The chromatin remodeling and mRNA splicing functions of the Brahma (SWI/SNF) complex are mediated by the SNR1/SNF5 regulatory subunit

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ABSTRACT

Nucleosome remodeling catalyzed by the ATP-dependent SWI/SNF complex is essential for regulated gene expression. Transcriptome profiling studies in flies and mammals identified cell cycle and hormone responsive genes as important targets of remodeling complex activities. Loss of chromatin remodeling function has been linked to developmental abnormalities and aggressive cancers. The Drosophila Brahma (Brm) SWI/SNF complex assists in reprogramming and coordinating gene expression in response to ecdysone hormone signaling at critical points during development. We used RNAi knockdown in cultured cells and transgenic flies, and conditional mutant alleles to identify unique and important functions of two conserved Brm complex core subunits, SNR1/SNF5 and BRM/SNF2-SWI2, on target gene regulation. Unexpectedly, we found that incorporation of a loss of function SNR1 subunit led to alterations in RNA polymerase elongation, pre-mRNA splicing regulation and chromatin accessibility of ecdysone hormone regulated genes, revealing that SNR1 functions to restrict BRM-dependent nucleosome remodeling activities downstream of the promoter region. Our results reveal critically important roles of the SNR1/SNF5 subunit and the Brm chromatin remodeling complex in transcription regulation during elongation by RNA Polymerase II and completion of pre-mRNA transcripts that are dependent on hormone signaling in late development.

INTRODUCTION

The SWI/SNF ATP-dependent chromatin remodeling complex facilitates early events in transcription through interactions with DNA binding transcription factors and recruitment of RNA polymerase II (PolII) (1). The complex assists transcription events by interacting with nucleosomal substrates to alter DNA:histone contacts (2) and facilitates DNA translocation within the nucleosome (3). The SWI/SNF complex associates with sites of PolII accumulation (4,5) and it may form transient associations with PolIII (6). Remodeling activities allow for transcription at promoters to initiate, while early elongation events are thought to be mediated by alternate chromatin remodeling activities (7). However, recent studies of transcription elongation and splicing regulation suggest there is even greater diversity in the modes of SWI/SNF regulation (8,9). For instance, possible links between mammalian SWI/SNF complex remodeling activities, the rate of RNA PolII movement, and alternative pre-mRNA splicing regulation have been reported. However, it has not yet been possible to obtain a clear understanding from these studies what regulatory mechanisms are in place to help coordinate either the timing and/or limit the extent of SWI/SNF complex remodeling activities in the developing organism.

The SWI/SNF complex is composed of a conserved set of core subunits, including SNF2/SWI2, SWI3 and SNF5 which are required for in vitro remodeling (10), and a set of accessory subunits (8–11 total). SWI/SNF counterparts have been identified in Drosophila (Brm) and vertebrates (BRG1/HBRM) (11) and have critically important functions in development (12), reprogramming somatic cells during differentiation (13), as well as establishment and maintenance of pluripotent and multipotent identities of murine embryonic stem cells (14–17). Mouse knockouts of

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genes encoding the core SWI/SNF subunits (SNF5/SMARCBL and SWI2/BRG1) are associated with peri-implantation lethality (17) and genetic studies in flies revealed that the complex is required throughout development (11,18). Loss of SWI/SNF complex components has also been directly linked to a number of aggressive cancers (19), including malignant rhabdoid tumors associated with SNF5/SMARCBL loss (20,21), and melanomas, prostate, lung and breast cancers linked to BRG1/HBRM loss (19,22).

Genetic and transcriptome profiling studies of the Drosophila Brahma (Brm) complex using dominant-negative mutant alleles of genes encoding the conserved components, SNR1(SNF5) and BRM(SNF2/SWI2), allowed for analyses of loss of subunit or complex function under conditions where the mutant subunit was properly assembled (18,23). During Drosophila wing vein and intervein cell development, snr1 and brm elicit opposite mutant phenotypes revealing that SNR1 serves to block BRM ATPase functions in intervein cells in cooperation with histone modifying proteins and gene-specific repressors (24,25). We previously identified the hormone regulated E\(\text{ig}\) (ecdysone inducible) genes as direct targets of Brm complex regulation (26). The E\(\text{ig}\) genes comprise a cluster of five divergently transcribed pairs with short intergenic regions (~260 bp). Peak expression occurs during early pupariation correlating with elevated hormone levels (27). Many of the E\(\text{ig}\) genes encode for proteins related to mammalian defensins that may function as secreted antimicrobial polypeptides involved in host defense during metamorphosis. This type of sensor-mediated innate immune response system is strongly conserved between flies and mammals (28). The E\(\text{ig}\) genes were generally upregulated in response to reduced snr1 function, but downregulated if brm function was reduced suggesting that remodeling activity was necessary for activation, while SNR1 was important for negatively regulating that activity (26). Brm complex regulation of the E\(\text{ig}\) genes mimics the interactions observed in the Drosophila wing suggesting a common mode of control. Thus, SNR1 acts as a regulatory subunit to restrict Brm complex-dependent chromatin remodeling activities during development on select target genes that control growth, differentiation and patterning, including genes that respond to hormone signaling (5,25,26).

