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Citation for published version:

Digital Object Identifier (DOI):
10.1093/nar/gkw801

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
Nucleic Acids Research

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Transcription-coupled changes to chromatin underpin gene silencing by transcriptional interference

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Received May 13, 2016; Revised August 17, 2016; Accepted August 31, 2016

ABSTRACT

Long non-coding RNA (IncRNA) transcription into a downstream promoter frequently results in transcriptional interference. However, the mechanism of this repression is not fully understood. We recently showed that drug tolerance in fission yeast Schizosaccharomyces pombe is controlled by IncRNA transcription upstream of the tgp1+ permease gene. Here we demonstrate that transcriptional interference of tgp1+ involves several transcription-coupled chromatin changes mediated by conserved elongation factors Set2, Clr6CII, Spt6 and FACT. These factors are known to travel with RNAPII and establish repressive chromatin in order to limit aberrant transcription initiation from cryptic promoters present in gene bodies. We therefore conclude that conserved RNAPII-associated mechanisms exist to both suppress intragenic cryptic promoters during genomic transcription and to repress gene promoters by transcriptional interference. Our analyses also demonstrate that key mechanistic features of transcriptional interference are shared between S. pombe and the highly divergent budding yeast Saccharomyces cerevisiae. Thus, transcriptional interference is an ancient, conserved mechanism for tightly controlling gene expression. Our mechanistic insights allowed us to predict and validate a second example of transcriptional interference involving the S. pombe pho1+ gene. Given that eukaryotic genomes are pervasively transcribed, transcriptional interference likely represents a more general feature of gene regulation than is currently appreciated.

INTRODUCTION

The organization of DNA into chromatin poses a significant physical challenge to eukaryotic transcription. In order to activate gene expression, chromatin must be opened in manner that allows transcription factors, co-activators, and RNA polymerase II (RNAPII) access to the DNA template (1). Active eukaryotic promoters therefore exhibit nucleosome-depleted regions immediately upstream of the transcription start site (TSS) (2). In contrast, developmentally regulated and stress-response gene promoters frequently display increased nucleosome density, which limits gene expression by masking key regulatory sequences in DNA when repression of such genes is required.

Numerous chromatin remodelers, histone chaperones, and chromatin-modifying activities cooperate to reorganize nucleosomes and permit transcription into gene bodies (3). These factors are often recruited directly or indirectly by histone modifications on nearby nucleosomes and/or by specific post-translational modifications to the C-terminal domain (CTD) of Rpb1, the largest subunit of RNAPII (4). For example, Ser-5 phosphorylation (Ser5P) on the Rpb1 CTD indirectly recruits histone methyltransferase (HMT) activity, which transfers three methyl groups on to lysine 4 of histone H3 (H3K4me3) at active promoters (5). This active histone mark is thought to simultaneously prevent the binding of repressive complexes and recruit histone acetyl transferases (HATs), which transfer acetyl groups to lysine residues on histone tails to bring about a more open chromatin structure that is permissive to transcription initiation (6–8). In contrast, histone deacetylase complexes (HDACs) remove acetyl groups from histone tails, while other HMTs deposit repressive histone marks (e.g. H3K9me2/3). Such activities create a much less accessible chromatin environment that silences gene expression, termed heterochromatin (9).

As RNAPII travels away from the initiation site, the Rpb1 CTD gradually loses Ser5P and acquires Ser2P (10,11). The Ser2P form of the Rpb1 CTD recruits the HMT Set2, which methylates H3K36 on nucleosomes positioned over the body of transcribed genes (12,13). The H3K36me3 mark serves as a docking site for Rpd3S (14), an HDAC that is co-transcriptionally recruited by direct interactions with RNAPII (15,16). Importantly, Rpd3S establishes a hypoacetylated chromatin environment over gene bodies to prevent aberrant transcription initiation from cryptic intragenic promoters (17,18). Thus, crosstalk between RNAPII
and the underlying chromatin tightly control chromatin states and gene expression.

Over the last decade, the location of complexes such as RNAPII and nucleosomes, including their variant modified forms, have been mapped genome wide in various organisms and cell types (19). Such studies complemented transcript-profiling analyses and revealed that eukaryotic genomes are pervasively transcribed by RNAPII (20). Apart from just generating messenger RNAs (mRNAs) from protein-coding genes, we now know that RNAPII also synthesizes long non-coding RNAs (lncRNAs) that overlap protein-coding genes on the sense and antisense strands, from within introns, and from intergenic regions (21). Although mRNAs and lncRNAs are both produced by RNAPII, these transcripts have notably different fates. Unlike stable mature mRNAs that are exported to the cytoplasm for protein synthesis, lncRNAs remain predominantly nuclear and are often rapidly degraded by RNA decay pathways (22). In addition, most lncRNAs are poorly conserved in primary nucleotide sequence when compared with mRNAs (23). While low steady-state levels and poor sequence conservation are obvious challenges for characterizing lncRNA functions, substantial progress has been made into assigning biological functions to an accumulating number of individual lncRNAs (24). However, this difficult task is confounded by the fact that subsequent studies regularly overturn the interpretations of previous reports (25,26), making lncRNAs arguably the least understood and most contentious products of eukaryotic genomes.

