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H3K9me-Independent Gene Silencing in Fission Yeast Heterochromatin by Clr5 and Histone Deacetylases

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Abstract
Nucleosomes in heterochromatic regions bear histone modifications that distinguish them from euchromatic nucleosomes. Among those, histone H3 lysine 9 methylation (H3K9me) and hypoacetylation have been evolutionarily conserved and are found in both multicellular eukaryotes and single-cell model organisms such as fission yeast. In spite of numerous studies, the relative contributions of the various heterochromatic histone marks to the properties of heterochromatin remain largely undefined. Here, we report that silencing of the fission yeast mating-type cassettes, which are located in a well-characterized heterochromatin region, is hardly affected in cells lacking the H3K9 methyltransferase Clr4. We document the existence of a pathway parallel to H3K9me ensuring gene repression in the absence of Clr4 and identify a silencing factor central to this pathway, Clr5. We find that Clr5 controls gene expression at multiple chromosomal locations in addition to affecting the mating-type region. The histone deacetylase Clr6 acts in the same pathway as Clr5, at least for its effects in the mating-type region, and on a subset of other targets, notably a region recently found to be prone to neo-centromere formation. The genomic targets of Clr5 also include Ste11, a master regulator of sexual differentiation. Hence Clr5, like the multi-functional Atf1 transcription factor which also modulates chromatin structure in the mating-type region, controls sexual differentiation and genome integrity at several levels. Globally, our results point to histone deacetylases as prominent repressors of gene expression in fission yeast heterochromatin. These deacetylases can act in concert with, or independently of, the widely studied H3K9me mark to influence gene silencing at heterochromatic loci.

Introduction
The mating-type region of the fission yeast *Schizosaccharomyces pombe* affords a well-defined system to investigate how heterochromatin histone modifications affect gene expression [1] (Figure 1A). The region comprises three cassettes, *mat1*, *mat2-P*, and *mat3-M*. *mat1* contains and expresses either the P- or M- mating-type genes and thereby determines the mating-type of a cell. *mat2-P* and *mat3-M* contain the same genes and internal promoters of transcription as *mat1*, however these two cassettes are not expressed. They act as repressors of gene expression in fission yeast heterochromatin. These deacetylases can act in concert with, or independently of, the...
is artificially disrupted [7,11]. Even when heterochromatin is artificially disrupted, RNAi mutants are capable of re-establishing wild-type levels of H3K9me in their mating-type region [11]. The phenotype of the RNAi mutants can be explained by a redundant recruitment of Clr4 through the CREB-like transcription factor Atf1 bound at two sites near the mat3-M cassette [12,13]. The recruitment of Clr4 by Atf1/Pcr1 might be via a direct interaction between Clr4 and Atf1/Pcr1 [12] or it might be facilitated indirectly by histone deacetylation following the association of Clr3 and Clr6 with Atf1/Pcr1 [13,14]. Positive feedback loops strengthen H3K9me in the mating-type region, in particular Swi6 facilitates H3K9me in the centromere-proximal half of the mating-type region that includes mat2-P [11].

Other redundancies in the silencing mechanisms operating in the mating-type region are made obvious by two classes of epistasis analyses. One class of experiments combined mutations in the HDACs Clr3 and Clr6 [3]. The second class of experiments combined cis- and trans-acting mutations. These latter experiments involve two small elements, REH and REIII, adjacent to mat2-P and mat3-M respectively (Figure 1A). When combined with a mutation in Clr4 or other mutations in the Clr4 epistasis group, deletion of either REH or REIII causes a strong expression of the adjacent cassette [15,16,17]. This indicates the existence of a class of factors acting redundantly with Clr4 to silence mat2-P and mat3-M through REH or REIII. We present here the first characterization of a factor in this class, Clr5.

