A Toggle Involving Cis-Interfering Noncoding RNAs Controls Variegated Gene Expression in Yeast

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Toggle involving cis-interfering noncoding RNAs controls variegated gene expression in yeast

Stacie L. Bumgarner, Robin D. Dowell, Paula Grisafi, David K. Gifford, and Gerald R. Fink

The identification of specific functional roles for the numerous long noncoding (nc)RNAs found in eukaryotic transcriptomes is currently a matter of intense study amid speculation that these ncRNAs have key regulatory roles. We have identified a pair of cis-interfering ncRNAs in yeast that contribute to the control of variegated gene expression at the FLO11 locus by implementing a regulatory circuit that toggles between two stable states. These capped, polyadenylated ncRNAs are transcribed across the large intergenic region upstream of the capped, polyadenylated ncRNAs are transcribed across the large regulatory circuit that toggles between two stable states. These capped, polyadenylated ncRNAs are transcribed across the large intergenic region upstream of the FLO11 ORF. As with mammalian long intervening (linc)ncRNAs, these yeast ncRNAs (ICR1 and PWR1) are themselves regulated by transcription factors (SF11 and Flo8) and chromatin remodelers (Rpd3L) that are key elements in hypothetical transitions in yeast. The mechanism that we describe explains the unanticipated role of a histone deacetylase complex in activating gene expression, because Rpd3L mutants force the ncRNA circuit into a state that silences the expression of the adjacent variegating gene.

FLO11 | intergenic transcription | Rpd3L histone deacetylase | transcriptional interference | regulatory RNAs

Recent genome-wide studies of eukaryotic transcriptional landscapes in yeast, mice, and humans have revealed extensive activity in regions previously expected to be transcriptionally inert (1–13). A subset of these noncoding (nc)RNAs are long ncRNAs transcribed across intergenic regions. In mammalian cells, transcription of numerous such long intervening (linc)ncRNAs is regulated by the binding of transcription factors critical to mammalian development, including Oct4, Nanog, and Sox2 (5). This observation has engendered speculation that mammalian lincRNAs have key roles in development by regulating expression of protein-coding ORFs via mechanisms distinct from the Dicer-dependent RNAi pathway (5, 14–16). However, experiments that would conclusively test the postulated roles for the vast majority of eukaryotic long ncRNAs have not yet been performed (5). Careful interrogation of specific loci is necessary to distinguish between ncRNAs that represent mere transcriptional “noise” and those that have a bona fide role in regulation and development (17–22). Long intergenic ncRNAs also exist in yeast, and despite the tractability of this model system, most remain uncharacterized.

Recent studies of an intergenic ncRNA that regulates the SER3 gene (23, 24), and other subsequent investigations at specific genes in yeast (25–27), have begun to reveal mechanisms, alternative to the RNAi pathways, via which ncRNAs regulate the expression of protein-coding ORFs. The detection in genome-wide studies of noncoding transcripts within promoter regions and numerous instances of overlapping complementary transcripts points to additional regulatory roles for yeast ncRNAs (2, 3, 8–11).

We have identified a pair of long cis-interfering ncRNAs in yeast that contribute to the control of gene expression at the FLO11 locus via a previously uncharacterized type of regulatory circuit, in which these ncRNAs toggle to control transcription of the downstream protein-coding ORF. Transcription of these yeast ncRNAs is regulated by transcription factors SF11 and Flo8, key players in FLO11-dependent developmental transitions that enable this organism to adapt to changing environments (28–35).

Functional characterization of the circuitry involving this pair of ncRNAs helps to explain two puzzling phenomena. First, FLO11 is expressed in a binary or “variegated” fashion in clonal populations of WT cells: FLO11 is transcribed at high levels (“on”) in some cells and is completely transcriptionally silenced (“off”) in others (35). In this report, we present evidence that these ncRNAs contribute to the variegated expression observed at FLO11 by toggling between the transcription of one or the other of these ncRNAs. Second, Rpd3L, a histone deacetylase (HDAC), has an unanticipated net activating effect on FLO11 transcription. Because it was the paradoxical role of Rpd3L as an activator of FLO11 transcription that led us to the discovery of the ncRNAs at the FLO11 locus, our presentation of experimental results begins there.