An emerging paradigm is that many lncRNAs contribute to the regulation of gene expression. For example, several individual lncRNAs have been reported to interact with and/or direct chromatin-modifiers to control gene expression, while others have been proposed to recruit transcriptional activators, repressors, or components of the transcription machinery itself (27). Although there is evidence that some lncRNAs regulate distant genes in trans, lncRNAs more frequently influence adjacent gene expression in cis. Notably, antisense transcription can compete with transcription on the sense strand to regulate gene expression (28). Functionally, this balance of sense and antisense transcription is required to control the expression of numerous meiotic and stress-response genes in different yeast species (29,30). The act of intergenic lncRNA transcription can also have a profound impact on the expression of nearby genes. For example, the activation of the fer1p+ gene in fission yeast (Schizosaccharomyces pombe) occurs in response to glucose starvation and requires upstream lncRNA transcription to evict promoter-associated repressors and permit transcription factor binding (31,32). Conversely, a phenomenon known as ‘transcriptional interference’ often involves transcription of lncRNAs into downstream gene promoters to repress their expression. While this form of gene repression has been documented in many organisms, ranging from prokaryotes to higher eukaryotes (33–39), a comprehensive molecular understanding of the mechanism is lacking. Perhaps the best-studied eukaryotic example of transcriptional interference involves lncRNA transcription into the budding yeast S. cerevisiae SER3 gene promoter. In serine-rich growth conditions, the act of lncRNA transcription prohibits transcription factor access to repress SER3 expression (36). Additional examples of gene regulation by the act of lncRNA transcription, rather than by the RNAs produced (40), underscore the biological significance of transcribing lncRNAs, even if the RNA products are themselves not functional.

Recently we reported that the S. pombe permease gene tgp1+ is regulated by transcriptional interference in response to changes in extracellular phosphate levels (34). While lncRNA transcription into the tgp1+ promoter is associated with increased nucleosome density and tgp1+ repression does not require the RNA interference (RNAi) pathway or heterochromatin components, little is known about the mechanism that mediates this repression. Here we show that numerous conserved transcriptional elongation factors (including Set2, the Rpd3S homolog Clr6CII, and histone chaperones Spt6 and FACT) are required to establish a repressive chromatin environment over the tgp1+ promoter in the wake of upstream initiating lncRNA transcription. Furthermore, the identification of key factors associated with transcriptional interference at the tgp1+ locus allowed us to demonstrate that a second phosphoreponse gene (pho1+) is regulated by a similar mechanism. We conclude that the mechanism of transcriptional interference appears to be well conserved between S. pombe, which retains active RNAi, and the distantly related budding yeast S. cerevisiae, which lacks the RNAi pathway. Thus, RNAi does not play a role in the mechanisms that repress genes by transcriptional interference. Rather, upstream lncRNA transcription-coupled changes in promoter chromatin status underpin gene silencing by transcriptional interference in two evolutionarily distant eukaryotes.

**MATERIALS AND METHODS**

**Yeast strains, plasmids, and standard techniques**

*S. pombe* strains used in this study are listed in Supplementary Table S1. Standard methods were used for fission yeast growth, genetics and manipulations (41). All strains were grown in YES medium (Yeast extract plus supplements) at 32°C, unless otherwise indicated. For phosphate starvation experiments, cells were grown to mid-log phase in EMMS (Edinburgh minimum medium with supplements) (Formedium), washed twice in dH2O, and then grown for indicated times in EMMS without phosphates (Formedium). *nmt1-nc-tgp1* cells were grown in phosphate-rich PMG (Pombe minimal glutamate) medium in the presence or absence of thiamine (15 μM). Endogenous genetic manipulations were carried out by lithium acetate transformation. Selections were performed on PMG/agar plates with according auxotrophy or on YES/agar plates with appropriate antibiotic(s) and grown at 32°C. Colony PCR confirmed all endogenous genetic modifications and crosses. For spotting assays, serial (1:4) dilutions of equal numbers of cells were spotted onto YES/agar and grown at 32°C. For drug-sensitivity experiments, cells were spotted onto YES/agar with vehicle (DMSO) or TBZ (20 μg/ml), HU (10 mM), caffeine (15 mM).
Chromatin immunoprecipitation

