Evidence for Regulation of ECM3 Expression by Methylation of Histone H3 Lysine 4 and Intergenic Transcription in Saccharomyces cerevisiae

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ABSTRACT Transcription of nonprotein-coding DNA is widespread in eukaryotes and plays important regulatory roles for many genes, including genes that are misregulated in cancer cells. Its pervasiveness presents the potential for a wealth of diverse regulatory roles for noncoding transcription. We previously showed that the act of transcribing noncoding DNA (ncDNA) across the promoter of the protein-coding SER3 gene in Saccharomyces cerevisiae positions nucleosomes over the upstream activating sequences, leading to strong repression of SER3 transcription. To explore the possibility of other regulatory roles for ncDNA transcription, we selected six candidate S. cerevisiae genes that express ncRNAs over their promoters and analyzed the regulation of one of these genes, ECM3, in detail. Because noncoding transcription can lead to changes in the local chromatin landscape that impinge on the expression of nearby coding genes, we surveyed the effects of various chromatin regulators on the expression of ECM3. These analyses identified roles for the Paf1 complex in positively regulating ECM3 transcription through methylation of histone H3 at lysine 4 (K4) and for Paf1 in controlling the pattern of intergenic transcription at this locus. By deleting a putative promoter for the noncoding transcription unit that lies upstream of ECM3, we provide evidence for a positive correlation between intergenic transcription and ECM3 expression. Our results are consistent with a model in which cotranscriptional methylation of histone H3 K4, mediated by the Paf1 complex and noncoding transcription, leads to activation of ECM3 transcription.

KEYWORDS noncoding RNA histone methylation RNA polymerase II cryptic unstable transcripts Paf1 complex

Widespread pervasiveness of transcription is a common feature of eukaryotic genomes. The importance of pervasive nonprotein-coding transcription is highlighted by the results of the human genome project, which revealed that over 80% of the human genome displays biochemical activities associated with transcription in at least one cell type, even though only about 1% of the transcribed regions contain protein-coding exons (Venter et al. 2001; Borel et al. 2008; ENCODE Project Consortium 2012). Noncoding transcripts carry out a diverse array of regulatory functions. For example, microRNAs (miRNAs) associate with Argonaute proteins to regulate gene expression at a posttranscriptional level or by directing chromatin modifications (Bartel 2004). Several long noncoding RNAs (lncRNAs), such as Xist and HOTAIR, two important developmental regulators, associate with and direct the Polycomb repressive complex, PRC2, to specific genetic loci. PRC2 is then able to alter the local chromatin state and lead to the regulation of gene expression (Rinn et al. 2007; Lee 2009; Tsai et al. 2010; Simon and Kingston 2013). PCGEM1, a lncRNA associated with prostate cancer, directly binds the transcription factor c-Myc, activates transcription of c-Myc target genes, and regulates several metabolic pathways including nucleotide and lipid biosynthetic pathways and the tricarboxylic acid cycle (Hung et al. 2014).

In these examples, the noncoding RNA (ncRNA) molecule itself plays a regulatory role. The act of transcribing ncDNA can also alter the local chromatin environment and the regulation of neighboring genes. Transcription can alter the occupancy and positions of nucleosomes, posttranslational histone modifications, and potentially higher order...
transcription elongation. During transcription of the FACT complex, chaperones place nucleosomes over the upstream regulatory sequences. In Smolle and Workman 2013). The histone modifications of H3K36 at the 5′ ends of transcription units, methylation of H3 K79 throughout the bodies of transcription units, and methylation of H3 K4 due to transcription of ncDNA at the GAL1-10 locus is required for histone deacetylation, which leads to repression of GAL1 and GAL10 in the presence of glucose (Houseley et al. 2008; Pinksaya et al. 2009). Two other S. cerevisiae genes, DCI1 and DUR3, are regulated by noncoding transcription across their promoters through a mechanism in which methylation of H3 K4 and subsequent Set3-mediated deacetylation of histones leads to gene repression (Kim et al. 2012). Transcriptional interference, as has been observed at the yeast IME4 gene, presents an alternative mode of regulation by intergenic transcription that does not require alteration of chromatin but can be explained by the collision of traveling Pol II complexes (Prescott and Proudfoot 2002; Hongay et al. 2006; Gelfand et al. 2011; Hobson et al. 2012).