Results

HDAC Rpd3L Is a Net Activator of FLO Gene Expression. Null mutations (Rpd3L−) in components of Rpd3L, including Cti6, Rxt2, and Pho23, result in increased silencing of the FLO11 and FLO10 promoters, indicating that Rpd3L is a net transcriptional activator of these genes. This role for Rpd3L is demonstrated in three ways. First, promoter activity was assayed in strains in which the endogenous promoter is fused to a reporter gene (PFLO11-URA3, Fig. 1A; PFLO11-GFP or PFLO10-GFP, Fig. 1A), which precisely replaces the FLO ORF (Table S1). Detection of ura− (5-FOA resistant) or gfp− cells in WT vs. Rpd3L− strains indicates that FLO promoter silencing is elevated in Rpd3L− cell populations. Second, Northern blot analysis (Fig. 1B) shows that FLO11 mRNA is reduced in Rpd3L− (cit8) compared with WT. Third, disruption of Rpd3L function results in loss of FLO11-dependent phenotypes. Homozygous Rpd3L− diploids fail to form pseudohyphae (Fig. 1C) and Rpd3L− haploids do not adhere to YPD agar (Fig. 1D). These phenotypes are observed in rpd3A deletion mutants, indicating that the catalytic component of the Rpd3L HDAC is required for net activation of FLO11. Rpd3L− strains transformed with a PTEF-FLO11 plasmid


The authors declare no conflict of interest.

See Commentary on page 18049.

1To whom correspondence may be addressed. E-mail: gfrink@mit.edu or gifford@mit.edu.

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recovery both diploid filamentation and haploid adhesion (Fig. 1C and D), demonstrating that the phenotypic defects observed in Rpd3L−/− strains are a direct consequence of their loss of FLO11 expression. These phenotypes are specific to the Rpd3L and not the Rpd3S complex. FLO11 promoter activity was assayed in haploids containing the P_{FLO11-URA3}reporter at the endogenous locus. Four-fold serial dilutions were spotted onto SC, -URA, and 5-FOA (0.1%) media. Cells with active FLO11 promoters are Ura+ and 5-FOA+, whereas silenced cells are Ura− and 5-FOA−. (B) Northern blot analysis with a probe for FLO11 (3502–4093 bp) shows that reporter assays reflect average steady-state FLO11 mRNA levels. (C) Pseudohyphal growth is lost in Rpd3L−/− diploids, but is restored by P_{TEF-FLO11} on a 2-μm plasmid. C1, cti6/ci6+; C2, cti6/ci6+ + P_{TEF-FLO11}; C3, WT; C4, WT + P_{TEF-FLO11}. (D) Loss of Rpd3L function abolishes haploid adhesion. The same plate, after (Left) and after (Right) washing, is shown. P_{TEF-FLO11} on a 2-μm plasmid restores adhesion. (part 1) WT; (part 2) fio8; (part 3) cti6 + P_{TEF-FLO11}; (part 4) cti6 + vector; (part 5) rtx2 + P_{TEF-FLO11}; (part 6) rtx2 + vector; (part 7) rpd3 + P_{TEF-FLO11}; (part 8) rpd3 + vector.

Fig. 1. The HDAC Rpd3L is a net activator of FLO11 transcription. (A) FLO11 promoter activity was assayed in haploids containing the P_{FLO11-URA3} reporter at the endogenous locus. Four-fold serial dilutions were spotted onto SC, -URA, and 5-FOA (0.1%) media. Cells with active FLO11 promoters are Ura+ and 5-FOA+, whereas silenced cells are Ura− and 5-FOA−. (B) Northern blot analysis with a probe for FLO11 (3502–4093 bp) shows that reporter assays reflect average steady-state FLO11 mRNA levels. (C) Pseudohyphal growth is lost in Rpd3L−/− diploids, but is restored by P_{TEF-FLO11} on a 2-μm plasmid. C1, cti6/ci6+; C2, cti6/ci6+ + P_{TEF-FLO11}; C3, WT; C4, WT + P_{TEF-FLO11}. (D) Loss of Rpd3L function abolishes haploid adhesion. The same plate, after (Left) and after (Right) washing, is shown. P_{TEF-FLO11} on a 2-μm plasmid restores adhesion. (part 1) WT; (part 2) fio8; (part 3) cti6 + P_{TEF-FLO11}; (part 4) cti6 + vector; (part 5) rtx2 + P_{TEF-FLO11}; (part 6) rtx2 + vector; (part 7) rpd3 + P_{TEF-FLO11}; (part 8) rpd3 + vector.