Cells were grown to mid-log phase at 32°C. For phosphate starvation experiments, cells in mid-log phase were washed twice in H2O before being grown in EMSS without phosphates (–PO4) for 6 h. For temperature sensitive strains, cells were shifted from 32°C to the restrictive temperature of 36°C for 1 h. ChIP was performed essentially as described (42). Briefly, cells were fixed with 1% paraformaldehyde (PFA) for 15 min at room temperature. Cells were lysed by bead beating (Biospec Products) and sonicated using a Bioruptor (Diagenode) sonicator at 5°C by bead beating (Biospec Products) and sonicated using a Bioruptor (Diagenode) sonicator at 5°C on high for a total of 30 min (30 s ON/OFF cycles). 2 μl Ser2P Rpb1 CTD antibody (abq095; Abcam), 2 μl H3 antibody (ab1791; Abcam), 2 μl H3K9ac antibody (39137; Active Motif), 2 μl H4K12ac antibody (39165; Active Motif), 2 μl H3K36me3 antibody (61101; Active Motif), 1 μl H3K9me2 antibody (5.1.1), and 2 μl GFP antibody (A11122; Life Technologies) were used per ChIP. Quantitative analysis was performed by qPCR.

RNA analysis

RNA was isolated from S. pombe using RNeasy Mini- or Midi-Kits as per manufacturer’s instructions (Qiagen). For quantitative reverse transcriptase PCR (RT-qPCR) experiments, first strand cDNA synthesis was performed on Turbo DNase (Life Technologies) treated RNA using random hexamers and Superscript IV (Invitrogen) as per manufacturer’s instructions. Negative controls lacking the reverse transcriptase enzyme (-RT) were performed alongside all RT-qPCR experiments. Quantitative analysis was performed by qPCR. To make RNA probes for northern analysis, DNA fragments specific to target transcripts were amplified from genomic DNA by PCR and gel-purified using the Wizard® SV Gel and PCR Clean-Up System (Promega). The T7 promoter was equipped at the end of the DNA fragment using an oligonucleotide containing a T7 promoter sequence at the 5'-end (TAATACGACT CACATATAGGGAGA). The T7 promoter containing PCR products were transcribed in vitro using the MaxiScript T7 Kit (Ambion) to produce UTP-32P-labelled RNA probes following the manufacturer’s instructions. Unincorporated radionucleotides were removed using NucAway Spin columns (Life Technologies) according to manufacturer’s instructions. The UTP-32P-labelled RNA probes were hybridized to membranes overnight in church buffer (0.5 M Na2HPO4 pH 7.2, 1 mM EDTA, 7% SDS) at 68°C in a rotating oven. Hybridized membranes were washed twice in a pre-warmed buffer containing 2× SSC and 0.1% SDS for 30 min at 68°C followed by two washes in a buffer containing 0.5× SSC and 0.1% SDS for 15 min at 68°C. To detect transcripts, northern blots were analyzed after 1–2 days of exposure on a Phosphor Screen (Molecular Dynamics) using a Typhoon Phosphorimagery (GE Healthcare Life Sciences).

qPCR

Primers used in this study are listed in Supplementary Table S2. Quantitative real-time PCR (qPCR) was performed using SYBR Green on a Roche Lightcycler. Data was analyzed with LightCycler 480 Software 1.5.0.39. RT-qPCR levels were calculated by normalizing product of interest to an internal reference gene (act1). Expression levels were expressed relative to levels detected in wild-type cells. ChIP enrichments were calculated as the ratio of product of interest from IP sample normalized to the corresponding input sample and expressed as %IP. Error bars represent standard deviation resulting from at least three independent replicates.

RESULTS

nc-tgpl transcription establishes Set2-dependent H3K36me3 over the tgpl+ promoter

Maintaining stable cellular phosphate levels is a challenge since inorganic phosphate availability can fluctuate unpredictably. To combat this, organisms have evolved complex strategies to sense extracellular phosphate levels and integrate this information into a transcriptional response that increases survival. The glycerophosphodiester permease gene tgpl+ is a core component of the phosphate regulon in S. pombe and is activated in phosphate-limited conditions by the Pho7 transcription factor (43). In addition, Pho7 has been shown to bind directly to phosphate regulated gene promoters, such as tgpl+ and phol+ promoters (43). When external phosphate levels are high, an upstream exosome-sensitive lncRNA termed nc-tgpl is transcribed in tandem with the tgpl+ gene and corresponds with increased nucleosome density and decreased Pho7 binding over the tgpl+ promoter (Figure 1A) (34,44,45). Although this repression occurs in an RNAi and heterochromatin-independent manner, it is possible that other transcription-coupled changes in chromatin status contribute to transcriptional interference at the tgpl+ locus.