In this study, we sought to expand our knowledge of gene regulatory mechanisms by focusing on genes that harbor noncoding transcription units in their promoters and exploring the importance of both chromatin regulatory proteins and the ncDNA in the regulation of these genes. To begin, we identified candidate genes that might be regulated by noncoding transcription and selected one of these genes, ECM3, for detailed study. Our analyses of ECM3 expression revealed an integral role for the Paf1 complex, H3 K4 methylation, and two histone acetyltransferases in the positive regulation of ECM3. In addition, our findings indicate that transcription of the intergenic ncDNA at ECM3 correlates with expression of the gene, potentially through establishment of a permissive chromatin structure.

**MATERIALS AND METHODS**

*S. cerevisiae* strains and media

*S. cerevisiae* strains used in this study are listed in Supplemental Material, Table S1. The strains used to perform the anchor away experiment are W303 derivatives purchased from Euroscarf or generously
provided by Patrick Cramer (Schulz et al. 2013). For anchor away experiments, cells were grown at 30° in YPD medium (1% yeast extract, 2% peptone, and 2% dextrose) until cultures reached a density of 2 × 10^6 cells per ml. Rapamycin was then added to cultures for 1 hr at a final concentration of 1 μg/ml from a stock of 1 mg/ml rapamycin suspended in ethanol. All other strains used in this study are derived from a GAL2^+ S288C isolate using standard genetic crosses and transformations (Winston et al. 1995). The EUCI promoter deletions were made by two-step integration of an HA-URA3-HA cassette that was PCR-amplified from the plasmid pMPY-3XHA (Schneider et al. 1995). This resulted in strains where a portion of the EUCI promoter has been replaced with a DNA sequence encoding one copy of the 3XHA tag, which is serving as spacer DNA. Cells were grown at 30° in YPD medium until cultures reached a density of 1–2 × 10^7 cells per ml for isolation of either RNA or chromatin for use in northern blotting, primer extension, and chromatin immunoprecipitation (ChIP) analyses.

**Northern blot analysis**

Northern blot analyses were performed using 20 μg total RNA samples resolved in gels containing 2% agarose, 6.5% formaldehyde, and 1 × MOPS as previously described (Ausubel 1987). Double-stranded probes were generated by random-primed labeling and single-stranded probes were generated by asymmetric PCR with α-32P-dATP (Rio 2011). Probe templates were amplified from genomic DNA to contain the following sequences relative to the +1 start codon of the protein-coding gene at each locus: EUCI (−541 to −100), ECM3 (+545 to +976), ARO2-CUT (−494 to −49), ARO8-CUT (−429 to −28), CLN3-CUT (−671 to −321), FET4-CUT (−479 to −114), KDH1-CUT (−496 to −235), and SCR1 (−182 to +284). SCR1 RNA levels serve as an internal loading control. The oligonucleotides used to generate probe templates are listed in Table S2. Images were generated by phosphorimaging and quantified using ImageJ software. For each experiment, the data from at least three biological replicates were averaged.

**Primer extension analysis**

Primer extension assays were performed as previously described using 20 μg total RNA samples (Ausubel 1987). Sequencing reactions were performed with Sequenase following the manufacturer’s guidelines (Affymetrix USB) using a purified PCR product as a template. Oligonucleotides were gel-purified and end-labeled with γ-32P-ATP and T4 polynucleotide kinase using standard protocols (Ausubel 1987). The EUCI and ECM3 transcription start sites were mapped by primer

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**Figure 2** The Paf1 complex and methylation of H3 K4 positively regulate ECM3 expression. (A) Representative northern blot analysis of ECM3 transcript levels in a wild-type strain (FY4) or strains lacking one of the five subunits of the Paf1 complex, either paf1Δ (YJ807), ctr9Δ (KY2170), rtf1Δ (YJ1788), cdc72Δ (KY2171), or leo1Δ (KY1805). (B) Representative northern blot analysis of ECM3 transcript levels in a wild-type strain (FY4) and strains where the genes encoding histone modifiers that work in concert with the Paf1 complex have been deleted (rad6Δ, KY1712; brf1Δ, KY1713; set1Δ, KY2720; set2Δ, KY2723; and dot1Δ, KY2725). (C) Representative northern blot analysis of ECM3 transcript levels in strains lacking a subunit of the Set3 HDAC complex (set3Δ, KY2782), the SAGA HAT complex (gcn5Δ, KY1743), or the NuA3 HAT complex (sas3Δ, ECY394) compared to wild-type levels (YJ1125). Quantitation below shows the average ECM3 mRNA levels relative to WT (set to 1) from at least three biological replicates. Error bars represent the SEM. SCR1 serves as a loading control.
The authors state that all data necessary for construction of conclusions presented in the article are represented fully within the article.