recover both diploid filamentation and haploid adhesion (Fig. 1 C and D), demonstrating that the phenotypic defects observed in Rpd3L−/− strains are a direct consequence of their loss of FLO11 expression. These phenotypes are specific to the Rpd3L and not the Rpd3S complex. FLO11 promoter activity is not affected in a strain lacking Eaf3 (Fig. 1A), unique to Rpd3S (36, 43). Experiments described below use null alleles of Cti6, unique to Rpd3L, to assay the effects of disrupting Rpd3L function.

Epistasis data suggest that (i) Rpd3L works upstream of FLO-specific transcription factors Sfl1 (repressor) (31, 33, 44) and Flo8 (activator) (28, 29, 33); and (ii) net activation of FLO11 by Rpd3L depends on Sfl1 function. The phenotype of the Rpd3L−/− sfl1 double mutant is indistinguishable from that of the sfl1 mutant, in which FLO11 promoter silencing is lost in all cells (Fig. 1A) (25). As in the flo8 strain, all cells have a silenced FLO11 promoter in the Rpd3L−/− flo8 double mutant (Fig. 1A). SFL1 mRNA levels in Rpd3L−/− mutant strains do not differ significantly from WT (Fig. S1B), indicating that the role of Rpd3L in activating FLO11 expression is not via an indirect mechanism involving transcriptional repression of SFL1.

Rpd3L Localization to the FLO11 Promoter Alters Transcription Factor Binding and Chromatin Remodeling. Genome-wide ChIP-chip detects Rpd3 localization at two regions within the upstream intergenic region of FLO11: ~1,250 and ~2,850 bp upstream of the ATG of FLO11 (Fig. 2A). Genomic specific ChIP shows that enrichment of Rpd3 upstream of FLO11 is at least 4-fold higher than at unbound regions, and exceeds enrichment at the INO1 promoter (Fig. 2A and Fig. S2A), where Rpd3 localization is reported (45).

Compared with WT, localization of the transcriptional activator Flo8 to the FLO11 promoter is significantly decreased in the Rpd3L−/− mutant and, as previously reported (33), is increased in sfl1 (Fig. 2B). In the Rpd3L−/− sfl1 double mutant, Flo8 binding is restored, but not to the levels observed in sfl1. Thus, Flo8 binding remains impaired in the Rpd3L−/− mutant even in the absence of Sfl1. Yeast TATA box-binding protein (TBP) localization to the FLO11 TATA box (~92 bp) is absent in Rpd3L−/− and is elevated above WT levels in sfl1 (Fig. 2C). Histone H4 localization shows that nucleosome eviction fails to occur at the FLO11 core promoter in Rpd3L−/− cells compared with sfl1 cells (Fig. 2D). Differential enrichment of TBP and H4 is not merely an artifact of differential overall signal on the arrays, because signal is similar at control regions (Fig. S2 C and D).

To quantitatively define the size of the ncRNAs upstream of FLO11, Northern blot analysis was performed on oligo(dT)-selected RNAs with strand-specific RNA probes (Fig. 3B–D). Probes for Crick-strand transcription detect a ~3.2-kb ncRNA, designated ICRI (interfering Crick RNA), transcribed across much of the upstream intergenic region of FLO11 (Fig. 3C). Low levels of an ~8-kb Crick-strand transcript, which may represent a species transcribed across the FLO11 promoter and ORF, are also detected in some mutants (Fig. 3 C and D). A probe specific for Watson-strand transcription at a region far upstream of the FLO11 ORF detects another ncRNA ~1.2 kb in length and designated PWRI (promoting Watson RNA) (Fig. 3C).