To assess the distribution of the elongating form of RNAPII over the tgpl+ locus in response to phosphate availability, the levels of Ser2 phosphorylated RNAPII (Rpb1-Ser2P) were assessed by quantitative ChIP in wild-type cells grown in the presence or absence of phosphate. These analyses revealed the presence of increased levels of Rpb1-Ser2P over the tgpl+ promoter in phosphate-replete cells (i.e. when the repressive lncRNA nc-tgpl is actively transcribed), compared to phosphate-starved cells (Figure 1B–D). This finding is consistent with the fact that following phosphate starvation tgpl+ induction is accompanied by reduced nc-tgpl transcription (34).

It is well established that the elongating Ser2P form of RNAPII recruits the H3K36 HMT Set2 (12,13). Examination of available ChIP-seq data revealed enriched levels of Set2 at the tgpl+ promoter in repressed phosphate-rich conditions (Supplementary Figure S1) (46), suggesting Set2 might contribute to tgpl+ regulation. Indeed, active nc-tgpl transcription in phosphate-replete cells correlated with increased levels of H3K36me3 over the tgpl+ promoter region (Figure 1E). To determine if nc-tgpl transcription into the tgpl+ promoter is required to establish Set2-dependent H3K36me3, we performed these analyses in cells lacking the promoter that drives nc-tgpl transcription (1343Δ). This manipulation prevented nc-tgpl transcription in phosphate-rich conditions and results in con-
Figure 1. nc-tgp1 transcription increases H3K36me3 levels over the tgp1+ promoter. (A) Schematic representation of the tgp1+ locus, including the nc-tgp1 lncRNA gene located immediately upstream. In phosphate-rich conditions (+PO4) the tgp1+ gene is repressed by nc-tgp1 transcription into the tgp1+ promoter. In contrast, reduced nc-tgp1 transcription, in response to phosphate starvation (−PO4) or following deletion of the nc-tgp1 promoter (1343Δ), permits tgp1+ induction (34). Primer pairs spaced over the tgp1+ locus are displayed below. (B and C) RT-qPCR analysis of tgp1+ mRNA levels (primer pair 1) and upstream nc-tgp1 lncRNA levels (primer pair 5) in wild-type cells grown in the presence or absence of phosphate, as well as in phosphate-replete 1343Δ cells. (D) ChIP-qPCR analysis of the Ser2P form of elongating RNAPII over the tgp1+ locus in response to changes in phosphate availability/nc-tgp1 transcription. (E) ChIP-qPCR analysis of H3K36me3 over the tgp1+ locus in response to changes in phosphate availability/nc-tgp1 transcription. Error bars represent standard deviation resulting from at least three independent experiments.

Constitutive tgp1+ expression (Figure 1D). Consistent with H3K36me3 being deposited during nc-tgp1 transcription elongation, removal of the nc-tgp1 promoter resulted in significantly reduced H3K36me3 levels upstream of the tgp1+ gene in the presence of phosphate (Figure 1E). Additionally, replacement of the nc-tgp1 promoter with a strong thiamine-repressive promoter (nmt1) brings nc-tgp1 under the control of thiamine, rather than phosphate. In these cells, Rpb1-Ser2P and H3K36me3 levels were significantly higher in the absence of thiamine (i.e. when nmt1-nc-tgp1 is transcribed) than in cells grown in the presence of thiamine. This manipulation demonstrates that nc-tgp1 transcription from even a heterologous promoter is sufficient to cause H3K36me3 to accumulate over the tgp1+ promoter. Together, these results demonstrate that the act of nc-tgp1 transcription stimulates Set2-dependent deposition of H3K36me3 over the tgp1+ promoter.

Loss of H3K36 methylation induces tgp1+ expression

Having established that the act of transcribing nc-tgp1 into the tgp1+ promoter directs the accumulation of H3K36me3, we next sought to determine if the presence of this mark plays a direct role in curbing tgp1+ expression. We measured tgp1+ mRNA levels in wild-type cells grown in the presence or absence of phosphate as well as in phosphate-replete cells lacking H3K36 methylation (i.e. set2Δ cells). As expected, northern analysis detected the tgp1+ mRNA in phosphate-starved cells but not cells grown in the presence of phosphate (repressed condition) (Figure 3A). Notably, elevated levels of the tgp1+ mRNA were detected in set2Δ cells grown in repressive phosphate-rich media (Figure 3A). Quantitative analyses confirmed a ~7-fold increase in tgp1+ expression in cells lacking Set2 (Figure 3B). This finding confirms microarray data indicating that tgp1+ expression increases in set2Δ cells (48). While this increase in tgp1+ mRNA levels is indeed significant, it is substantially lower than that detected in phosphate-starved wild-type cells (Figure 3A), or phosphate-replete 1343Δ cells (Supplementary Figure S1), suggesting that other factors must cooperate with Set2 to mediate full repression of tgp1+.