To better understand how Brm complex remodeling activities are regulated within the context of a developing organism, we undertook a genetic approach to uncover the functional role of SNR1 and the Brm complex using the dominant negative snr1\(^{E1}\) and brm\(^{K804R}\) mutants. We found that repression of ecdysone inducible gene expression by the Brm complex is due to restraint of complex chromatin remodeling activity leading to the stalling of PolIII elongation. Further, we make the novel finding that the restraint is mediated through the functions of SNR1, while BRM ATPase activity is required for subsequent chromatin remodeling following release of the stalled polymerase. We found that promoter distal nucleosome structures can impede or stall PolIII on certain developmentally regulated genes. In contrast to prevailing views, a consequence of Brm complex-dependent polymerase stalling is reduced splicing and the retention of introns that may function to control gene expression at a post-transcriptional level. This aspect of Brm (SWI/SNF) complex function has never been described and thus our findings represent an important advance in our understanding of in vivo developmental functions of chromatin remodeling.

**MATERIALS AND METHODS**

**Genetic manipulations and strains**

Fly strains and manipulations for snr1\(^{E1}\), UASBrm\(^{K804R}\) and UAS-shNELF have been described (23,26,29). Rpl121\(^{C4}\) and UAS-shDSIF stocks were from the Bloomington Drosophila Stock Center. Expression of UAS\(\text{GAL4}\) transgenes was controlled using P\((\text{GawB})\)69B-GAL4 driver with crosses performed at 29°C. Animals were staged according to standard guidelines using morphological landmarks (30). Staging was independently verified by monitoring expression of the ecdysone inducible gene, Eip93F (31) (Supplementary Figure S1). Blue gut and clear gut larvae were differentiated by growth on food supplemented with 0.05% bromophenol blue (32).

**Drosophila cell culture and RNAi**

S2 cells were cultured on standard medium, with addition of 20-hydroxyecdysone (Sigma) to a final concentration of 1 \(\mu\)M for 24 or 48 h. RNAi mediated knockdowns of snr1 and brm in cultured cells were performed with double-stranded RNA as described (26).

**RNA analysis**

Total RNA was prepared and semi-quantitative RT-PCR was performed as described (26). SYBR Green quantitative real time PCR on reverse transcriptase reactions (qRT-PCR) was performed in triplicate using GoTaq qPCR Master mix (Promega). The qPCR reactions were carried out in triplicate. Levels of mRNA were analyzed by comparative Ct method. The Drosophila rp49 ribosomal gene was chosen as the endogenous reference. Primers used for splice form analysis were designed similar to the strategy described by Hargreaves et al. (56). Primers within a single 3’ exon were used to determine total expression (precursor). Exonic primers that crossed an intron were used for detection of spliced transcripts. Primer sequences are listed in Supplementary Table S1.

**CHART-PCR Assay**

Nuclease accessibility assays were performed essentially as described (33). Treated and untreated DNAs were used to perform SYBR Green real time PCR in triplicate. A standard curve was generated with serial dilutions of genomic DNA to correlate Ct values obtained from real time PCR to percent accessibility. MNase accessibility was calculated as a percentage of the accessibility observed in the untreated DNA (34).
Chromatin immunoprecipitation

Chromatin immunoprecipitation (ChIP) was performed as described in both S2 cells (26) and Drosophila-staged animals (35). For qPCR analysis, fold enrichment was measured against IgG negative control and values were normalized to ChIP input. Antibodies included zSNR1 and zBRM (5); zH3-trimethyl-K4 (07-473), zH3–trimethyl K27 (07-449), zH3-acetyl K9,14 (06-599), zH3-dimethyl K36 (07-274) from Upstate (Lake Placid, NY, USA); zH3 (ab1791), zIgG (ab27478), zH3–trimethyl K9 (ab1186) from Abcam (Cambridge, MA, USA); zOSA from DSHB (University of Iowa, Department of Biology, Iowa City, IA, USA). RNA PolII antibodies (8WG16, H5 and H14) were from Covance (Berkeley, CA, USA). Antibodies to Cyclin T (D. Price), NELF-E (D. Gilmour) and POLYBROMO (P. Verrijzer) were gifts.