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RESULTS

Identification of genes with promoter-localized cryptic unstable transcripts (CUTs)

With the goal of identifying chromatin-mediated gene regulatory mechanisms associated with ncDNA transcription, we selected candidate genes that might be regulated by transcription across their promoter regions. Our selection criteria for candidate genes were intentionally simple to minimize the introduction of bias. The only criterion that we required of a candidate gene was the presence of a noncoding transcript over the promoter of a protein-coding gene in a tandem orientation, resembling the structure of the SEC1-SER3 locus. Several types of noncoding transcripts have been characterized in S. cerevisiae. We focused on our studies on cryptic unstable transcripts (CUTs), which are short transcripts that are terminated by the Nrd1-Nab3-Sen1 termination pathway, polyadenylated by the TRAMP complex, and degraded by the nuclear exosome (Arndt and Reines 2015; Porrua and Libri 2015). Enabling their detection, degradation of CUTs can be disrupted by deletion of TRF4, which encodes a subunit of the TRAMP complex, or RRP6, which encodes a catalytic subunit of the nuclear exosome (Wyers et al. 2005; Arigo et al. 2006; Davis and Ares 2006). Although we anticipate that regulation by intergenic transcription is not limited to the nature of the intergenic transcript, we limited this study to CUTs, as they are rapidly degraded. Due to the instability of CUTs in wild-type cells, we reasoned that regulatory events associated with CUT expression would likely be due to the act of transcription rather than the ncRNA molecule itself. We selected genes from microarray expression data, which mapped CUTs genome-wide (Neil et al. 2009), and confirmed that Pol II occupancy was detected across the promoters of these genes in genome-wide ChIP studies (Steinmetz et al. 2006). The genes we selected for initial characterization were AR02, AR08, CLN3, ECM3, FET4, and KNH1.

To confirm the microarray expression data in our strain background, we performed northern analyses to detect CUT expression over the candidate gene promoters. Using wild-type strains and strains lacking either Rrp6 or Trf4, we were able to detect CUTs across the promoter regions of all six candidate genes (Figure 1A).

We focused our attention on the ECM3 locus for mechanistic characterization. ECM3 is a nonessential protein-coding gene that was first identified in a screen for sensitivity to the cell wall stressor, calcofluor white (Lussier et al. 1997). For this reason, it is thought that ECM3 might be involved in cell wall maintenance. We detected two major transcription start sites for ECM3 (Figure S1), which were also detected by TIF-Seq analysis (Pelechano et al. 2013) and which overlap with the 3′ end of the upstream CUT as observed in microarray expression data (Neil et al. 2009). This presented an opportunity to observe isoform-specific regulation. We refer to the CUT across the ECM3 promoter as the ECM3 upstream CUT (EUC1). Upon deletion of the RRP6 gene, we did not detect a significant change in ECM3 expression, suggesting that extension using two different oligonucleotides for each major start site listed in Table S2.

ChIP

Chromatin was isolated and sheared by sonication using a Misonix 3000 sonicator as previously described (Shirra et al. 2005). Immunoprecipitations were performed by incubating sheared chromatin with 5 μl antisera to histone H3 (Tomson et al. 2011) or 2.5 μl of antibody to H3 K4me3 (Active Motif, catalog number 39159) at 4°C overnight, followed by precipitation using Protein A sepharose beads (GE Healthcare) for 2 hr at 4°C. All ChIP results were determined by quantitative PCR amplification of immunoprecipitated DNA compared to input DNA. Real-time PCR reactions were performed using SYBR green reagents (Fermentas) and a Step One Plus instrument (Applied Biosystems). The oligonucleotides used for qPCR amplification are listed in Table S2. Data were analyzed using the Pfaffl relative quantitation method (Pfaffl 2001). H3K4me3 occupancy values were normalized to total H3 occupancy values.