**Results**

Relative contributions of H3K9me and histone deacetylation to gene silencing in the mating-type region

The mat2-P cassette contains two genes, Pi and Pc, transcribed from an internal promoter [2] (Figure 1A). Whether these genes are expressed or not can be conveniently assayed in cells containing a stable, unswitchable, mat1-M cassette (mat1-Msmt-0). Because mat1-Msmt-0 cells cannot switch to mat1-P, they form colonies containing only cells of the M mating-type that fail to mate and sporulate due to the absence of compatible mating partners of the P mating-type in the same colony. The

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**Author Summary**

In eukaryotes some histone modifications are preponderantly associated with silent chromosomal domains, however the extent to which distinct modifications contribute to the silencing of gene expression is often not known. A well-studied chromosomal domain in which histone modifications have been extensively characterized is the fission yeast mating-type region. There, histone hypoacetylation and histone H3 lysine 9 methylation (H3K9me) are associated with a domain refractory to gene expression. Contrary to a general assumption, we found that genes naturally present in the mating-type region of wild-type strains remain repressed in the absence of the H3K9 methyltransferase Clr4. Their repression depends on histone deacetylases and on a hitherto uncharacterized factor, Clr5. Our results reveal an unsuspected robustness in the silencing mechanism, where H3K9me and deacetylation cooperate to ensure that the genes naturally present in the mating-type region remain silent in conditions where their expression would otherwise kill the cells.
Gene silencing by Clr5

Clr5 contains a conserved domain defining a new protein family

Transcriptional signature of clr5Δ mutant

A striking overlap was observed between genes upregulated in clr5Δ cells and in cells overexpressing the master regulator of cell differentiation Ste11, or in cells in which the meiotic program had been induced (Figure 5A, 5B, and Figure S3). Ste11 is a transcription factor regulated by phosphorylation and by positive transcriptional feedback as cells respond to pheromones, prepare for mating, and undergo meiosis. In wild-type cells Ste11 activates the transcription of a series of genes involved in mating and sporulation including the two M-specific genes contained in mat1-M and the two P-specific genes contained in mat1-P. Our microarrays suggest that Ste11 itself, and possibly some of its downstream targets, are repressed by Clr5.

The fact that the same promoters of transcription are present in mat2-P and mat3-M as in respectively mat1-P and mat1-M including Ste11-binding sites (Figure 1A) raised the possibility that the increased expression of mat2-P in clr5Δ swi6-115 cells results from

same time as cenH transcripts in Figure 2D, potential effects of Clr5 at centromeres were not investigated further.
increased Ste11 activity in these cells. However, induction of Ste11 by nitrogen starvation in mat1-Msmt-0 swi6-115 cells (Figure 2A), or expressing Ste11 from the thiamine-regulatable nmt1 promoter in these cells (Figure 5C), did not lead to the high frequency of haploid meioses caused by clr5 in the same genetic background, indicating the effects of clr5 in the mating-type region are not simply due to derepression of Ste11.

In addition to its effects on ste11+ and downstream effectors, we found that Clr5 acts together with the Clr6 deacetylase on a number of other targets (Figure 5A). The overlapping function of Clr5 and Clr6 is fully consistent with the epistasis analysis presented above suggesting that Clr5 and Clr6 repress the mating-type region together (Figure 2A and 2D). Clr5 and Clr6 also have non-overlapping roles in gene regulation consistent with Clr6 participating in various protein complexes.
Figure 4. Features of the Clr5 protein. (A) The N-terminus of Clr5 (first 120 amino acids) was compared to NCBI and Broad Institute databases by BLAST. Protein sequences retrieved in the searches were aligned using Multalin and manually annotated. Twenty four sequences are displayed below.


B

Disorder tendency

Amino acid position

Identity

C

S. pombe

P. nodorum

T. stipitatus

P. marneffei

M. canis

C. posadasi

P. triticirepentis

A. clavatus

A. nidulans

N. fischeri

P. anserina

P. marneffei

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Ankyrin repeat regions (ANK_REP_REGION, PS50297) with Ankyrin repeats (ANK_REPEAT, PS50088) shown in a lighter shade.

between S. pombe using IUPred. The transcript was clearly increased in the double mutants mat1-Msmt-0 clr5 (Figure 6A). These observations show that Clr5 contributes to the repression at mat3-M.