RESULTS

Eig genes are poised for activation

Our previous gene expression profiling study using conditional dominant-negative mutant alleles of snr1 and brm identified the hormone regulated Eig genes as significant in vivo targets of Brm complex regulation, and cultured cell studies confirmed that the regulation was direct (26). Eig71Ef–i gene transcripts are normally undetectable in cultured Drosophila Schneider (S2) cells in the absence of ecdysone hormone and transcripts first appear ~48 h after hormone addition (26); however, RNAi knockdown of snr1 prior to adding hormone resulted in the accelerated appearance of the completed Eig71Ef transcript within 24 h (Figure 1A, left panel). Other Eig genes showed an identical response (data not shown), consistent with a function for SNR1 in repressing EIG expression.

Close relationships between chromatin remodeling and epigenetic histone modifications involved in gene regulation have been described (36). Since the upregulation of the Eig genes following RNAi depletion of snr1 in S2 cells was similar to the in vivo mutant effects of snr1 (26), we sought to determine if these effects were the result of changes in histone modifications. ChIP analyses revealed (26) no obvious differences in the profile or relative levels of histone modification marks tested on Eig71Ef chromatin (and Eig71Ef, Ef and Eeg) upon snr1 knockdown compared to control cells (data not shown). However, in both cases, addition of ecdysone led to the appearance of epigenetic marks associated with active transcription (H3-acetyl K9, K14 and H3-K4me3) coexisting with repressive histone marks (H3-K9me3 and H3-K27me3) suggesting that the Eig genes were poised for activation. Surprisingly, dimethylated histone H3-K36, a covalent modification frequently associated with transcription elongation (37), was detected within the Eig gene coding exons 24 h after hormone addition in normal S2 cells, suggesting that transcripts had been initiated but not fully elongated (Figure 1A, right panel). Therefore, hormone triggers the appearance of epigenetic marks associated with active transcription, while full-length transcripts are delayed. Depletion of the Brm complex using RNAi did not cause dramatic changes in these marks, but accelerated the appearance of completed transcripts.

The Brm complex regulates Eig transcript elongation

The accelerated appearance of completed Eig transcripts following snr1 knockdown could result from elevated transcription initiation and/or elongation by RNA PolII. We focused our analyses of Brm complex functions on Eig71Ef as Eig71Ef–i represent the most robustly regulated divergent gene pair within the Eig gene cluster (26) and they share common promoter regulatory elements (Figure 1B). ChIP experiments using PolII antibodies that recognize the phosphorylation status of the carboxyl-terminal domain (CTD) revealed that a paused PolII (Ser5P-CTD)–Ser5P–CTD, CycT (P-TEFb) and pausing factor, NELF and DSIF and the release of phosphorylated forms. CycT associates with the Cdk9 kinase to form P-TEFb that is required for the phosphorylation of Ser2-CTD, NELF and DSIF and the release of paused PolII. Bulk chromatin was isolated from untreated S2 cells and cells exposed to prolonged incubation with ecdysone. There was no significant accumulation of PolII or elongation factors in untreated cells (Figure 1E, left). The Eig71Ef 5' exon transcript was detected after 24 h of treatment coincident with the appearance of the Ser5P-CTD, CycT (P-TEFb) and releasing factor, NELF
After 48 h of ecdysone treatment, the 3′ exon appeared (Figure 1E, right) indicating a full-length transcript. Importantly, histone H3 was present throughout prolonged ecdysone treatment suggesting no significant changes in nucleosome density occurred within the Eig chromatin.

We next sought to determine whether the Eig genes were regulated through control of transcription elongation during normal development. The Eig71Eh–i transcribed regions and primers used for RTPCR analysis. Primers spanning the promoter regions (p) and 5′ and 3′ exonic regions are depicted. (C) ChIP analysis of PolII phosphorylated forms on Eig71Eh–i promoter. S2 cells treated with control or snr1 RNAi plus ecdysone followed by ChIP using antibodies specific to Ser2P-CTD (elongating) or Ser5P-CTD (initiating) PolII and PCR using Eig71Eh–i promoter primer pairs (p). (D) RNA analysis of S2 cells treated with ecdysone and RNAi for snr1, brm and control. Agarose gel analysis of RT-PCR products using primers specific to 5′ and 3′ coding exons as depicted in (A) and RP49 control. Quantitative RT-PCR of 5′ and 3′ exons performed (left); ratios 3′-end/5′-ends plotted (right). (E) Hormone-dependent recruitment of elongation factors to Eig71Eh genomic region. ChIP analysis of cultured S2 cells (+/−) ecdysone. Agarose gel analysis of RT-PCR products (center panel) and qRT-PCR (right) of Eig71Eh 5′- and 3′-ends from S2 cells 24 and 48 h after ecdysone treatment.

