA Degradation; mRNA Export

1. INTRODUCTION

The CCR4 protein is involved in several processes controlling the metabolism of mRNA in the cell: mRNA initiation, elongation, and degradation. CCR4 was originally identified as a mutation that suppressed the increased ADH2 expression on glucose caused by a spt10 allele, cre1-1 [1]. SPT10 is known to function in part by controlling histone gene expression, which in turn can alter chromatin structure and gene expression at sensitive loci [2]. The interaction of CCR4 with SPT10 is not limited to the ADH2 promoter, as ccr4 also suppressed spt10 at the his4-912δ locus [3]. CCR4 is also required for maximal expression of ADH2 and other nonfermentative genes [1] and appears involved in other processes such as cell wall integrity, amino acid metabolism, cell cycle progression, and DNA repair [4-8]. The effects of CCR4 at ADH2 and presumably many of these other processes occur at the transcriptional level implicating CCR4 in the control of mRNA initiation.

CCR4 functions in the context of two CCR4-NOT complexes, 1.0 and 1.9 MDa in size. The 1.0 MDa complex contains CCR4, CAF1, the five NOT proteins (NOT1-5) and three other proteins, CAF40, CAF130 and BT1 [6,9,10]. In addition to CCR4, mutations in both CAF1 and NOT4 suppress the effects of an spt10 mutation at ADH2 and affect the derepression of ADH2, suggesting that they also are involved in the activation of transcription [6,11].

The NOT1-5 proteins, however, are clearly involved in the repression of transcription [12,13], initially identified by their binding and restricting TFIID access to non-canonical TATAA sequences [14]. In addition, the CCR4-NOT proteins have been suggested to play a role in mRNA elongation [15]. Recent studies indicate that the CCR4-NOT complex is responsible for restarting transcription after transcriptional arrest has occurred [16].

One defined biochemical function for CCR4 is that it is the catalytic component of the cytoplasmic deadeylase complex [18-20]. CCR4 mRNA poly (A) deadeylation is the first step in targeting the mRNA for degradation and caf1 or not4 defects also lead to defects in deadeylation [19,20]. A ccr4 defect, therefore, in stabi-
lizing mRNA would augment mRNA levels. This effect would be opposite in nature to the ccr4 suppression of spr10 effects at ADH2 or the requirement of CCR4 for ADH2 and other genes’ syntheses. The CCR4 effect on ADH2 RNA accumulation implies that it operates by mechanisms other than or in addition to controlling mRNA degradation.

To gain further insight into the mechanisms of how CCR4 activates gene expression, we have re-conducted the screen for factors that can suppress spr10-enhanced expression at ADH2. The only known suppressors of spr10 effects are defects in the CCR4, CAF1 and NOT4 proteins, all components of the CCR4-NOT complex, and the DBF2, SRB9 and SRB10 proteins, which are known to associate with the CCR4-NOT complexes [5, 21]. The SRB9 and SRB10 proteins have been shown to be part of mediator, the transcriptional activator complex [21, 22]. Hence, the ability to suppress spr10-enhanced ADH2 expression reflects a common factor related to CCR4 function, and possibly to a role not directly involving effects on mRNA degradation. Utilizing this screen for suppressors of spr10, we have identified three new genes which when mutated are capable of suppressing spr10: NUP159, LSM6 and EBS1. These three factors, like CCR4, CAF1 and NOT4 are known or presumed to be involved in controlling mRNA export or degradation. These results suggest that defects in factors involved in post-transcriptional regulation of mRNA metabolism may result in corresponding decreases in transcriptional initiation. The CCR4 requirement at ADH2 may, therefore, result from indirect effects involving the integration of mRNA synthesis with the subsequent nuclear export and degradation of mRNA.

2. MATERIALS AND METHODS

2.1. Yeast Strains and Growth Medium

Yeast strains are listed in Table 1. Strains were grown on YEP medium (1% yeast extract/2% Bacto-peptone) supplemented with 2% glucose and 2% agar (YD plates). Allyl alcohol was added to YD plates in the concentration indicated in the test. ADH assays were conducted as previously described [6].

2.2. Analysis of spr10 Suppressors

Standard genetic techniques were used to identify complementation groups. Yeast transformations were conducted with either an YCp50-LEU2, YEpl3, or YEp24 based genomic library. Western analysis was conducted as described [6] using antibody specific to CCR4-NOT protein components [23].