The response to nitrogen starvation [19], and recently this region was found to the Clr4/Swi6 pathway, but the transcript levels are not as high placed in the mating-type region is alleviated in mutants belonging to the centromere-proximal edge of the heterochromatin domain, is close to the centromere-proximal edge of the hetero-

Heterochromatin spans ~20 kb in the mating-type region. mat2-P is close to the centromere-proximal edge of the heterochromatin domain, mat3-M close to its centromere-distal edge, and ~15 kb of heterochromatin separate the two cassettes (Figure 1A). Clr5 was identified because it represses mat2-P. We investigated whether Clr5 also represses mat3-M and/or reporter genes placed between mat2-P and mat3-M.

Whether Clr5 represses mat3-M was assayed using cells containing a stable mat1-P allele (mat1-PA17; Figure 6A). Expression of mat3-M was monitored in these cells by measuring haploid meiosis – driven by the co-expression of mat1-P and mat3-M – and by RT-PCR. The RT-PCR conditions we used failed to detect mat3-M transcripts in the cb3A and cb4A single mutants, however we observed occasional haploid meioses in cb3A or cb4A colonies indicating a low level of mat3-M transcription occurs in these mutants. In the double cb3A cb5A and cb4A cb5A mutants, both haploid meioses frequency and mat3-M transcript levels were increased. These effects of Clr5 at mat3-M appeared much less pronounced than the effects of Clr5 at mat2-P as judged by the iodine staining of mat1-PA17 cb3A cb5A (or cb4A) colonies compared with mat1-Manot-0 cb3A cb5A (or cb4A) colonies, however the abundance of mat3-M transcript was clearly increased in the double mutants (Figure 6A). These observations show that Clr5 contributes to the repression of mat3-M – albeit to a comparatively low level – and that, at mat3-M, like at mat2-P, repression by Clr5 is redundant with repression by Clr3 or Clr4 (Figure 6A).

As mentioned above the transcriptional repression of transgenes placed in the mating-type region is alleviated in mutants belonging to the Clr4/Swi6 pathway, but the transcript levels are not as high as when the genes are transcribed from a euchromatic location [17,21,22]. It is therefore possible to ask whether factors of interest contribute to the repression redundantly with Clr5 or Swi6 by examining the mat4 transcript levels in double mutants. We observed that mat4 inserted near mat2-P (Figure 1; mat2-P(XbaI);ura4) was more strongly expressed in the cb3-142 swi6-115 double mutant than in either single mutant (Figure 6B and Figure S4). We also observed increased accumulation of cenH transcripts in the cb3-142 swi6-115 and cb3-142 cb4A double mutants (Figure 2D and Figure 6B). These widespread effects strengthen the conclusion that Clr5 does not act solely through Ste11 to activate the mating-type genes specifically.

H3K9me-Independent Gene Silencing by Clr5

The RNAi pathway has been proposed to recruit Clr4 to the mating-type region by acting upon non-coding transcripts generated from the cenH element. Consistent with this proposal, deletion of cenH affects H3K9me in the mating-type region. Cells lacking cenH adopt one of two semi-stable epitypes: one similar to wild type displaying normal levels of H3K9me and one similar to the cb3A mutant characterized by reduced H3K9me [11,23,24]. The fluctuations between two phenotypes can be understood in the frame of models postulating that the establishment and maintenance of heterochromatin proceed through distinct mechanisms. One such model would be that cenH facilitates the establishment of H3K9me in wild-type cells without being necessary to the subsequent maintenance of the H3K9me state. The fluctuations between two epigenetic states can be followed experimentally using reporter genes, for example replacement of cenH with ade6 leads to variegated ade6+ expression [25]. Noticeably, mat2-P remains silent in cenH/Δade6 cells regardless of the expression state of ade6+ (Figure 6C) in agreement with H3K9me being dispensable for the repression of mat2-P. Our observations with cb3A cb4A mutants suggested that combining cb3A with cenHΔ should lead to a cumulative derepression of mat2-P. Indeed, deleting cb5 in cenHΔ cells increased the expression of mat2-P (Figure 6C). Furthermore, as with cenHΔ single mutants, fluctuations between two phenotypes still occurred. Similarly, deleting cb5 in a cb1A background released the repression of mat2-P in a variegated manner (Figure S5). We conclude from these observations that Clr5 insures a cenH/RNAi-independent silencing in the mating-type region.