We and others have shown that RNAi depletion of individual core subunits of the Brm complex in S2 cells resulted in complex instability and possible degradation of subunits (24,26,38). In this report, we find that loss of the Brm complex by RNAi depletion of either snr1 or brm in S2 cells mimics effects on Eig regulation observed with our conditional snr1E1 mutant in vivo (26), in which transcription was upregulated in response to reduced SNR1 function. In contrast, we had previously found that the BRM subunit exerts a positive role in Eig gene regulation in vivo using a dominant-negative brm mutant allele (brmK804R) that is impaired in ATPase function but still assembled into Brm complexes (23). To more precisely uncover the role of the Brm complex, in particular the (LP), the Eig gene transcripts are undetectable (see EP versus LP control lanes in Figure 3B).
SNR1 subunit, in regulating transcription elongation during development we used snr1E1 and brmK804R dominant negative mutants and carried out RT-PCR analyses of Eig71Eh during the EP stage that corresponds to the snr1E1 temperature-sensitive period (Figure 2A and B). Thus, unlike the RNAi depletion studies in tissue culture, the conditional snr1 and brm dominant negative mutant alleles afforded us the opportunity to assess the function of the individual subunits within the assembled complex (18,23). Comparing to wild-type (WT), we found that the Eig71Eh transcript was elevated at both 5' and 3'-ends in the snr1E1 mutant; however, the 5'-end transcript was much reduced and transcription of the 3'-end was undetectable in a brmK804R mutant. Quantitative RT-PCR using 3' exon-specific primers verified that transcription was upregulated 13-fold in the snr1 mutant and reduced 8-fold in the brm mutant compared to WT. It is important to note, ChIP analyses of histone marks in S2 cells and in early pupae (Figures 1E and 2A) indicated that histones were present throughout Eig transcribed regions including those that correlated with polymerase stalling.

The requirement for BRM ATPase activity in transcription elongation suggests that nucleosomes need to be remodeled for release of the stalled polymerase and that the Brm complex would need to be present at nucleosome positions embedded within distal exons. Therefore, we next sought to examine the distribution of the Brm complex on the Eig71Eh genomic region. ChIP analyses revealed that SNR1E1 was associated with Eig71Eh in a pattern identical to WT SNR1 (Figure 2C); although, the mutant protein accumulated at higher levels within promoter and 5'-exon regions, possibly reflecting the elevated transcription observed in the snr1E1 mutant.

We next addressed whether misregulation of the Eig genes in a snr1E1 mutant could possibly be the result of alterations in Brm complex accessory subunit composition. Two subclasses of the SWI/SNF complex exist in a number of eukaryotes. Eukaryotic transcription factors (transcriptional activators) bind to DNA via a leucine zipper domain, and are typically recruited to the same DNA sequence by the SWI/SNF ATPases. The SWI/SNF ATPases play a role in the remodeling of chromatin structure by removing nucleosomes from DNA.
of organisms, including Drosophila, that share seven common core subunits while alternate subunits contribute to functional specificity. OSA/BAF250 subunit is found within mammalian BAF or Drosophila BAP complexes, while POLYBROMO (PB)/BAF180 and BAP170/BAF200 are subunits of mammalian PBAF or Drosophila PBAP complexes (38,39). It is not known which subcomplex participates in Eig71Eh–Ei gene regulation. To address these questions, quantitative ChIP of Eig71Eh chromatin was performed using PB and OSA antibodies in both WT and mutant animals. These experiments revealed that PB protein, in contrast to OSA, is enriched at the promoter and throughout the transcribed regions in a pattern identical to SNR1 in both WT and snr1E1 mutant (Figure 2D). PB enrichment was observed during the EP stage when Eig71Eh–Ei transcripts were accumulating, suggesting that PBAP complexes most likely regulate Eig71Eh–Ei transcription elongation. Thus, misregulation of Eig71Eh transcription in the snr1E1 mutant is not due to either altered accessory subunit composition or impaired Brm complex binding to chromatin.

Our data suggests that, while the BRM subunit ATPase activity is required for chromatin remodeling following release of the paused polymerase, the Brm complex-dependent restraint on transcription elongation is mediated through the functions of SNR1. In this context, SNR1 could act either as a physical block to PolII movement or to restrain remodeling activities of the Brm complex. If SNR1 acts as a barrier to PolII movement, we would predict an inverse correlation between binding of the Brm complex to chromatin and active elongation. As an example, NELF dissociates from the Hsp70 gene upon activation by heat shock and a stalled PolII is released (40). Alternatively, if SNR1 functions to restrain remodeling during elongation, we would expect enhanced recruitment of the complex coincident with hormone-dependent activation. We examined the distribution of SNR1 and PolII CTD-phosphorylated forms on chromatin at the larval BG stage before transcription of Eig genes was initiated and compared that with the EP stage when transcripts were accumulating. SNR1 and PolII (Ser2P-CTD and Ser5P-CTD) were further enriched throughout transcribed regions in the EP stage compared with the earlier BG stage (Figure 2E) consistent with recruitment of the Brm complex to assist in elongation events when transcription was maximal. Interestingly, Ser5P-CTD showed the greatest change in recruitment during transcription of the Eig genes.