2.3. RNA Analysis

S1 nuclease protection assays were conducted to quantitate ADH2 mRNA levels as described [17, 24]. The rates of ADH2 mRNA half-lives were determined following growth of yeast on YEP medium containing 2% glycerol/2% ethanol and shifting to YEP medium containing 8% glucose as previously indicated [17].

Table 1. Yeast strains.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>553-4b</td>
<td>MATα adh1-11 adh3 cre1-1 ura3 leu2 trp1</td>
</tr>
<tr>
<td>553-4b-10</td>
<td>MATα adh1-11 adh3 cre1-1 ccr4-10 ura3 leu2 trp1</td>
</tr>
<tr>
<td>43-2B</td>
<td>MATα adh1-11 adh3 ura3 his4</td>
</tr>
<tr>
<td>43-2B-M1</td>
<td>MATα adh1-11 adh2-1 adh3 ura3 his4</td>
</tr>
<tr>
<td>1076-2c</td>
<td>MATα ura3 his3 leu2 trp1 ccr4::URA3</td>
</tr>
<tr>
<td>1005-2-3c</td>
<td>MATα adh1-11 his3 ura3 trp1 leu2 caf1::LEU2 spr10::trp1</td>
</tr>
<tr>
<td>1005-2-3c-s</td>
<td>MATα adh1-11 his3 ura3 trp1 leu2 caf1::LEU2 spr10::trp1</td>
</tr>
<tr>
<td>BA1-1</td>
<td>MATα adh1-11 leu2 asg1::4-6</td>
</tr>
<tr>
<td>BA2-1</td>
<td>MATα adh1-11 leu2 his4 ebs1-1-42</td>
</tr>
<tr>
<td>BA3-1</td>
<td>MATα adh1-11 leu2 lsm6-5-17</td>
</tr>
<tr>
<td>BA4-1</td>
<td>MATα adh1-11 leu2 trp1 asg4-4-33</td>
</tr>
<tr>
<td>BA5-1</td>
<td>MATα adh1-11 leu2 trp1 asg5-5-37</td>
</tr>
<tr>
<td>BA6-1</td>
<td>MATα adh1-11 trp1 nap1-20-6-72</td>
</tr>
<tr>
<td>994-2</td>
<td>MATα adh1-11 his3 ura3 leu2 spr10::TRP1</td>
</tr>
<tr>
<td>994-2-ΔEBS1</td>
<td>MATα adh1-11 his3 ura3 leu2 spr10::TRP1 ebs1::URA3</td>
</tr>
<tr>
<td>LGY101</td>
<td>MATα rad5-1 his3Δ200 ura3-5-2 leu2Δ1</td>
</tr>
<tr>
<td>AEMY19</td>
<td>MATα trp1Δ1 his3Δ200 ura3-1 leu2-3-1 lsm6::URA3</td>
</tr>
</tbody>
</table>

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3. RESULTS

3.1. A Screen for Suppressors of spt10 at ADH2

In order to identify other factors that are functionally related to the CCR4-NOT proteins, we conducted a search for additional suppressors of the spt10 effects at the ADH2 locus using a strain carrying the defective adh1-1 allele. The increased expression of ADH2 caused by spt10 results in an inability of strains to grow in the presence of allyl alcohol. Allyl alcohol can be converted by ADH enzymes to acrolein that kills the cells. While ccr4 alleles were previously identified by such a screen [1], in order to identify new suppressors we used a modified selection process. In the previous screen, mutations that allowed growth on allyl alcohol-containing plates were then tested for sensitivity to the respiratory inhibitor Antimycin A; complete loss of both ADH I and ADH II enzyme activity in the cell would require the utilization of oxidative phosphorylation rendering such cells Antimycin A sensitive. This secondary requirement resulted in the elimination of nearly 90% of the allyl alcohol revertants [1]. Since there is a narrow range of ADH enzyme activities that allows growth on both allyl alcohol and resistance to antimycin A we were intent on identifying new suppressors of spt10 that resulted in ADH II activity that fell into this range.

Strain 553-4b, containing a spt10 mutant allele called cre1-1, was chosen for this screen since the cre1-1 allele, unlike an spt10 deletion, does not result in phenotypes typically associated with ccr4 or not defects: these phenotypes include temperature sensitivity, slow growth, and sensitivity to caffeine. Approximately 1 × 10⁸ cells of strain 553-4b were spread on YD plates containing 10 mM allyl alcohol. 198 allyl alcohol resistant colonies were selected for analysis. Complementation analysis, following mating each of these revertants to strain 43-2B-M1 carrying a defective adh2 allele, identified 99 of these revertants as containing mutations in the ADH2 gene (data not shown).