We tested in a similar manner whether Clr5 exerts its effects through the REII or REIII silencing elements found near mat2-P and mat3-M respectively by combining cb5A with deletions of these elements. Deleting cb5 in cells lacking the mat3-M-adjacent element REIII lead to a small cumulative, variegated, derepression of mat3-M (Figure 6D) placing cb5 in a pathway different from the REII pathway. In contrast to the situation with cenH or REII, deleting cb5 in cells that lack REII did not increase the expression of mat2-P (Figure 6D). This supports the notion that Clr5 acts through REII, a proposition substantiated by the effects of cb5A on ectopic silencing reporters (see below) and by the fact that an REII insertional mutant had been obtained in the same genetic screen as the cb3-LEU2 mutants.

REI-mediated silencing at an ectopic site requires Clr5

To further test whether REI and Clr5 participate in the same silencing mechanism, we asked whether REI-mediated silencing at an ectopic site depends on Clr5. Insertion of a cenH sequence adjacent to an ade6+ reporter gene at an ectopic site confers partial heterochromatic silencing on ade6+ [26]. Changes in the expression state of ade6+ can be monitored at the colony level by a color test. Cells expressing ade6+ produce white colonies while cells that fail to express ade6+ produce red colonies or sectors due to the accumulation of a red byproduct in the adenine biosynthetic pathway. Hence, establishment of silencing can be monitored as a change from white to red and loss of silencing as a change from red to white. Silencing of ade6+ is established at a very low
Figure 5. Transcription signature of clr5Δ mutant. (A) and (B) The list of genes upregulated 2-fold in clr5Δ cells was compared with the list of genes upregulated 2-fold in respectively clr6-1 cells [18], cells over-expressing Ste11 [65], and cells induced to undergo meiosis by 4 hours of nitrogen starvation [19]. P-values reflect the significance of gene list overlaps. (C) Over-expressing Ste11 from the pREP1-ste11 plasmid does not confer the same sporulation phenotype as deleting clr5Δ to a swi6-115 mutant. Sporulation was assayed on MSA medium lacking leucine and thiamine. mat1-Msmt-0 cells were PG1789 (wt); SPK29 (swi6-115); SPK464 (clr5Δ) and SPK142 (clr5-142 swi6-115). A switching-competent h90 strain was used as an additional control for sporulation, WT139. (D) As A and B but comparing with clr3Δ clr6-1 double mutant. (E) Transcriptional signature (mutant/wt ratios) of genes from a subtelomeric region of chromosome 1 (this study), [18]. Asterisks represent missing data points. Stippled lines indicate 2 fold.
up- or down-regulation. The inset examines the distribution of genes upregulated >2 fold in the clr5Δ mutant (average of two arrays) for part of chromosome 1, plotting the probability of the observed distribution in a 20-gene sliding window. The orange line represents a P value of 0.05 while the red line represents a P value of 0.001. The peak is a 20-gene window centered on SPAPJ695.01c (P = 1.1e⁻²⁸).

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rate, but it is epigenetically maintained for several generations. Rates of establishment and stability of silencing are markedly enhanced by inserting REII [26] (Figure 7) or REIII (Figure 7) adjacent to the ade6⁺-cenH construct.