Hormone-dependent recruitment of elongation factors

We sought to more directly examine the individual roles of elongation factors on Eig regulation and, in particular, determine whether loss of NELF and DSIF had similar effects on Eig transcription as Brm complex mutants. We performed in vivo RNA knockdown of NELF and DSIF using short hairpin containing transgenes (shRNAi). NELF has been shown to have both positive and negative roles in regulating polymerase elongation (40). Expression of a shNELF driven by the GAL4 expressing P(GawB)69B driver produced crumpled wing phenotypes indicating important functions in tissue development (Figure 3A). Depletion of NELF in the EP stage caused an unanticipated reduction of full length transcripts by 6-fold (Figure 3A), with the 3’ mRNA almost

![Figure 3. Eig’s are regulated by PolII pausing factors. (A) NELF positively regulates Eig’s. (Top left) qRT-PCR analysis of Eig71Eh full length transcripts in EP expressing shRNA to NELF or control with no driver. Depletion of NELF in early pupae causes an unanticipated reduction of Eig71Eh 3’ transcript. (Top right) Agarose gel analysis of RT-PCR products. (Bottom) shRNAi depletion of NELF causes developmental wing defects. Show are representative wings from P(GawB)69B-GAL4 driver alone and P(GawB)69B-GAL4 > UAS-shNELF. A dorsal view of an shNELF adult is shown on the right. (B) DSIF negatively regulates Eig’s. (Left) RNA analyzed from shDSIF and control (no driver alone) EP animals by qRT-PCR. (Right) Agarose gel analysis of RT-PCR products from EP and LP animals with specific primers. (C) qRT-PCR analysis from EP (left) and LP (right) animals described in panel (B).]
undetectable, suggesting that NELF has a positive function in regulating Eig71Eh transcription. Other Brm complex targets were upregulated by knockdown of NELF (data not shown) (40). Thus, the Brm complex and NELF are both required for production of Eig71Eh 3' transcripts. In contrast, expression of shDSIF resulted in a 23-fold upregulation of Eig71Eh expression in EP-staged animals compared to controls (Figure 3B) suggesting a negative regulatory role. Similar upregulation was observed for other Eig genes (Figure 3B; data not shown). RT-PCR using exon-specific primers for Eig71Eh and Eig71Ei verified the transcripts were elevated at both 5'- and 3'-ends compared to control (Figure 3B gel analysis and Figure 3C qPCR measurements). Surprisingly, at the LP stage when transcripts are normally absent in WT, strong expression was observed upon shDSIF knockdown. Inappropriate transcription was also observed in the LP stage snr1E1 mutant (data not shown). Thus, loss of the negative pausing factor DSIF shows a similar enhancement of Eig transcription as snr1E1 mutant flies. The promiscuous transcription of Eig genes in both snr1E1 and in the shDSIF knockdown flies in late development suggests that stalling of PolII at distal exons in response to nucleosome impediments may be also required for the return to a transcriptionally inactive state (41).

SNR1 negatively regulates splicing

In human cell lines, the SWI/SNF complex regulates RNA splicing by decreasing the PolII transcription elongation rate resulting in increased accumulation of PolII on variant exons and by interacting directly with splicing factors (8,9). Since a decreased elongation rate represents a form of RNA polymerase pausing, we looked in snr1E1 mutants for altered splicing regulation. Our expectation was that if PolII was not appropriately paused in the snr1E1 mutant, an increased transcription elongation rate might result in a pool of RNA species with retained introns. Examination of Eig RNA accumulation at developmental stages subject to ecdysone regulation revealed that predominantly non-spliced RNA first accumulates at the WPP stage in WT animals (Figure 4A). Conversion to a smaller spliced form is most evident during the later EP stage even though a non-spliced RNA subpopulation persists. No RNA is detected later in pupariation (see LP, Figure 3C). Thus, the ratio of spliced to non-spliced Eig RNA steadily increases over developmental time, indicating that Eig splicing is developmentally regulated. Unexpectedly and in contrast to WT, analysis of RNA accumulation in the snr1E1 mutant revealed that the spliced form predominated at all developmental stages where the transcript was detected (Figure 4A and B). The largest differential between snr1E1 and WT was measured at the WPP stage, in which we observed 79-fold increased spliced product and 23-fold greater total expression. By early pupal development, the difference in spliced product in snr1E1 is 11-fold over WT with 28-fold greater total expression. Thus, the enhanced intron removal of Eig71Eh and Eig71Ei RNAs in the snr1E1 mutant reveals an unanticipated role for SNR1 in regulating splicing/RNA maturation.