Nonetheless, these results suggest that Set2 activity contributes to the efficient silencing of tgp1+ mediated by upstream nc-tgp1 transcription.

Constitutive tgp1+ expression renders S. pombe cells hypersensitive to growth in the presence of various compounds (34), such as the microtubule destabilizing drug thiabendazole (TBZ), DNA-synthesis inhibitor hydroxyurea (HU) and caffeine (CAF), a potent inhibitor of cyclic AMP phosphodiesterase. This tgp1+-dependent phenotype must result from greater drug uptake in cells expressing elevated...
Figure 2. nmt1-driven nc-tgp1 transcription directs the accumulation of H3K36me3 over the tgp1+ promoter in response to thiamine. (A) Replacing the nc-tgp1 promoter with a strong thiamine-regulated nmt1 promoter brings nc-tgp1 transcription under the control of thiamine. (B) ChIP-qPCR for Ser2P, the elongating form of RNAPII, over the tgp1+ locus in nmt1-nc-tgp1 cells grown in the presence or absence of thiamine. (C) ChIP-qPCR for H3K36me3 levels over the tgp1+ locus in nmt1-nc-tgp1 cells grown in the presence or absence of thiamine. Error bars represent standard deviation resulting from at least three independent replicates.

Figure 3. Set2 represses tgp1+ expression. (A) Northern analysis of tgp1+ mRNA levels in wild-type cells grown in the presence or absence of phosphate and set2Δ cells grown in the presence of phosphate. (B) RT-qPCR analysis of tgp1+ mRNA levels in phosphate-replete wild-type and set2Δ cells. Error bars represent standard deviation resulting from three independent experiments. (C) Serial dilutions of wild-type cells, 1343Δ (nc-tgp1 promoter deleted; constitutive tgp1+ expression), the tgp1Δ1343Δ double mutant, set2Δ, and the tgp1Δset2Δ double mutant spotted on non-selective YES medium or in the presence of the following compounds: thiabendazole (TBZ: 20 μg/mL), hydroxyurea (HU: 10 mM), or caffeine (CAF: 15 mM).
levels of the \( tgp1^{+} \) permease. Interestingly, in our growth assays we found that \( set2^{\Delta} \) cells are also sensitive to growth in the presence of these three compounds (Figure 3C). Deletion of the \( tgp1^{+} \) gene in the \( set2^{\Delta} \) background revealed that cells lacking both \( T_{gp1} \) and \( Set2 \) (\( tgp1^{\Delta} set2^{\Delta} \)) were more resistant to growth in the presence of TBZ, HU, and CAF than cells lacking \( Set2 \) alone (Figure 3C). Thus, increased \( tgp1^{+} \) expression contributes to the increased drug sensitivity observed in \( set2^{\Delta} \) cells. Overall, these findings support a role for lncRNA transcription-coupled Set2 recruitment in the repression of \( tgp1^{+} \) by transcriptional interference.

HDAC Clr6CII participates in lncRNA-dependent repression of \( tgp1^{+} \)