Since ccr4 and defects in other CCR4-NOT complex components are sensitive to caffeine and a number of other factors such as high temperature and elevated salt concentration, the remaining 99 revertants were tested for sensitivity to these conditions. Sixteen of the 99 showed sensitivity to one or more of the following conditions: 8 mM caffeine, 37°C, 16°C, 0.75 M MgCl₂, or 0.2 M LiCl (Table 2; data not shown) and were chosen for further analysis.

3.2. Identification of Known Suppressors of spt10

To test if any of these 16 revertants generated in this screen were ccr4 mutations, Western analysis was conducted on each strain to determine if the CCR4 protein was absent. Extracts from only one revertant, 553-4b-1-65, lacked detectable CCR4 protein (data not shown; see also Figure 1). In addition, genetic complementation analysis was conducted by crossing a ccr4-containing strain to all the revertants. In this case, only revertant 553-4b-1-65 failed to complement a ccr4 allele. Similarly, a caf1 strain, 1005-2-3c-s, was crossed to all revertants to identify those that contained caf1 mutations. Revertants that allowed growth on allyl alcohol-containing plates and sensitivity to caffeine were then tested for sensitivity to the respiratory inhibitors Antimycin A and creb. These revertants are described in Table 2.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Allele</th>
<th>8 mM Caff</th>
<th>YD 37°C</th>
<th>0.2 M LiCl</th>
</tr>
</thead>
<tbody>
<tr>
<td>553-4b-10</td>
<td>ccr4-10</td>
<td>w/+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>1-65</td>
<td>ccr4-1-65</td>
<td>w/–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>4-26</td>
<td>caf1-4-26</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>1-42</td>
<td>ebs1-1-42/asm2</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>5-17</td>
<td>lsm6-5-17/asm3</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>6-72</td>
<td>nup159-6-72/asm6</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>4-6</td>
<td>asg1-4-6</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<td>1-36</td>
<td>asg1-1-36</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<tr>
<td>1-52</td>
<td>asg1-1-52</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<tr>
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<td>+</td>
<td>–</td>
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<tr>
<td>5-84</td>
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<td>–</td>
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<td>–</td>
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<tr>
<td>6-16</td>
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<td>–</td>
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<td>–</td>
</tr>
<tr>
<td>4-33</td>
<td>asg1-4-33</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
</tbody>
</table>

Yeast strains were grown on YEP medium containing 2% glucose supplemented with 8 mM caffeine (8 mM caff) or 0.2 M LiCl. Growth was at 30°C except as indicated. “w/+”: very good growth; “w/-”: good growth; “w/-”: poor growth; “-”: no growth.

Figure 1. nup159, lsm6 and ebs1 alleles do not affect the expression of CCR4-NOT components. Western analysis was conducted on yeast extracts with antibodies directed against CCR4, CAF1, NOT4, and CAF40. Left lane—(wt) strain 553-4b; other lanes—strain 553-4b except containing the allele as indicated.
The ADH II assay values that were obtained confirm that growth on ally1 alcohol was due to reduced expression of caf1 mutations. To clarify this result, the mutation in revertant 553-4b-4-26 was cloned by complementation using a genomic library and the complementing gene was shown to contain the complete CAF1 gene following DNA sequence analysis. Subsequent retransformation of the CAF1 containing genomic clone into revertant 553-4b-6-72 failed to complement its defects, demonstrating that 553-4b-4-26 is the only caf1 mutation produced by this screen. Crosses with strains containing either a dbf2 or not4 mutation showed that none of the remaining revertants carried mutations in either of these genes.

Additional complementation analysis grouped the remaining 14 revertants that displayed pleiotropic effects into four complementation groups (Table 2). Most of the complementation groups were represented by a single revertant, whereas complementation group designated asg1 contained 10 members.

ADH II enzyme activity assays were conducted on the 16 revertants from each of these complementation groups, the parent strain 553-4b, and 553-4b-10, which contains the previously characterized ccr4-10 allele (Table 3). The ADH II assay values that were obtained confirm that growth on ally1 alcohol was due to reduced expression of ADH2. As expected, values for many of the revertants were not as low as the previously characterized parent strain 553-4b, and 553-4b-10, which contains 16 revertants from each of these complementation groups, whereas complementation group designated asg1 contained 10 members.