Data availability

The authors state that all data necessary for confirming the conclusions presented in the article are represented fully within the article.
**ECM3** expression is not regulated by stability of the **EUC1** transcript itself (Figure 1, B and C).

### The Paf1 complex and methylation of H3 K4 positively regulate ECM3 expression

Because noncoding transcription can alter the local chromatin environment in a way that impinges upon protein-coding gene regulation (Fu 2014; Rinn and Guttman 2014; Yang et al. 2014), we surveyed various chromatin regulators for their effects on **ECM3** expression. Through these analyses, we determined that the **Paf1** complex positively regulates **ECM3** expression, as deletion of any one of the five members of the **Paf1** complex results in reduced **ECM3** transcript levels (Figure 2A).

The **Paf1** complex associates with Pol II during transcription elongation and plays a crucial role in establishing patterns of histone modifications across transcribed loci (reviewed in Tomson and Arndt 2013). Therefore, to investigate the mechanism by which the **Paf1** complex stimulates **ECM3** transcription, we analyzed **ECM3** mRNA levels in strains that lack histone modifiers known to depend on the **Paf1** complex for function. Our results indicate that ubiquitylation of H2B K123 and methylation of H3 K4 are required to activate **ECM3** as the enzymes that perform these modifications, the ubiquitin conjugase **Rad6** and ubiquitin-protein ligase **Bre1** for H2B K123 ubiquitylation and the H3 K4 methyltransferase **Set1**, are required for normal **ECM3** expression (Figure 2B). Other histone modifications dependent on the **Paf1** complex, H3 K79 di- and trimethylation and H3 K36 trimethylation, do not appear to play a role in stimulating **ECM3** transcription. Mutations that delete **DOT1** or **SET2**, which encode the H3 K79 and H3 K36 methyltransferases, respectively, did not reduce **ECM3** mRNA levels (Figure 2B). Targeted mutation of H3 K4 to an unmodifiable residue, H3 K4A, reduced **ECM3** transcript levels, consistent with the idea that **Set1** stimulates **ECM3** expression by methylating H3 K4 (Figure 2C). The magnitude of the decrease in **ECM3** mRNA levels was greater for the **set1**Δ mutant than for the H3 K4A mutant. In addition to methylating H3 K4, it is possible that **Set1** targets a nonhistone substrate that contributes to **ECM3** expression. Alternatively, because the H3 K4A mutant has only a single copy of the H3 and H4 genes, reduced H3-H4 dosage may partially rescue the H3 K4A effect on **ECM3** transcription. A previous study has shown that histone dosage impacts expression of a gene regulated by noncoding transcription as deletion of a single copy of the H3 and H4 genes, **HHT1** and **HHF1**, results in **SER3** derepression (Hainer and Martin 2011). Furthermore, histone dosage affects the expression of many genes in **S. cerevisiae** (Wyrick et al. 1999). Collectively, these data indicate that H2B K123 ubiquitylation by **Rad6-Bre1**, and subsequent H3 K4 methylation by **Set1**, positively regulate **ECM3** expression.

Methylation of H3 K4 may serve as a signal to downstream activators of **ECM3** expression. To test this, we explored the effects of complexes that recognize various H3 K4 methylation states on **ECM3** expression. The recruitment of SAGA, NuA3, and NuA4 histone acetyltransferase complexes and the **Set3** histone deacetylase complex is stimulated by methylated H3 K4 in **S. cerevisiae** (Martin et al. 2006; Ginsburg et al. 2009, 2014; Kim and Buratowski 2009; Bian et al. 2011). We evaluated the contributions of **Set3**, SAGA, and **NuA3** to **ECM3** regulation by northern analysis using strains lacking a single member of each complex. Consistent with previous studies showing that the **Set3** histone deacetylase complex represses transcription (Kim et al. 2012), we did not observe a strong or consistent positive effect of **SET3** on **ECM3** expression (Figure 2D). The **NuA3** and SAGA complexes have various effects on chromatin and have been generally associated with transcriptional activation. Deletion of the genes encoding **Gen5** and **Sas3**, the catalytic subunits of SAGA and **NuA3**, respectively, caused a dramatic reduction in **ECM3** expression (Figure 2D). We note that **ECM3** transcript levels are lower in **gen5Δ** and **sas3Δ** mutants than in the **set1**Δ mutant. SAGA and **NuA3** are both large, multisubunit complexes that associate with chromatin through multiple interactions. It is possible that the loss of H3 K4 methylation results in a partial loss of SAGA and **NuA3** activity at **ECM3** and that some function may be retained through other interactions.