We examined whether ade6⁺ silencing in strains where the ectopic ade6⁺-cenH construct was fused to either REII or REIII depends on Clr5 or Dcr1. Consistent with cenH-mediated silencing relying on RNAi, deletion of dcr1 abolished silencing in both strains (Figure 7). In contrast, deletion of clr5 affected silencing of the REII-ade6⁺-cenH construct, but not silencing of the REIII-ade6⁺-cenH construct (Figure 7). Hence Clr5 participates specifically in REII-mediated silencing at the ectopic site.

Histone modifications in clr5 mutants

The genetic interactions between clr5, clr3, clr6, and clr4 suggested the chromatin structure of the mating-type region might change in some of the double mutants, accounting for changes in gene expression. Hence, H3K9 methylation (H3K9me2) and
acetylation (H3K9Ac) were examined at the REII element and mat2-P in single and double mutants (Figure 8). The expression of mat2-P was measured in the same strains (Figure 8A and 8B). This experiment gave the following insights in the molecular mechanisms responsible for the effects observed in the various mutants.

First, as predicted from the phenotypic analysis described above, lack of H3K9me2 is not sufficient to derepress mat2-P. This could be seen in the clr3A and clr4A mutants, both of which lacked H3K9me2 at REII and mat2-P, yet failed to express mat2-P to a detectable level (Figure 8A and 8C). Deletion of clr3 in either of these strain backgrounds lead to a ~50 fold increase in mat2-P expression indicating Clr5 is necessary for the H3K9me-independent repression of mat2-P in clr3A and clr4A cells (Figure 8B and 8D), a result also corroborating our genetic analysis. Clr5 itself showed no sign of directly affecting H3K9me2, the level of H3K9me in clr3A or clr5-142 was not significantly different from wild-type (Figure 8C; please note that clr5-142 is in all likelihood a loss of function allele due to LEU2 insertion at the beginning of the gene. No clr5 transcripts were detected in clr5-142 cells (Figure S1).

Changes in H3K9Ac were also observed at REII and mat2-P in the various mutants examined. The greatest increase in H3K9Ac occurred in the clr3A clr6-1 double mutant consistent with the two HDACs acting redundantly on this substrate. Furthermore H3K9Ac increased in the clr4A clr5A and clr3A clr5A double mutants relative to each single mutant (which were not significantly different from wild-type) supporting the idea that Clr5 acts together with an HDAC. One should bear in mind when interpreting these data that histone deacetylases tend to be promiscuous affecting more than one of the numerous nucleosomal lysines that are subject to acetylation and they might furthermore deacetylate proteins other than histones hence changes other than H3K9Ac might take place in the mutants we examined and also affect gene expression.

Finally, only strains with both abnormally low H3K9me and abnormally high H3K9Ac expressed mat2-P. These were the clr4A clr5A, clr3A clr5A and clr4A clr6-1 double mutants. Strains lacking H3K9me but showing no increase in H3K9Ac (clr3A and clr4A) failed to express mat2-P. Conversely, a small increase in H3K9Ac that was not accompanied by loss of H3K9me in the clr6-1 clr5A double mutant did not lead to mat2-P expression. These results epitomize the redundancy of silencing mechanisms at the mat2-P cassette.

**Discussion**

The mechanisms by which H3K9me is brought about in defined chromosomal regions of fission yeast have been extensively studied in the last decade. Perhaps because of this widespread interest, H3K9me tends to be equated with heterochromatin while histone deacetylation in the same regions has often been presented as a simple pre-requisite for H3K9me. Recent studies have
proposed an additional, more direct, role of histone deacetylation in heterochromatic gene silencing [14,27–30]. However, this role has been discussed exclusively in the context of H3K9me, that is, histone deacetylation has been presented only as a facilitating factor for, or consequence of, H3K9me. Arguing against these widespread views we found that some essential properties of heterochromatin are largely independent of H3K9me and rely instead on deacetylation and on a hitherto uncharacterized factor, Clr5. These H9K9me-independent mechanisms of repression act in parallel and/or cooperate with H3K9me-dependent mecha-