Cloning of ASG2, 3, and 6
In order to clone the respective genes for the remaining unidentified complementation groups, a representative from each group was transformed with either or both low and high copy yeast genome libraries. Depending on the phenotype of the representative mutant, selection for complementing plasmids was conducted on different media. Repeated attempts to complement asg1 failed, however, and complementing clones were only obtained for asg2, asg3 and asg6.

For strain 553-4b-6-72 (asg6), complementing plasmids were selected on 8 mM caffeine plates. A single plasmid (6-72-1), derived from a YCp50-LEU2 genomic library, was identified and was shown to contain an 8.4 Kbp fragment of Chromosome IX. Three genes were identified on this plasmid that could potentially be responsible for complementing 553-4b-6-72: YIL113w, POR2 and NUP159. Given the function of NUP159 as involved in mRNA transport out of the nucleus and that a defect in such a gene could result in lowered gene expression, a nup159 strain (LGY101) was obtained carrying the rat7-1 mutation (RAT7 is the same as NUP159). Crossing strain LGY101 to strain 553-4b-6-72, resulted in diploids that failed to grow on 8 mM caffeine plates, indicating that the asg6-6-72 mutation could not complement the rat7-1 mutation. asg6-6-72 was therefore designated as an allele of NUP159. The NUP159 protein has recently been shown to play an important role in mRNA transport by aiding DBP5 remodeling of the mRNP complex [25], but otherwise has no direct role in mRNA expression.

Revertant 553-4b-5-17 (asg3) when transformed with the yeast genomic library YEp13 yielded one transformant that was caffeine resistant and that was also unable to grow on 10 mM ally1 alcohol media. The insert contained in plasmid 5-17-1 was determined to be a 6.5 Kbp fragment of chromosome IV containing three genes, ATRIP17, LSM6 and RGA2. RGA2 has been described as a GTPase activating protein, LSM6 is involved in RNA splicing processing and mRNA decapping [26,27].

### Table 3. ADH2 expression in sp10 revertants.

<table>
<thead>
<tr>
<th>Allele</th>
<th>ADH II enzyme activity</th>
<th>ADH2 mRNA</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Glc</td>
<td>EtOH</td>
</tr>
<tr>
<td>wt</td>
<td>52</td>
<td>2400</td>
</tr>
<tr>
<td>ccr4-10</td>
<td>16</td>
<td>620</td>
</tr>
<tr>
<td>ccr4-1-65</td>
<td>22</td>
<td>730</td>
</tr>
<tr>
<td>caf1-4-26</td>
<td>19</td>
<td>250</td>
</tr>
<tr>
<td>ebs1-1-42</td>
<td>27</td>
<td>1700</td>
</tr>
<tr>
<td>lem6-5-17</td>
<td>15</td>
<td>1400</td>
</tr>
<tr>
<td>nup159-6-72</td>
<td>26</td>
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<tr>
<td>asg1-4-6</td>
<td>24</td>
<td>570</td>
</tr>
<tr>
<td>asg1-4-33</td>
<td>43</td>
<td>940</td>
</tr>
</tbody>
</table>

ADH II enzyme activities were conducted as described previously following growth in YEP medium supplemented with 8% glucose (Glc) or 3% ethanol (EtOH) [46]. The standard error of the mean (SEM) for all ADH assays was less than 20% and the values represent the average of at least four determinations. ADH2 mRNA levels were quantitated using an S1 nuclease protection assay as described in Figure 2 using 4CT1 mRNA levels as a standard. The ADH2 mRNA levels were normalized against levels found in the parent strain 553-4b which is given a value of 1.0. The SEMs for the ADH2 mRNA levels were less than 20% except for lem6 and caf1 under ethanol growth conditions in which the values were 37% and 28%, respectively.
ATP17 is a subunit of ATP synthase. A BamHI-Sall fragment of plasmid 5-17-1 that contained ATP17 and LSM6 was subcloned into pRS315, a single copy plasmid containing a LEU2 gene. This plasmid was able to complement the caffeine sensitive phenotype of 5-17, showing that one of these two genes, but not RG42, was responsible for this complementation. Also, following transformation of a YCp50-LEU2, single copy yeast genomic library, into 553-4b-5-17, a single caffeine resistant colony was obtained that contained a plasmid with both ATP17 and LSM6 genes (data not shown). An lsm6-containing strain, AEMY19, was crossed to 5-17, and the resulting diploid strain failed to grow in the presence of 8 mM caffeine. This failure to complement indicates that the asg3-5-17 mutation is an allele of lsm6.