### Transcription of the EUC1 ncDNA does not require H3 K4 methylation

Expression of many genes is influenced by the regulation of neighboring transcription units. To determine if methylation of H3 K4 could be regulating **ECM3** indirectly by acting farther upstream to regulate transcription of **EUC1**, we analyzed **EUC1** RNA levels in strains lacking H3 K4 methylation. Northern analysis of **EUC1** transcription in an **rep6Δ** background showed only a slight reduction in **EUC1** transcript levels in

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**Figure 4** Deletion of putative **EUC1** promoter sequences 5' of **ECM3** results in reduced **ECM3** expression. Representative northern blot analysis of RNA isolated from strains carrying an **RRP6** deletion and containing either a WT **ECM3** locus (YJ1126) or the indicated **EUC1** promoter deletion mutations. Promoter deletion mutations were introduced at the endogenous **ECM3** locus and replaced either 50 bp (p**EUC1Δ1**; region −400 to −350 deleted; YJ1128) or 100 bp (p**EUC1Δ2**; region −400 to −300 deleted; YJ1131) upstream of the +1 start codon of **ECM3**, as diagrammed below. The locations of a PIC identified by Rhee and Pugh (2012) and a putative TATA sequence are indicated on the diagram below. **SCR1** serves as a loading control. CUT, cryptic unstable transcript; PIC, preinitiation complex; WT, wild-type.
the absence of H3 K4 methylation (rrp6Δ set1Δ strain), although ECM3 mRNA levels remained low (Figure 3, A and B–D). In the rtf1Δ rrp6Δ double mutant, EUC1 levels were lower than those detected in rrp6Δ or set1Δ rrp6Δ strains (Figure 3, A and B–D), consistent with the observation that Rtf1 has functions in addition to regulating H3 K4 methylation (Warner et al. 2007). In the absence of Pafl, levels of the EUC1 isoform present in rrp6Δ cells, termed EUC1 SC for short CUT, were not significantly altered (Figure 3, A and B–D). However, a larger, more abundant EUC1 isoform, which we refer to as EUC1 LC for long CUT, was enriched in the paflΔ rrp6Δ strain (Figure 3, A and C). Thus, although the set1Δ, paflΔ, and rtf1Δ mutations all reduce ECM3 expression (Figure 3, A and D), they do not affect the pattern of EUC1 transcripts in the same way. Instead, the correlation with ECM3 expression is most clearly related to the loss of H3 K4 methylation. Fitting with this idea, a set2Δ rrp6Δ double mutant, which lacks H3 K36 methylation, does not show a change in EUC1 or ECM3 expression compared to the rrp6Δ control strain (Figure 3). These data do not exclude a role for EUC1 in ECM3 regulation; however, ECM3 transcript levels remain low in the absence of H3 K4 methylation even though an EUC1 transcript is produced in the rrp6Δ set1Δ double mutant strain. Thus, if EUC1 transcription is involved in ECM3 regulation, methylation of H3 K4 may work downstream of this effect. These results suggest that H3 K4 methylation does not indirectly regulate ECM3 expression by acting farther upstream to modulate the levels of EUC1 transcription.