Cap-dependent RACE was used to map the 5′ and 3′ ends of ICRI and PWRI. The 5′ RACE identified start sites for ICRI over a 250-bp range, 3.445–3.197 bp upstream of FLO11 (Fig. 3B and Table S2). The 5′ RACE identified a strong stop site for ICRI 209 bp upstream of FLO11 and other stops closer to (6, 4, and 2 bp upstream) and within (+10 and +24 bp) the FLO11 ORF itself (Fig. 3B and Table S2). The 5′ RACE for PWRI identified start sites over a 160-bp range, 2,190 to 2,339 bp upstream of FLO11 (Fig. 3B and Table S3). This configuration suggests that ICRI initiates, between 3246 and 3409 bp upstream of FLO11 (Fig. 3B and Table S3).
Titative PCR was performed on IP and WCE using primers specific for the anti-Myc antibody normalized to the whole-cell extract (WCE). (Inset) Quanitative PCR was performed on IP and WCE using primers specific for the FLO11 promoter (−1,400 bp), for positive binding control P necr, and for unbound regions APL2 and ARG2. Data were normalized to unbound region ARK1 and are expressed as fold enrichment ± SD. (B) Localization of Flo8 using a Myc-tagged allele in WT and mutant haploids was assayed by qPCR with primers specific for the FLO11 promoter on IP (anti-Myc) and WCE. Data were normalized to unbound region. (C) Northern blot analysis was performed on poly(A) RNA from haploid WT (lane 1), cti6 (lane 2), sfl1 (lane 3), and for unbound (lane 4) where the entire FLO11 locus is shown. In the plots, each circle represents a probe with log signal intensity indicated on the axis. Circles positioned above each x axis indicate Watson-strand transcription. Circles positioned below each x axis indicate Crick-strand transcription. Results from two arrays are shown. (Upper) Transcription in WT (red circles) vs. cti6 (blue circles); (Lower) Transcription in WT (red circles) vs. sfl1 (blue circles). Faded circles represent probes that were not called as part of a transcript in the analysis. A larger version of these plots is provided in Fig. S3. (D) Map of ncRNAs detected upstream of FLO11 and probes used in Northern blot analysis. Probes a, b, and c hybridize to regions located 284–819, 1653–2255, and 2631–3226 bases upstream of FLO11, respectively. Vertical lines at the 5′ ends of ICR1 and PWRI ncRNAs show the range of start sites identified by RACE (Tables S2 and S3). Arrowheads at the 3′ ends of the ncRNAs indicate the range of stop sites identified by RACE (Tables S2 and S3). (E) Northern blot analysis was performed on poly(A) RNA from haploid WT (lane 1), cti6 (lane 2), sfl1 (lane 3), and ΔFLO11 (lane 4) where the entire intergenic region upstream of FLO11 is deleted. FLO11 is, by convention, encoded on the Crick strand; other transcripts encoded on this strand are designated “Watson-strand.” Circles positioned above each x axis indicate Watson-strand transcription. Circles positioned below each x axis indicate Crick-strand transcription. Results from two arrays are shown. (Upper) Transcription in WT (red circles) vs. cti6 (blue circles); (Lower) Transcription in WT (red circles) vs. sfl1 (blue circles). Faded circles represent probes that were not called as part of a transcript in the analysis. A larger version of these plots is provided in Fig. S3. (B) Map of ncRNAs detected upstream of FLO11 and probes used in Northern blot analysis. Probes a, b, and c hybridize to regions located 284–819, 1653–2255, and 2631–3226 bases upstream of FLO11, respectively. 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transcription. The analogous pair of ncRNAs transcribed upstream of FLO11 (Fig. S3) adds support to this model.

There is an inverse correlation observed between ICR1 and PWR1 transcription. ICR1, but not PWR1, is transcribed at the highest levels detected in this study in mutants (Rpd3L−, flo8, Rpd3L−/flo8, Rpd3L−/flo8 sfl1; Fig. 3 C and D) where transcription of FLO11 is largely silenced. These data implicate Flo8 and Rpd3L as repressors of ICR1. ICR1 is barely detectable in sfl1 mutants in which Rpd3L function is still intact, indicating that Sfl1 function normally promotes ICR1 transcription. PWR1 is detected only in the strains in which FLO11 is also transcribed at high levels (Figs. 1 A and B and 3 C and D). PWR1 transcription requires Flo8 and is promoted by Rpd3L activity, but is repressed by Sfl1 function (Fig. 3 C and D). Both PWR1 and ICR1 are detected in the mixed population of FLO11 on and off cells in the variegating WT strain (Fig. 3C). Quantitative (q)PCR assays support the presence of the ICR1 transcript, the quantitative differences in its transcription observed by Northern blot analysis, and an inverse correlation between ICR1 and FLO11 transcription (Fig. 3E and Fig. S4).