Strain 553-4b-1-42 (asg2) after transformation with a YEpl3 high copy yeast genomic library yielded a single plasmid that could complement the ability to grow at 37°C and the allyl alcohol phenotype. The insert was found to be a 4.3 Kbp region of chromosome IV containing a single gene, EBS1. EBS1 was initially reported to be involved in telomere maintenance based on its sequence similarity to EST1 [28] but more recently it has been shown to be the ortholog of the higher eukaryotic nonsense-mediated decay protein SMG7 [29]. Its involvement in nonsense mediated decay may be only one means that its is involved in mRNA expression, as it has also been demonstrated that EBS1 binds eIF4E, the mRNA cap binding protein required for translational initiation. In fact, EBS1 is a negative regulator of translation [30]. EBS1 also binds DCP1 [31], a component of the mRNA decapping complex [20]. Its exact role in decapping is not understood, as it does not clearly affect mRNA degradation rates (R. Parker, pers. commun), and more recent studies indicate that it does not affect MFA2 decapping [29]. Removal of amino acids 456-783 from EBS1, that overlap a putative RNA recognition motif, resulted in an EBS1-expressing plasmid that was unable to complement the 37°C growth defect of the 553-4b-1-42, demonstrating that the EBS1 gene complemented 553-4b-1-42 and that this deleted region is required for EBS1 function. We also showed that deleting ebs1 gave the same phenotype as the ebs1-1-42 allele in that it was capable of suppressing an spt10 deletion in its effects on either ADH2 or HIS4 (data not shown).

3.4. spt10 Suppressors Affect ADH2 Expression at the Transcriptional Level

The identification of three additional suppressors of spt10 as factors involved in mRNA degradation (LSM6 and EBS1), translation (EBS1), and transport (NUP159) coincide with the role of the other spt10 suppressors, CCR4, CAF1 and NOT4, that have known roles in post-transcriptional control of mRNA metabolism, including that of mRNA degradation, translation, and elongation [17-20,32]. We subsequently investigated whether the effects of these new spt10 suppressors were the result of reducing ADH2 mRNA expression. ADH2 mRNA levels were quantitated by S1 analysis and are summarized in Table 3 (see also Figure 2, where the zero time points are representative assays conducted under ethanol growth conditions). Each of the lsm6-17, ebs1-1-42, nup159-6-72 and asg1-4-6 alleles reduced spt10-enhanced ADH2 mRNA expression by around two-fold or more under glucose growth conditions and by a similar level following ethanol growth conditions. It should be mentioned that the spt10 allele does not affect ADH2 enzyme levels following ethanol growth conditions [1,3]. Therefore, the effects of these suppressor mutations on ADH II activity following non-fermentative growth represent direct effects on ADH2 expression. These results indicate that these alleles reduce ADH II enzymatic levels by primarily reducing the steady state levels of ADH2 mRNA levels. Therefore, as previously found for CCR4 and CAF1 [3,11] (Table 3), these new spt10 suppressors are required for activating ADH2 expression. It should be noted, however, that under ethanol growth conditions the actual steady state reduction in ADH2 mRNA levels by lsm6 and nup159 did not appear to directly correlate with the degree of reduction in the levels of ADH II enzyme activity (Table 3). The cause for this is unclear but could result from the unknown nature of the mutation or possibly even from pleiotropic effects on the translatability or expression of the mRNA.

3.5. lsm6, ebs1, and nup159 Alleles Do Not Affect Expression of CCR4-NOT Complex Components

One likely cause for the suppression of spt10 and of ADH2 gene expression by the lsm6, ebs1 and nup159 alleles is that they reduce the levels of key CCR4-NOT complex components. The levels of CCR4-NOT complex proteins were subsequently determined by Western analysis in strains carrying these mutant alleles. As shown in Figure 1, lsm6, ebs1 and nup159 had no effect on the relative abundance of CCR4, CAF1, and other complex components. We also found that the integrity of the CCR4-NOT complex, as evidenced by co-immunoprecipitation, to be unaffected by the lsm6, ebs1, and nup159 alleles (data not shown). These data indicate that lsm6, ebs1, and nup159 affect ADH2 expression by a means other than through indirect effects on the CCR4-NOT complex.