**Loss of EUC1 transcription correlates with a reduction in ECM3 transcription**

As the Pafl complex associates with actively transcribing polymerases and H3 K4 methylation patterns are established during transcription, one possible model is that transcription of EUC1 functions to place this modification over the ECM3 promoter to positively regulate ECM3 expression. To investigate a possible role for EUC1 transcription in regulating ECM3 expression, we devised a strategy to disrupt the EUC1 promoter and eliminate CUT transcription. To identify putative EUC1 promoter elements, we performed a sequence alignment of the intergenic region 5′ of ECM3 in four related yeast species (S. cerevisiae, S. mikatae, S. bayanus, and S. paradoxus) (Figure S2). This analysis identified a conserved putative TATA sequence 344 nucleotides upstream of the ECM3 start codon. In ChiP-exo analyses, Rhee and Pugh (2012) identified a site of preinitiation complex (PIC) assembly 382 nucleotides upstream of the ECM3 start codon. Guided by this information, we generated promoter deletion mutations at the endogenous ECM3 locus using a two-step integration method, which replaced the putative EUC1 promoter sequence with an unrelated DNA sequence (177 bp encoding the 3XHA tag and linker DNA). Deletion 1 (pEUC1Δ1) replaced bases −400 to −350 and deletion 2 (pEUC1Δ2) replaced bases −400 to −300 relative to the ECM3 start codon. These deletions eliminate the detected site of PIC assembly and pEUC1Δ2 also eliminates the putative TATA sequence (Rhee and Pugh 2012). Both deletions greatly reduce EUC1 transcript levels (Figure 4). A very small amount of a slightly larger transcript is detected with the EUC1 probe in RNA isolated from these promoter deletion strains. Based on the location of the northern probes, the nature of the promoter deletion mutations, and the size of the RNA product, this transcript may initiate downstream of the major EUC1 start sites and extend partially into ECM3. Because the amount of this transcript in pEUC1Δ2 strains is very small, we continued our analyses with this mutation. Interestingly, both deletions also lower ECM3 mRNA levels (Figure 4). These results indicate that EUC1 transcription is positively correlated with ECM3 transcription.

**Loss of EUC1 transcription is associated with a reduction in H3 K4me3 levels at the ECM3 promoter**

To further investigate the connections between H3 K4 methylation and ECM3 transcription, we analyzed the local chromatin landscape of the
**EUC1-ECM3** locus by ChIP analysis. In particular, we analyzed the levels of H3 K4 trimethylation (me3) in the presence and absence of **EUC1** transcription as well as in **paf1Δ** and **set1Δ** mutants, which served as controls for loss of the modification. As expected, H3 K4me3 levels were nearly undetectable in the **paf1Δ** and **set1Δ** mutants (Figure 5). In wild-type cells, two peaks of H3 K4me3 were observed, one over the 5’ end of **EUC1** and one over the 5’ end of **ECM3**. Interestingly, deletion of the putative EUC1 promoter in the **pEUC1Δ2** mutant reduced H3 K4me3 levels at both of these locations (Figure 5), consistent with the possibility that **EUC1** transcription positively regulates **ECM3** transcription by promoting H3 K4me3.

### The Paf1 complex and EUC1 impact ECM3 transcription through independent pathways

To determine if Paf1 regulates **ECM3** transcription in a manner that requires synthesis of the upstream CUT, we analyzed **ECM3** transcript levels in **pEUC1Δ2 paf1Δ** double mutants. In combination, deletion of the putative EUC1 promoter and deletion of **Paf1** caused a greater defect in **ECM3** expression than either mutation alone (Figure 6). Although the interpretation of these data are complicated somewhat by the fact that the **pEUC1Δ2** mutation is not equivalent to an **EUC1** null allele, as it does not completely eliminate **EUC1** transcription (Figure 4), the results are consistent with the Paf1 complex and EUC1 transcription having separable roles that contribute to **ECM3** expression. Our data suggest that one shared role of **EUC1** and the Paf1 complex is promoting methylation of H3 K4 (Figure 5), but each of these factors may have other contributions to **ECM3** regulation that remain to be identified.

### Defective termination of EUC1 is not sufficient to repress ECM3 expression

We next investigated whether the long isoform of **EUC1** (LC), which is enriched in **paf1Δ** strains (Figure 3), plays a role in repressing **ECM3** transcription. Northern analysis using strand-specific probes to detect sense transcripts showed that the LC isoform, like the SC isoform, is transcribed from the sense strand relative to the **ECM3** ORF (Figure S3). Neither the SC nor the LC isoform is detected with an antisense strand-specific northern probe. In addition, the LC transcript is not detected in **paf1Δ** strains carrying a wild-type **RRP6** allele, indicating that it is also unstable (Figure S3). Because Paf1 is required for proper termination by the Nrd1-Nab3-Sen1 pathway (Sheldon *et al.* 2005; Tomson *et al.* 2011, 2013), we hypothesized that the longer **EUC1** isoform might be a read-through product of the smaller isoform that terminates farther downstream. In support of this, primer extension analysis revealed that **paf1Δ** strains use the same **EUC1** transcription start sites as an **rrp6Δ** control strain, which are located between 344 and 364 nucleotides upstream of the **ECM3** start codon (Figure 7).