Histone acetylation promotes an open chromatin configuration that accompanies transcriptional activation (48). We predicted that \( H3K36me3 \) deposition over the \( tgp1^{+} \) promoter during \( nc-tgp1 \) transcription would recruit the \( S. \ pombe \) Rpd3S complex (termed Clr6CII) and that this would result in hypacetylated chromatin over the region upstream of \( tgp1^{+} \). ChIP analyses revealed that the levels of histone acetylation (\( H3K9ac \) and \( H4K12ac \)) over the \( tgp1^{+} \) promoter were highest in cells with active \( tgp1^{+} \) expression (phosphate-starved cells), while much lower levels of histone acetylation were observed in wild-type cells grown in the presence of phosphate (Figure 4A and Supplementary Figure S1). In addition, the partial activation of \( tgp1^{+} \) expression in \( set2^{\Delta} \) cells was also accompanied by increased histone acetylation levels over the \( tgp1^{+} \) promoter (Figure 4A), suggesting histone deacetylation is involved in mediating transcriptional interference at the \( tgp1^{+} \) gene. To directly test if Clr6CII promotes transcriptional repression, \( tgp1^{+} \) mRNA levels were measured in cells lacking \( Pst2 \) or \( Alp13 \), two critical subunits of the HDAC Clr6CII complex also display increased levels of \( tgp1^{+} \) expression (Supplementary Figure S2) (46). Therefore, a prime candidate was the \( pho1^{+} \) gene, which exhibits exosome-sensitive lncRNA transcription that initiates upstream and overlaps the phosphate-regulated \( pho1^{+} \) gene (Figure 6A) (45). Impaired exosome-mediated degradation of this overlapping lncRNA was previously reported to result in the accumulation of \( H3K9 \) methylation at the \( pho1^{+} \) gene (45,51). Nevertheless, the mechanism of \( pho1^{+} \) regulation in wild-type cells remain unclear since genome-wide analyses of \( H3K9 \) methylation do not detect this repressive heterochromatin mark at the \( pho1^{+} \) gene in wild-type cells grown under normally repressive phosphate-rich conditions (52–54). In contrast, ChIP-seq analysis reveal that \( Set2 \) is enriched upstream of the \( pho1^{+} \) gene in phospate-rich media (Supplementary Figure S2) (46). Therefore, a mechanism of transcriptional interference similar to that observed for \( tgp1^{+} \) regulation might also be involved in silencing \( pho1^{+} \) expression in wild-type cells grown in the presence of phosphate.

\( pho1^{+} \) repression is mediated by transcriptional interference

The above analyses demonstrate that \( tgp1^{+} \) regulation by upstream lncRNA transcription requires several conserved transcription elongation factors to direct the assembly of repressive chromatin over the \( tgp1^{+} \) promoter. To identify other genes that may be similarly regulated we surveyed other nutritionally regulated genes in \( S. \ pombe \) that display similar hallmarks of transcriptional interference (e.g. upstream initiation of lncRNA, elevated \( Set2 \) levels at promoters, etc.). A prime candidate was the \( pho1^{+} \) gene, which exhibits exosome-sensitive lncRNA transcription that initiates upstream and overlaps the phosphate-regulated \( pho1^{+} \) gene (Figure 6A) (45). Impaired exosome-mediated degradation of this overlapping lncRNA was previously reported to result in the accumulation of \( H3K9 \) methylation at the \( pho1^{+} \) gene (45,51). Nevertheless, the mechanism of \( pho1^{+} \) regulation in wild-type cells remain unclear since genome-wide analyses of \( H3K9 \) methylation do not detect this repressive heterochromatin mark at the \( pho1^{+} \) gene in wild-type cells grown under normally repressive phosphate-rich conditions (52–54). In contrast, ChIP-seq analysis reveal that \( Set2 \) is enriched upstream of the \( pho1^{+} \) gene in phosphate-rich media (Supplementary Figure S2) (46). Therefore, a mechanism of transcriptional interference similar to that observed for \( tgp1^{+} \) regulation might also be involved in silencing \( pho1^{+} \) expression in wild-type cells grown in the presence of phosphate.

Consistent with \( pho1^{+} \) regulation by transcriptional interference, our analyses demonstrate that \( pho1^{+} \) expression was induced in phosphate-replete cells lacking \( Set2 \) (Figure 6D). We note that increased \( pho1^{+} \) transcription is also evident in expression profiling data from \( set2^{\Delta} \) cells (47). In addition, \( pho1^{+} \) mRNA levels similarly accumulated in cells lacking the activity of Clr6CII (\( pst2^{\Delta} \) or \( alp13^{\Delta} \)), \( Set6 \) (\( sp6^{\Delta} \) and FACT (\( sp16^{\Delta} \) or \( poh3^{\Delta} \)) (Figure 6E, and Supplementary Figure S2). These analyses show that
Figure 4. Clr6CII HDAC activity is required to suppress tgp1+ expression. (A) The levels of acetyl-histones (H3K9ac) at the tgp1+ promoter primer pair 3 (see Figure 1A) were measured by ChIP-qPCR in wild-type cells grown in the presence or absence of phosphate and set2Δ cells grown in the presence of phosphate. (B) RT-qPCR analysis of tgp1+ mRNA levels in phosphate-replete wild-type cells and cells lacking either Pst2 or Alp13, each of which are critical HDAC subunits of Clr6CIIpd3S. Error bars represent standard deviation resulting from three independent replicates. (C) Northern analysis of tgp1+ mRNA levels in wild-type cells grown in the presence or absence of phosphate and in phosphate-replete cells with compromised Clr6CIIpd3S activity (pst2Δ).