3.6. lsm6, ebs1, nup159 Decrease or Have No Effect on ADH2 mRNA Half-Lives

Both LSM6 and EBS1 have known or suggested roles in
controlling the rate of mRNA degradation, with \textit{lsm6} slowing mRNA decapping and \textit{ebs1} interacting with the decapping complex or controlling at least nonsense mediated decay [26,27,29]. It was theoretically possible, however, that the \textit{lsm6} and \textit{ebs1} alleles identified in this \textit{spt10} screen were mutations that enhanced the rate of \textit{ADH2} mRNA degradation, thereby suppressing \textit{spt10} effects on the initiation of \textit{ADH2} synthesis and reducing \textit{ADH2} expression under non-fermentative growth conditions. To test this hypothesis we examined the rate of \textit{ADH2} mRNA degradation in each of these mutated strains. \textit{ADH2} mRNA half-lives were determined following pre-growth of yeast under ethanol (non-fermentative conditions) and shifting them to glucose growth following pre-growth of yeast under ethanol (non-fermentative growth). This allowed us to calculate the rate of mRNA degradation. In fact, \textit{ADH2} mRNA half-life is much less than found under non-fermentative conditions [1,3]. The mechanism by which it and other factors related to it, such as \textit{CAF1} or \textit{NOT4}, are required for maintaining \textit{ADH2} mRNA levels has remained, however, obscure [5,6,11,21]. The identification of the CCR4-NOT complex as involved in mRNA deadenylation, with CCR4 and \textit{CAF1} as deadenylases [17-20,32,34], indicate that \textit{ccr4} deletions actually stabilize \textit{ADH2} mRNA and hence raise its mRNA levels, not lower them [17,33]. In this report we identify three new factors, NUP159, LSM6 and EBS1, whose defects, like those of \textit{caf1} and \textit{ccr4}, suppress \textit{spt10}-enhanced \textit{ADH2} expression and decrease the ability of \textit{ADH2} to derepress. The known or putative roles of NUP159, LSM6, and EBS1 in the post-transcriptional regulation of mRNA suggests, therefore, a functional link to CCR4 and \textit{CAF1} and a common mechanism by which they all affect \textit{ADH2} expression.

The \textit{lsm6-5-17}, \textit{nup159-6-72} and \textit{ebs1-1-42} alleles effect on \textit{ADH2} mRNA levels were not the result of increasing the rate of \textit{ADH2} mRNA degradation. In fact, \textit{lsm6} and \textit{nup159} stabilized \textit{ADH2} mRNA, indicating that their effects on the synthesis of the mRNA was at least two-fold greater than that observed from monitoring \textit{ADH2} steady state mRNA levels. Similar conclusions

<table>
<thead>
<tr>
<th>Allele</th>
<th>\textit{ADH2} mRNA half-life (min)</th>
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<tbody>
<tr>
<td>\textit{wt}</td>
<td>12 ± 0.40</td>
</tr>
<tr>
<td>\textit{ebs1-1-42}</td>
<td>13 ± 0.90</td>
</tr>
<tr>
<td>\textit{lsm6-5-17}</td>
<td>29 ± 9.1</td>
</tr>
<tr>
<td>\textit{nup159-6-72}</td>
<td>26 ± 0.16</td>
</tr>
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</table>

\textit{ADH2} mRNA half-lives were calculated as described [17]. \textit{ADH2} mRNA levels were quantitated by S1 nuclease protection assays. The value ± SEMs represent the average of three to five determinations except for \textit{lsm6} whose value is the average of two determinations.
can be made for ccr4 and caf1 defects that caused increased stabilization of ADH2 mRNA and yet, concurrently, reduced overall ADH2 mRNA levels [3,17,33] (Table 3). We also showed that the lsm6, nup159 and ebs1 alleles did not alter the abundance of CCR4-NOT complex components, indicating that their effects were not indirectly through lowering CCR4 and CAF1 abundance in the cell. In addition, the role of EBS1 in negatively regulating translation [30] cannot directly explain how it would function as an activator of ADH2.

spr10 results in a low level of ADH2 expression under glucose growth conditions by an unknown mechanism that could involve affecting ADH2 chromatin structure [2, 35,36]. The observation that lsm6, nup159, ebs1, ccr4 and caf1 can each suppress spr10 effects at ADH2 could suggest that these factors function downstream of spr10 on chromatin structure. However, our previous analyses indicated that CCR4 acted independently of SPT10 to affect ADH2 expression [36]. Also, the fact that lsm6, nup159, ebs1, caf1 and ccr4 reduce ADH2 expression under ethanol growth conditions when spr10 has no effect on ADH2 transcription further supports an effect of these alleles on ADH2 independently of spr10.