We also analyzed the potential effect of alternative **EUC1** termination by depletion of **Nrd1** from the nucleus by the anchor-away method (Haruki *et al.* 2008). Upon depletion of **Nrd1** from the nucleus by addition of rapamycin to a **NRD1-FRB** strain, a prominent **EUC1** transcript, which comigrated with the LC isoform observed in the **paf1Δ** background, was observed. This result is consistent with the idea that the LC isoform detected in **paf1Δ** **rrp6Δ** strains arises from transcriptional read-through of a CUT terminator. In the **Nrd1**-depleted strain, an additional transcript was detected by the **EUC1** probe and this transcript corresponds to the size of an **EUC1** transcript reading through (RT) the entire **ECM3** ORF (Figure 8A). The relative locations of these isoforms based on northern probe hybridization and relative size are diagrammed in Figure 8C. The RT isoform overlaps with the **ECM3** mRNA bands in the northern blot in Figure 8A and is included in quantitation of **ECM3** levels. Upon addition of rapamycin, there is no significant change in **ECM3** transcript levels in the control strain used for the anchor away technique (labeled WT in Figure 8). There is also no significant fold change in **ECM3** transcript levels in the **NDR1-FRB** strain after addition of rapamycin (Figure 8B). This result indicates that a defect in **Nrd1**-dependent termination of the **EUC1** CUT does not significantly change the overall level of **ECM3** transcripts. Although we have not ruled out a role for the longer **EUC1** isoform in fine-tuning **ECM3** expression, these data indicate that transcription of the long **EUC1** isoform alone is not sufficient to regulate **ECM3** expression under these conditions. Therefore, of the two described functions of the Paf1 complex that we have explored, stimulation of H3 K4 methylation is important for **ECM3** transcription, while regulation of **EUC1** termination plays little if any role in...
the expression of ECM3. As indicated by our genetic data (Figure 6), we anticipate that the Paf1 complex has multiple functions that contribute to ECM3 regulation that will be interesting to explore.

**DISCUSSION**

Prompted by previous mechanistic work that revealed a repressive effect of noncoding transcription on expression of the yeast SER3 gene, we sought to identify additional cases in which transcription of intergenic DNA upstream of a protein-coding gene impacts the expression of that gene. We focused on the ECM3 locus, where a promoter-associated CUT, EUC1, is synthesized in the sense direction relative to the ORF. We investigated the role of transcription-associated chromatin alterations in the regulation of ECM3, as many genes regulated by intergenic transcription employ mechanisms that alter the local chromatin environment. A survey of transcription-associated chromatin regulators uncovered an integral role for the Paf1 complex in the positive regulation of ECM3 expression. Each of the five subunits of the Paf1 complex is necessary for proper ECM3 expression. Our data suggest that the role of the Paf1 complex in promoting H3 K4 methylation is required for proper ECM3 expression. Loss of Set1, the histone methyltransferase for H3 K4, or the ubiquitin conjugase and ligase enzymes that catalyze H2B K123 monoubiquitylation, results in reduced ECM3 expression. Additionally, we provide evidence that the role of H3 K4 methylation may be to serve as a signal for HAT activity at the ECM3 promoter. Loss of catalytic subunits of the SAGA and NuA3 HAT complexes, which both recognize methylated states of H3 K4, results in a dramatic reduction of ECM3 expression. In addition to the stimulatory role of this network of chromatin modifiers, ECM3 transcription appears to be positively correlated with noncoding transcription across its promoter. Differences in the levels and isoforms of the EUC1 noncoding transcripts do not strongly affect ECM3 transcription. Instead, the common link between factors stimulating ECM3 expression appears to be their role in promoting H3 K4 methylation. Consistent with this idea, a EUC1 promoter deletion reduced H3 K4me3 levels across both the EUC1 and ECM3 transcription units.