Figure 5. Spt6 and FACT are required to suppress tgp1+ expression. (A) Histone density over the tgp1+ locus was measured by histone H3 ChIP-qPCR experiments in phosphate-replete wild-type cells, Stp6 mutant cells (spt6-1), and cells lacking the activity of the FACT subunit Spt16 (spt16-18) grown for 1 h at the restrictive temperature of 36°C. (B) Northern analysis of tgp1+ mRNA levels in wild-type cells, 1343Δ cells with constitutive tgp1+ expression (i.e. cells lacking the promoter that drives repressive nc-tgp1 transcription), and in cells with compromised Spt6 or FACT activity grown at the restrictive temperature for 1 h. (C) RT-qPCR analysis of tgp1+ mRNA levels in phosphate-replete wild-type cells, spt6-1 cells, and spt16-18 cells grown at the restrictive temperature for 1 h. Error bars represent standard deviation resulting from at least three independent replicates.
**DISCUSSION**

The orientation of closely arranged protein-coding genes in dense yeast genomes means that most acts of transcription impinge on the activity of nearby genes. For instance, non-coding antisense transcripts emanating from bidirectional gene promoters can interfere with the activation of adjacent genes and insulate against interfering acts of transcription (55,56). While networks of closely arranged genes are less prevalent in higher eukaryotes, intergenic regions are still pervasively transcribed (57). In fact, pervasive eukaryotic transcription implies that transcriptional interference mediated by intergenic IncRNA transcription might be a much more general feature of gene regulation in higher eukaryotes than is currently appreciated. Individual examples of this phenomenon have been observed in diverse biological
Figure 7. lncRNA transcription regulates \textit{pho1} by transcriptional interference. (A) Schematic depiction of the \textit{pho1} locus, including the lncRNA \textit{prt} gene that occupies the \textit{pho1} promoter and overlaps the gene body downstream. Primer pairs spaced over the \textit{pho1} locus are displayed below. (B) ChIP-qPCR for Ser2P, the elongating form of RNAPII, over the \textit{pho1} locus in response to changes in phosphate availability. (C) Nucleosome density over the \textit{pho1} locus was measured by histone H3 ChIP-qPCR experiments in wild-type cells grown in the presence or absence of phosphate. (D) ChIP-qPCR for H3K36me3 levels over the \textit{pho1} locus in phosphate-replete and phosphate-starved wild-type cells. (E) Histone density was measured by histone H3 ChIP-qPCR experiments in wild-type cells, Stp6 mutant cells (\textit{spt6-1}), and FACT mutant cells (\textit{spt16-18}) grown in the presence of phosphate and at the restrictive temperature of 36°C. Error bars represent standard deviation resulting from at least three independent replicates.

systems ranging from free-living unicellular yeasts to multicellular organisms, including mammals (33,34,36–38,58–60). In addition, the genetic disease alpha thalassemia is caused by an intergenic single nucleotide polymorphism that creates a new promoter and initiates novel transcription that interferes with the expression of the alpha globin gene downstream (61). Transcriptional interference also plays a role in controlling human immunodeficiency virus-1 (HIV-1) latency (62,63). More recently, cells infected with herpes simplex virus-1 (HSV-1) and renal cancer cells have been observed to display defects in transcription termination that result in genome-wide read-through transcription (64,65), which is capable of repressing adjacent genes by transcriptional interference (66). Collectively, these findings suggest that transcriptional interference is a widely conserved mechanism for modulating gene expression and plays an important role in human health and disease. Nevertheless, it is remains unclear how widespread concerted gene regulation by this specific mechanism actually is. In order to determine the prevalence of transcriptional interference in eukaryotic genomes, greater mechanistic insight is required in order to pinpoint the features associated with this elusive process.

Research from diverse organisms suggests that transcription elongation is itself too rapid to mediate strong repression of downstream genes (67). In bacteria, interference between two transcription units is achieved primarily by upstream transcription pausing, which occludes underlying promoter sequences (68). While most transcription factors in prokaryotes recognize long sequence motifs (up to 30 nt or longer) (69), eukaryotic transcription factors generally recognize much shorter motifs (70). Such short regulatory elements could more easily escape occlusion by stalled RNAPII alone, which might explain why examples of transcriptional interference in eukaryotes frequently implicate transcription-associated changes in chromatin. For example, repression of the \textit{S. cerevisiae} \textit{SER3} gene by transcriptional interference requires histone chaperones, such as Spt6 and FACT, to bring about increased nucleosome density over the \textit{SER3} promoter and prevent transcription factor binding (71). Here we show that the conserved counterparts of Spt6 and FACT are required to mediate transcriptional interference of two genes in \textit{S. pombe} (\textit{tgp1} and
Figure 8. Model for transcriptional interference at tgp1\(^+\) and pho1\(^+\) in S. pombe. (A) Reduced upstream lncRNA transcription corresponds with decreased nucleosome density over the tgp1\(^+\) and pho1\(^+\) promoters to permit expression of these phosphate response genes following phosphate-starvation. (B) In phosphate-replete conditions, lncRNA transcription upstream of tgp1\(^+\) and pho1\(^+\) results in transcription-coupled deposition of Set2-dependent H3K36me3 and recruitment of the Clr6 HDAC (Clr6CII). In addition, histone chaperones Spt6 and FACT travel with RNAPII and reorganize nucleosomes during lncRNA transcription in order to limit Pho7 transcription factor binding and suppress downstream gene expression.