One possible model for how CCR4 and CAF1 function in activation is that they influence action of the RNA polymerase II holoenzyme through their contacts to SRB-9, -10, and -11 mediator components [21]. Alternatively, CCR4 and CAF1 could serve as coactivators by somehow mediating the action of activators such as ADR1 at ADH2. However, this latter model seems unlikely in that ADR1 is not required for spr10-enhanced ADH2 expression [1,11].

Based on the results presented in this paper, we suggest a different model for how CCR4, CAF1, LSM6, NUP159 and EBS1 act as activators at the ADH2 locus. The primary roles for these factors appear to be the mRNA degradative process, in mRNA transport from the nucleus, or in mRNA elongation. Studies have increasingly linked transcription initiation processes with post-transcriptional processing and transport of mRNA [37]. It is, therefore, conceivable that interfering with mRNA degradation and transport could result in slower processing and movement of mRNA through the cell. These effects could then result indirectly in reducing transcriptional initiation of particularly sensitive genes. A variant of this model would be that proteins involved in post-transcriptional mRNA processing are loaded onto the mRNA during its synthesis. Defects in these processing components would interfere with this loading process that again indirectly influences the corresponding initiation of transcription from certain promoters. In this regard CCR4-NOT complex is known to play a critical role in mRNA elongation [15,16,38]. Its function as an activator of transcriptional elongation would therefore be a very direct way for components of this complex to function as activators of ADH2 expression. For example, if transcription through the ADH2 gene were particularly prone to transcriptional arrests that the CCR4-NOT complex would be especially able to bypass by restimulating transcription [16], then a positive role for CCR4-NOT proteins would be substantiated. But no evidence for ADH2 susceptibility to transcriptional arrest is known and the EBS1, NUP159 and LSM6 factors do not have clear roles in elongation.

Finally, it has been recently shown that the nuclear pore factors may have diverse and direct effects on chromatin structure and hence gene expression [39]. Given these interactions between mRNA transport and transcription, the NUP159 protein and the CCR4-NOT complex, which has been shown to interact with the mRNA export pathway [40], may exert their respective effects on ADH2 chromatin structure and expression by virtue of their effects on mRNA export. Since the SPT10 protein is specifically involved in affecting chromatin structure [2,35,36], this could be one means by which defects in NUP159 and CCR4-NOT components suppress spr10 effects.

In contrast to the above models, given that CCR4, CAF1, LSM6, NUP159 and EBS1 defects might be expected to have broad affects on the mRNA degradation and/or transport of many genes [39-41], it remains possible that the mRNA for certain key transcriptional initiation factors might be specifically sensitive to corresponding defects in mRNA degradation or transport. For instance, the mRNA for holoenzyme or core initiation components might be specifically affected by such defects, resulting again, indirectly, in reduced ADH2 gene expression. However, whole genome microarray analysis with ccr4, caf1 and not4 deletions did not identify specific core transcriptional factors under the regulation of any of the CCR4-NOT factors [10].

In that ccr4, caf1, lsm6 and nup159 defects all reduce ADH2 steady state mRNA levels and at the same time reduce the rate of ADH2 mRNA degradation indicates an additional difficulty with interpreting the actual mechanisms by which factors control gene initiation. A number of factors thought to control initiation of transcription (HPR1, RTF1, PAF1, SPT5) have been shown to be involved in post-initiation processes [33,38,42-45]. Whether these original effects on transcription initiation were merely the consequences of indirect effects derived from their post-initiation sites of action has not been determined. At least for the case of CCR4-NOT factors understanding how their effects on ADH2 mRNA degradation rates can exert opposite effects on ADH2 synthesis may shed new light on the total integration of mRNA metabolism.

5. ACKNOWLEDGEMENTS

We would like to thank Dr. C. Cole and J. Beggs for yeast strains, B.
REFERENCES


in vivo evidence that defects in the transcriptional elongation factors RPβ2, TFIIIS and SPT5 enhance upstream poly(A) site utilization. 


the zinc-finger region of the yeast regulatory protein
ADR1 affect both DNA binding and transcriptional acti-