If ICR1 transcription across the FLO11 promoter has a causal role in repressing FLO11, then termination of the ICR1 transcript should block this inhibition and restore FLO11 expression. This prediction was tested with strains in which ICR1 is terminated by constructs (T1–T3) containing a transcriptional terminator (Fig. 4A). The control construct (C) contains an ORF sequence with no terminator (Fig. 4A). Insertion of T1, T2, or T3 at a site 3,041 bp upstream of FLO11 (~350 bp downstream of ICR1 initiation) restores FLO11-dependent adhesion in Rpd3L− mutants (Fig. 4D). The extent of rescue correlates directly with the strength of the terminator (Fig. 4C) and the resulting increase in FLO11 expression (Fig. 4B). Control construct C inserted at the same site does not terminate ICR1 and does not restore adhesion to the Rpd3L− mutant (Fig. 4B–D).

ICR1 and PWR1 show evidence of reciprocal transcriptional interference. This interference is suggested by the inverse correlation in their transcription and by Northern blot bands indicative of a range of transcript sizes that could result from interference (Fig. 3 C and D). A genomic comparison of four yeasts closely related to Saccharomyces cerevisiae (49, 50) shows that the region of overlap between PWR1 and ICR1 represents the least conserved DNA sequence in this region, suggesting that transcription per se, rather than specific DNA sequence, is important there (Fig. S4B). A URA3 gene inserted as a surrogate-initiated similarly to ICR1 revealed PWR1-imposed interference on URA3 expression (Fig. S5). Last, termination of ICR1 increases PWR1 levels in the Rpd3L− background (Fig. 4C). The fact that low level ICR1 is detected even in sfl1 mutants (Fig. 3 C and D) suggests that ICR1 may be constitutive, supporting a model in which its levels are tuned by PWR1 transcription.

The insertion of a terminator into just one copy of the FLO11 promoter in Rpd3L− diplotypes up-regulates expression of the downstream ORF only in cis (Fig. 4E). Overexpression of ICR1 or PWR1 in trans has no effect on FLO11 promoter activity in WT, sfl1, flo8, or Rpd3L− strains (Fig. S6). These results show that ICR1 and PWR1 function in cis to regulate FLO11 transcription.

Together, these data support a mutual interference between PWR1 and ICR1, and suggest a model for transcriptional variation at the FLO11 locus involving a toggle between these ncRNAs (Fig. 5).

Discussion
We report the discovery of two long intergenic ncRNAs, ICR1 and PWR1, that have key roles in regulating transcription of the nearby protein-coding ORF FLO11. The ~3.2-kb ICR1 ncRNA is initiated far upstream (~3.4 kb) from the FLO11 ORF and is transcribed across much of the large promoter of FLO11 (53), repressing FLO11 transcription in cis. Our data support a “promoter occlusion” model (23, 24), in which transcription of ICR1 blocks access to general transcription factors and to chromatin remodelers required for nucleosome ejection. The ~1.2-kb PWR1 ncRNA is transcribed from the strand complementary to that encoding ICR1, and promotes FLO11 transcription by interfering with ICR1.

In our model (Fig. 5), the competitive binding of Sfl1 or Flo8 at their respective binding domains (33) initiates events that...
expected to occupy its site more often and Flo8 less often (Fig. 2B) in an Rpd3L− mutant. When both Rpd3L and Sfl1 functions are lost, Flo8 could access its binding site more readily (Fig. 2B). However, we cannot exclude the possibility that up-regulation of PWR1 itself in sfl1 dominates over the repressive effects of increased ICR1 when Rpd3L function is also lost, a consequence of the coupled regulation in this toggle switch. Weak Rpd3 localization detected −2,850 bp upstream of FLO11 (Fig. 2A) and the observation that ICR1 transcription is lower in the sfl1 flo8 double mutant compared with the Rpd3L− sfl1 flo8 triple mutant (Fig. 3D) point to the possibility of some Sfl1-independent role for Rpd3L in repressing ICR1 transcription. ICR1 and PWR1 are implicated in controlling an epigenetic phenomenon in yeast (35) that involves the reversible transition from a chromatin state that is competent for transcription of a protein-coding ORF to one that is silenced for its transcription. The roles proposed for these ncRNAs, which share features with mammalian lincRNAs (5), may have general significance for epigenetic regulation in other eukaryotes. There is evidence that epigenetic phenomena, such as imprinting and X-inactivation in mammals, involve ncRNAs (58). Our discovery of a circuitry involving two ncRNAs at the yeast FLO11 locus suggests that regulation of other epigenetic phenomena that involve a progression from an unstable or bistable condition to a stable transcriptional state (either on or off) may, like the FLO11 gene, be controlled by underlying ncRNA regulatory networks.