Splicing of the Eig genes does not depend on the PolII elongation rate

It has been suggested that the mammalian hBRM (SWI/SNF) complexes might regulate splicing through ‘slowing down’ RNA Polymerase on gene templates (8).
RNA polymerases paused near gene promoters frequently exhibit Ser5P-CTD, with increased Ser2P-CTD observed upon release of the pause (42). The Ser2P-CTD form is processive and can associate with splicing factors. PolII associated with hBRM changes from a predominantly Ser2P-CTD status on CD44 gene constant exons to the Ser5P-CTD form on variant exons during alternative splicing events in HeLa cells, suggesting that mammalian SWI/SNF complexes participate in affecting CTD phosphorylation patterns on variant exons and contribute to the recruitment of elongation/pausing factors (8).

To account for the enhanced Eig splicing efficiency we observed, we first determined whether the phosphorylation pattern of the CTD was altered in the snr1E1 mutant EP animals. In WT animals, Ser5P-CTD was detectable in both 5’ (Figure 4C) and 3’ (Figure 4D) exonic regions of Eig71Eh. In striking contrast, a reciprocal profile is exhibited in the 3’ exonic region in snr1E1 compared to WT, as the PolII found there is predominantly enriched for Ser2P-CTD phosphorylation.

In previous studies, co-purification of RNA PolII with the mammalian SWI/SNF complex has been reported (43), though not in stoichiometric quantities. In addition, it has been reported that the association of PolIII with the Drosophila salivary gland chromosomes is drastically impaired in a brm mutant, suggesting that Brm complex remodeling is important for stabilizing PolIII on chromatin (4). The influence of the Brm complex on PolII could be direct through assisting PolII binding and processivity, or indirect through remodeling of nucleosomes ahead of the elongating polymerase, thus increasing chromatin accessibility. Based on the differences in PolIII CTD phosphorylation status we observed on the 3’ exon of Eig71Eh we questioned whether the enhanced Eig splicing in the snr1E1 mutant could be due to direct effects of the mutant Brm complex on PolIII processivity. To address this question, we examined whether the elongation rate of PolII was important for Eig71Eh splicing regulation using a ‘slow’ RNA polymerase mutant (RpII215C4) in Drosophila that exhibits a lower elongation rate, the human equivalent of which has been shown to affect alternative splicing (44,45). The single point mutation in the largest PolII subunit (RpII215C4) impairs its ability to read through intrinsic elongation blocks, resulting in defective movement of the polymerase (46). We found that the lower elongation rate in the ‘slow’ RNA PolII mutant resulted in reduced Eig71Eh expression compared to WT by the EP stage in development, the time point in which the spliced form of the Eig71Eh transcript typically predominates. As development proceeded from the WPP to EP stage in WT, total Eig expression increased 4-fold with a 47-fold increase in the spliced product. During this same developmental transition period in the RpII215C4 homozygous mutant, total Eig71Eh expression decreased by half with only a 7-fold enrichment in spliced transcript (Figure 5A). However, a fold comparison of spliced versus total Eig71Eh expression between the two stages in WT and RpII215C4 mutant revealed nearly identical ratios (Figure 5B). Importantly, since the Eig71Eh splicing pattern in the RpII215C4 slow RNA polymerase mutant animals was identical to WT, these results are most consistent with the view that PolIII elongation rate or processivity during transcription is not the crucial determinant for splicing outcome.

Chromatin in the snr1E1 mutant exhibits altered nuclease accessibility

Our results comparing the WT and slow mutant polymerases suggest that the presence of a nucleosomal barrier, rather than the rate of transcription elongation, contributes more directly to Eig splicing and removal of the barrier is dependent on Brm complex remodeling activity. If the changes in splicing that result from loss of SNR1 function are not due to alterations in PolIII processivity or rate, then the Eig71Eh splicing enhancement we observed in the snr1E1 mutant animals could be attributed to effects on nucleosome remodeling of the underlying chromatin, thereby altering interactions of PolII with the chromatin landscape. To test this hypothesis, we examined and compared the chromatin structure within the Eig71Eh genomic region in both WT and the snr1E1 mutant. Three nucleosomes have been mapped to the Eig71Eh genomic region (47). The first is centered at +122 within the first exon, the second is centered at +347 spanning the intron and proximal portion of the second exon, and the third is centered at +529 including the distal portion of second exon and transcription termination site (Figure 6A). Developmental associated changes in chromatin accessibility were examined by micrococcal nuclease digestion and quantitative CHART assay. The intergenic promoter and 5’ primer 1 region that includes 59nt upstream of the start of transcription were found to be highly accessible to nuclease digestion in both WT and snr1E1 mutant backgrounds (Figure 6B and C). The WT chromatin was largely inaccessible within the first exon (5’ primer 2 and 3 regions) around the mapped nucleosome site. There was partial accessibility within the 3’ exon and intron in WT CG and WPP stages, which then diminished by the EP stage. In contrast, Eig71Eh chromatin was substantially more accessible in snr1E1 compared to WT at all developmental stages. Thus, the increased nucleosome accessibility in the snr1E1 mutant would likely minimize barriers to transcription, allowing elongation by PolIII to proceed with little or no stalling. These results further strengthen the hypothesis that SNR1, acting within the context of the Brm complex, restrains PolII elongation through effects on chromatin. Thus, the transcription and splicing enhancement we observed in the snr1E1 mutant are most consistent with the misregulation of Brm complex chromatin remodeling events.