This requirement for Spt6 and FACT is consistent with earlier observations demonstrating that both factors disassemble/reassemble nucleosomes in a manner that reduces transcription from cryptic promoters within active transcription units (50). Moreover, Spt6 facilitates Set2-dependent H3K36 methylation (46,72), which is required for optimal repression of tgp1\(^+\) and pho1\(^+\) by transcriptional interference (Figures 3 and 6). The requirement for Set2 to mediate transcriptional interference in S. cerevisiae is less clear. While repression of the S. cerevisiae IME1 gene requires interfering transcription-coupled H3K36me3 deposition by Set2 (60), suppression of the SER3 gene does not require Set2 activity (71). To explain this discrepancy, it has been proposed that the lncRNA upstream of SER3 is too short (only ~500 nt) to allow the transcriptional elongation phase of RNAPII to deposit sufficient H3K36me3 over the SER3 promoter (60). This explanation is supported by the fact that Set2/Rpd3S predominantly limits intragenic transcription initiation on longer genes (73). Our data strengthen the concept that Set2 is required for transcriptional interference involving longer lncRNAs since the transcripts mediating Set2-dependent tgp1\(^+\) and pho1\(^+\) repression are each initiated ~2 kb upstream of their respective target gene (34,51). It is also possible that the act of RNAPII progression through a promoter may contribute to the displacement and/or limit transcription factor binding, however, our findings in S. pombe along with those in the evolutionarily distant S. cerevisiae demonstrate that transcription elongation-associated chromatin changes are pivotal for mediating transcriptional interference in eukaryotes.

Since numerous elongation factors that are known to prevent intragenic transcription initiation also contribute to the effectiveness of gene silencing by transcriptional interference, we suggest that gene promoters occluded by upstream initiating transcripts are in essence themselves cryptic promoters residing within the interfering transcription unit. Importantly, elongation factors are widely conserved in eukaryotes. A prediction therefore is that the basic mechanistic features of transcriptional interference revealed in both S. pombe and S. cerevisiae, two highly divergent yeast species separated by hundreds of millions of years of evolution, will also be conserved in metazoans. Indeed, Spt6 and FACT have already been implicated in transcriptional interference of the Ubx gene in Drosophila (38), while H3K36 methylation appears to contribute to transcriptional interference in mammals (33,64). Extensive analyses are required to identify additional components of the regulatory circuit that promotes transcriptional interference. Such information will provide a much more comprehensive understanding of the underlying mechanism, in addition to explaining mechanistic variability (such as the involvement or not of Set2). Furthermore, conserved features of transcriptional interference might provide useful hallmarks for assessing how widespread this regulatory mechanism truly is in various eukaryotic genomes. Maps of the genomic locations of specific transcription-coupled histone modifications along with factors known to be involved in mediating transcriptional interference (e.g. Set2, Spt6, FACT) should help to uncover additional examples of genes regulated by this mechanism. Complementary methods, such as native elongating transcript sequencing (NET-seq), which allows nascent transcript locations to be determined (74), should also facilitate the identification of novel interfering upstream transcripts. Together, we expect that such approaches should provide information regarding the potential scale and prevalence of transcriptional interference in different genomes. Finally, examples of transcriptional interference associated with diverse human diseases (61–65) imply that a more comprehensive understanding of the underlying mechanism of this form of gene regulation should better inform the molecular basis of pathologies that result from alterations in transcription dynamics.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

ACKNOWLEDGEMENTS

We would like to thank Alison Pidoux, Manu Shukla, and Sharon White for their technical expertise and input. We are grateful to Takeshi Urano for the H3K9me2 (5.1.1) antibody and Dennis Wykoff for strains.

FUNDING

Darwin Trust of Edinburgh (to R.A.); The Centre for Cell Biology is supported by core funding from the Wellcome Trust.
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