Materials and Methods

Strains, Media, Microbiological Techniques, and Growth Conditions. Yeast strains used in this study (Table S1) are derived from Σ1278b (28). Standard yeast media were prepared and genetic manipulation techniques were carried out as described (59). For experiments with Pmyt-URA3 strains, YPD liquid cultures were grown overnight, diluted 1:50, and grown to OD600 0.8–1.2. Culture densities were adjusted to equivalence, serially diluted 4-fold, and spotted onto synthetic complete (SC), SC-Ura, and SC + 5-FOA (0.1%) agar plates (60). Haploid adhesion tests were performed as described (30). To induce pseudohyphal growth, strains were grown on SLAD media (61). For Northern blot analysis, qPCR, ChIP, RACE, and microarray analysis, cells were grown overnight in YPD liquid, diluted 1:50, and grown to OD600 0.8–1.2 for use in experiments. Plasmids are listed in Table S1.

Northern Blot Analysis. For the Northern blot analysis in Fig. 18, total RNA isolated by standard acid phenol extraction was used. For all other blots, total RNA was oligo(dt)-selected to enrich for polyadenylated transcripts. RNAs were separated on formaldehyde-agarose denaturing gels and blotted as described (62). Hybrid membranes were hybridized with 32P (exo-) Klenow-labeled DNA probes (Fig. 1C and load controls) or 3P-labeled RNA probes generated with the Ambion T7 Maxscript Kit (all other hybridizations).

ChIPs. Protocols have been described (63). Bacteria were infected with Dnal Protein G magnetic beads preincubated with antibodies against Myc-epitope (Covance 9E-11 MMS-164P), yeast TBP (Santa Cruz SC-33736), or histone H4 (Upstate Millipore 05-808). For gene-specific ChIP, SYBR Green qPCR (Applied Biosystems) was performed on IP and WCE using specific primers. For ChIP-Chip, Cy-5 labeled IP and Cy-3 WCE were hybridized to Σ1278b custom genomic microarrays (Agilent, strand-specific probes − every 50 bp). Data were normalized as follows: Cross-talk normalization provided coefficients for Cy5 is 3.2x10^-7 and Cy3 is 3.2x10^-7 to correct intensities in each channel. Resulting values were median normalized. The data were transformed under the assumption that Cy3 − Cy5 is a good fit. JBD algorithm identified binding events (64).

qPCR. Total RNA obtained by standard acid phenol extraction was reversed transcribed (Qiagen QuantiTect Kit); cDNAs were analyzed with primers specific to targets, SYBR Green reagents (Applied Biosystems), and the ABI 7500 qPCR system.

Genome-wide Transcription Profiling. Cy3- or Cy5-labeled cDNAs were generated using SuperScript II Reverse Transcriptase on Poly(A) RNA, hybridized to Σ1278b custom genomic microarrays (Agilent, strand-specific probes − every 25 bp), and scanned (Agilent). Data were normalized as follows: Cross-talk normalization provided coefficients for Cy5 − Cy3 and Cy3 − Cy5 to correct intensities in each channel. Resulting values were median normalized. The data were trans-
formed under the assumption that Cy3 – Cy5 is a good fit. Differential expression between samples on the same array was determined as the difference in median intensity of the set of probes associated with a given transcript.

**RACE.** Mapping of 5′ and 3′ ends of capped, polyadenylated RNA was carried out with specific primers and the Invitrogen GeneRacer Kit. RACE products were cloned (pCR4-TOPO) and sequenced.