DISCUSSION

Approximately 20–30% of genes may be enriched for PolIII near their 5’-ends and release of the paused polymerase is a rate-limiting step for transcript completion (48,49). Paused polymerases allow for a rapid transcriptional response to stimuli, hormones and developmental cues
and are typically detected within 30–50 nt from the transcription start site (50–52).

We have identified a class of genes that appears to undergo two pausing/stalling events. The first pause is NELF and DSIF dependent and further stabilized by the Brm complex as evidenced by NELF and DSIF recruitment in both tissue culture and in vivo, NELF RNAi knockdown and Eig transcription regulation in vivo, as well as evidence which suggests that the Brm complex stabilizes the Ser5-CTD form of PolII in the vicinity of the transcription initiation region. We have also identified a second PolII elongation block within the transcribed region regulated by Brm complex remodeling functions that is mechanistically distinct from a typical
promoter proximal pause. Using a brm dominant negative conditional mutant, we found that chromatin remodeling is necessary for release of the second elongation block and subsequent completion of the 3′-end of the transcript, suggesting that promoter distal nucleosome structure acts as a barrier to elongation. A crucial finding from our work is that Brm complex remodeling function at this distal elongation barrier is regulated by the SNR1 subunit. In the present study, CHART analysis revealed that chromatin in the snr1E1 mutant was highly accessible even at developmental stages preceding hormone-dependent induction of transcription, leading us to speculate that a premature nucleosome remodeling event had occurred during early development as a consequence of the snr1E1 mutant’s inability to restrain Brm complex activities. As a result, nucleosomes in the Eig71Eh region would no longer be a barrier to future transcription in the snr1E1 mutant and elongation would proceed unimpeded once the NELF/DSIF-dependent promoter proximal pause is alleviated during early metamorphosis. These data are consistent with our previous findings that snr1 had an important role in transcription repression through effects on chromatin (5).

An unanticipated finding is that the Brm complex negatively regulates pre-mRNA splicing. Recent studies have highlighted the importance of positioned nucleosomes in exon definition and pre-mRNA splicing (53,54). Moreover, SWI/SNF remodeling complexes have been associated with splicing factors (8,9) and it has been suggested that hBrm promotes inclusion of alternative exons by decelerating PolII (8). If elongation rate is important for splice site recognition, then unimpeded transcription should produce a pool of unspliced message. Unexpectedly, we found that the snr1E1 mutant exhibits enhanced splicing of the Eig71Eh transcript at all developmental time points when transcripts are detected. In contrast to existing models (55), our data suggests that SNR1-dependent pausing of PolII enhances retention of the intron, producing unspliced transcripts in WT animals.

A reduced rate of transcription elongation by PolII associated with hBrm in alternative exons is accompanied by an alteration in the phosphorylation status of PolII from predominately Ser2P-CTD to Ser5P-CTD, thus resembling the status of paused polymerases. Our results with Brm complex knockdown indicated that the complex likely serves to stabilize the initiating form of PolII within the 5′ transcribed region. The Ser5P-CTD predominates in all regions of Eig71Eh in WT animals even though we detect Ser2P-CTD in both the 5′- and 3′-ends. We cannot differentiate whether transcription of the Eig genes occurs primarily with Ser5P-CTD or whether there is an eventual conversion to Ser2P-CTD as the chromatin becomes remodeled. In contrast, the snr1E1 mutant showed enrichment for Ser2P-CTD within the 3′ transcribed region, suggesting that SNR1 may directly affect associations of the Brm complex with PolII. However, studies employing a PolII ‘slow’ mutant in combination with the CHART analysis of the Eig region are consistent with the view that the effects on transcription elongation and splicing we observe in the snr1E1 mutant are most likely the result of alterations in the chromatin landscape. Full-length transcription with Ser5P-CTD is not unprecedented. Primary response genes use Ser5P-CTD PolII to produce unspliced full length transcripts in the absence of stimulation and thus lack cotranscriptional processing (56). The generation of processed transcripts in this case, however, required the signal-dependent recruitment of P-TEFb and Ser2P-CTD of PolII. In contrast, for the Eig genes we found that an ecdysone pulse is required even before unspliced transcripts can be detected. Thus, restraining PolII elongation through pausing by SNR1 at nucleosomal barriers to transcription and subsequent remodeling by the Brm complex ultimately determines the quality of the transcript produced. Our results strongly suggest that nucleosome remodeling regulation and chromatin architecture can play important roles in determining whether initial messages produced from a transcribed region will be co-transcriptionally processed.