One explanation for our observations is that transcription of EUC1 positively regulates ECM3 expression by promoting the methylation of H3 K4, which may lead to downstream histone acetylation at the ECM3 promoter. A key result in support of this model is that deletion of a 50 bp sequence just upstream of the EUC1 transcription start sites severely impaired both EUC1 and ECM3 expression. Although we cannot completely rule out the possibility that this deletion (pEUC1Δ1) may remove a transcription factor binding site that could directly activate the ECM3 promoter, several pieces of data indicate that this sequence most likely contains key regulatory elements of the EUC1 promoter. First, our ChIP data show two distinct peaks of H3 K4me3 expression. A DNA sequencing ladder is shown on the left. (B) A schematic diagram of the ECM3 locus with the positions of the upstream EUC1 CUTs and the pEUC1Δ1 and pEUC1Δ2 mutations indicated. For simplicity, the EUC1 SC and LC isoforms are diagrammed as initiating at a single start site to reflect that the closely positioned start sites detected in (A) do not appear as distinct isoforms by northern blot analysis. CUT, cryptic unstable transcript; LC, long CUT; SC, short CUT; PIC, preinitiation complex.
unsuccessful. Introduction of an exogenous terminator sequence within *EUC1* had nonspecific effects on *ECM3* transcription start site selection, and targeted mutation of the predicted TATA element failed to eliminate *EUC1* transcription. This is consistent with previous reports detecting PIC assembly further upstream of the putative TATA sequence and indicates that this TATA element is not likely to be the predominant site of PIC assembly for the *EUC1* transcript. The overall AT-richness of this region may allow for transcription initiation at multiple sites that may not be abolished by targeted mutations.

While both appear to be important for establishing the H3 K4 methylation pattern across the *ECM3* promoter, *EUC1* transcription and the Paf1 complex also have separable functions in facilitating *ECM3* expression. A double mutant lacking both *EUC1* transcription and *PAF1* is more severely compromised for *ECM3* expression than either single mutant strain. This indicates that the Paf1 complex stimulates *ECM3* transcription through a mechanism in addition to its role in promoting H3 K4 methylation. This is further evidenced by the *Leo1* subunit of the Paf1 complex having a positive role in *ECM3* regulation, despite the fact that *Leo1* is not required for H3 K4me3 (Ng et al. 2003). Although termination of the *EUC1* transcript is altered in a *paf1Δ* strain, our results of Nrd1 depletion do not support a major role for alternative termination of *EUC1* in regulating levels of *ECM3* expression. However, it is possible that there are transient isoform-specific effects or that these isoforms have different roles under biologically relevant conditions. An intriguing feature of the locus is that the *EUC1* and *ECM3* transcripts overlap in a region of DNA occupied by a nucleosome (Mavrich et al. 2008). It is interesting to speculate that the position and modification state of this nucleosome could be a major determinant in promoting or preventing transcription of *ECM3*. This nucleosome could also be a determinant in which isoforms of *EUC1* and *ECM3* are expressed. It would be interesting to relate the position of this nucleosome with where termination of *EUC1* and initiation of *ECM3* occur.

Our finding of a positive role for H3 K4 methylation at a gene that lies downstream of a noncoding transcription unit is interesting, as others have shown this modification to be repressive to initiation of transcription at the *GAL1-10, DCI1*, and *DUR3* loci (Houseley et al. 2008; Pinskaya et al. 2009; Kim et al. 2012). In these cases, noncoding transcription places H3 K4 methylation across the promoters of these genes and results in the recruitment of HDACs, such as Set3. Our data indicate that the functionally important readers of the H3 K4 methyl marks at *ECM3* are the HAT complexes SAGA and NuA3, which would explain the opposite effect of H3 K4 methylation on *ECM3* expression compared to *GAL1-10, DCI1*, and *DUR3*. Differential recruitment of readers could depend on whether the histones at the promoters of these genes display predominantly tri- or dimethylation of H3 K4 or other differences in the local chromatin environment. The observation that one histone modification associated with noncoding transcription can have opposite effects on the regulation of a neighboring gene adds to the increasing diversity of mechanisms by which noncoding transcription can regulate gene expression. This points to a potential plethora of regulatory mechanisms imparted by noncoding transcription that will be important to study at individual genes.

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