Based on our findings we propose the following model (Figure 7). In WT blue gut larvae prior to the ecdysone pulse that induces metamorphosis, the Brm complex and PolII are localized within promoter regions, with the PolII CTD phosphorylated on Ser5 and paused near the promoter. This pause is likely NELF and DSIF dependent and Ser5P-CTD PolII is stabilized by the Brm complex. During the clear gut stage P-TEFb and additional Brm complex are recruited, DSIF and NELF become phosphorylated and the promoter proximal pause is released. The CTD converts to Ser2P and transcription proceeds along the template until PolII approaches and encounters a nucleosome within exon one when it decelerates and stalls, as the nucleosome acts as an intrinsic barrier to transcription. As a consequence of stalling, Ser5P-CTD predominates and splicing factors likely disengage from the polymerase. Brm complex remodeling of the nucleosome is necessary for subsequent PolII elongation and the SNR1 subunit functions to prevent inappropriate remodeling, thereby stabilizing the nucleosome barrier. As the ecdysone titer rises by the WPP stage, SNR1 inhibitory function on remodeling is alleviated, the stall is released and elongation proceeds with Ser5P-CTD PolII. Elongation by Ser5P-CTD is not processive and co-transcriptional splicing may not occur so the majority of the transcripts have retained introns. Several different mechanisms, not addressed in this work, may account for the transition from mainly unspliced to spliced transcripts as development proceeds. In one scenario, as the chromatin becomes remodeled, stalling is alleviated and during subsequent transcription a population of PolII is eventually phosphorylated on serine 2, and splicing factors associate. A pool of co-transcriptional spliced products is generated de novo, and continues to accumulate up until the EP stage. In the second scenario, introns are removed from pre-existing messages post-transcriptionally and spliced transcripts slowly accumulate through the EP stage.

In snr1E1 larval BG animals, we envision the first NELF- and DSIF-dependent pause occurs normally with a Ser5P-CTD paused at its promoter proximal position. After the ecdysone pulse at larval CG stage,
PolII becomes phosphorylated on serine 2 and transcription proceeds to the first nucleosome within exon one. In contrast to WT, as a consequence of increased nucleosome accessibility in \textit{snr1E1} animals (possibly due to a prior remodeling event earlier in development), Ser2P-CTD PolII does not stall at the first nucleosome. Furthermore, since there is no stall, PolII does not convert back to the Ser5P-CTD form. Elongation continues to be processive with Ser2P-CTD and proceeds with little or no impediments. RNA processing factors are engaged with Ser2P-CTD PolII so splicing occurs co-transcriptionally. Transcription continues unimpeded and the yield of fully spliced transcripts continues to increase until the EP stage.

What are the possible biological implications of SNR1’s role in the regulation of paused target genes? The Brm complex appears to promote a developmental delay in splicing of the \textit{Eig} genes resulting in the retention of introns during early transcription. Intron retention in pre-mRNAs is a post-transcriptional form of gene regulation that enhances gene expression (57) and promotes mRNA stability (58). Unspliced transcripts are enriched in quiescent hematopoietic stem cells (HSC) (59) and serve as a means to control HSC activation post-transcriptionally. Additionally, intron retention is a form of alternative splicing (60). However, translation of \textit{Eig} intron containing transcripts would generate non-functional proteins. Since \textit{Eig} genes encode components of the humoral immune response the regulation of paused transcripts by the Brm complex could result in a ready reserve of \textit{Eig} pre-mRNA that could be spliced, allowing for a rapid response to infection during the vulnerable metamorphic period when massive tissue histolysis occurs. Interestingly, recent transcriptome analyses in Drosophila indicate that ~6000 transcripts have retained introns, suggesting that intron retention may represent an important developmental mechanism of post-transcriptional gene regulation (61,62).

What are the implications of our findings for human disease? Highly aggressive malignant rhabdoid tumors (MRT) result from inactivation of \textit{hSNF5/Ini1/SMARCB1}, the human counterpart of Drosophila \textit{snr1} (20). Almost all cases of MRT are associated with bi-allelic loss of \textit{SMARCB1}, and inactivation of murine \textit{mSNF5} resulted in rapid tumor formation with 100\% penetrance that was accelerated by loss of p53 (63), classifying the gene as a potent tumor suppressor. We previously found that the patterning defects resulting from reduced SNR1 function could be compensated by reduced BRM activity (18,26,64), suggesting that rhabdoid tumors may result from oncogenic activation of hSWI/SNF targets. Our current data support this view and reveals that SNR1 has vital functions in regulating SWI/SNF complex targets through restraint of chromatin remodeling activities. These findings highlight the unique and essential role that the SNR1 and hSNF5/INI1 subunit plays in regulating target genes in normal development and cancer.

**SUPPLEMENTARY DATA**

Supplementary Data are available at NAR Online: Supplementary Table 1 and Supplementary Figure 1.

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