Figure 8. Chromatin modifications and mat2-Pc expression in clr5 mutants. (A) and (B) mat2-Pc RNA levels in various mutants. RNA was prepared from cells starved for nitrogen for 5 hr to induce expression of the mating-type genes. Changes in mat2-Pc expression relative to wild-type (PG1789) were estimated by real-time PCR and plotted, using actin for normalization. The means of two biological experiments are displayed. Strains analyzed in (A) were WT: PG1789; clr4Δ: SPK450; clr3Δ: PG3564; clr6-1: SP1240; clr5Δ: PG3631; clr5-142: SPK368; and clr3Δ clr6-1: PG3577. Strains analyzed in (B) were WT: PG1789; clr4Δ: SPK450; clr3Δ: PG3564; clr6-1: PG3577; clr4Δ clr5Δ: PG3633; clr6-1: PG3630; clr5-142: SPK493. (C) and (D) Chromatin Immunoprecipitation (ChIP) analysis of H3K9me2 at the REII and mat2-Pc locus of the mating-type region compared with the adh1+ locus measured by real-time PCR. Enrichment of H3K9me2 was normalized to the values derived for a strain that lacks H3K9me2 (clr4Δ, SPK450). Values represent the means of two independent ChIP experiments except for clr6-1 mutant were only one ChIP experiment is shown. Strains analyzed in (C) were as in (A). Strains analyzed in (D) were as in (B). (E) and (F) Chromatin Immunoprecipitation (ChIP) analysis of H3K9Ac at the REII and mat2-Pc locus of the mating-type region compared with the adh1+ locus measured by real-time PCR. Values were normalized to the wild-type strain (PG1789) and represent the means of two independent ChIP experiments. Strains analyzed in (E) were as in (A). Strains analyzed in (F) were as in (B). doi:10.1371/journal.pgen.1001268.g008
Histone acetylation, examined at various levels of acetylation, showed H3K9me is not necessary for silencing. Repression was largely retained in cells lacking Clr4 (Figure 1, Figure 2, Figure 6, Figure 8; data not shown) showing H3K9me is not necessary for silencing. Repression was much more strongly affected in the double clr3 drl6-1 HDAC mutant. Histone acetylation, examined at mat2-P, was as expected increased in the clr3A drl6-1 mutant correlating with mat2-P expression (Figure 8). Whether increased acetylation was the sole cause for derepression of the mating-type region in the clr3A drl6-1 mutant is unclear since this mutant also lacked H3K9me at mat2-P (Figure 8D) leaving open the possibility that loss of silencing results from a combination of increased acetylation and reduced H3K9me. More generally full expression of mat2-P was observed only in mutants lacking both a H3K9me pathway component (Swi6, Clr3 or Clr4) and a component belonging to the REII/Clr6/Clr5 epistasis group (Figure 1, Figure 2, Figure 6, Figure 8; data not shown) showing H3K9me is not necessary for silencing. Repression was much more strongly affected in the double clr3A drl6-1 HDAC mutant. Histone acetylation, examined at mat2-P, was as expected increased in the clr3A drl6-1 mutant correlating with mat2-P expression (Figure 8). Whether increased acetylation was the sole cause for derepression of the mating-type region in the clr3A drl6-1 mutant is unclear since this mutant also lacked H3K9me at mat2-P (Figure 8D) leaving open the possibility that loss of silencing results from a combination of increased acetylation and reduced H3K9me. More generally full expression of mat2-P was observed only in mutants lacking both a H3K9me pathway component (Swi6, Clr3 or Clr4) and a component belonging to the REII/Clr6/Clr5 epistasis group (Figure 1, Figure 2, Figure 6, Figure 8; data not shown) showing H3K9me is not necessary for silencing. Repression was much more strongly affected in the double clr3A drl6-1 HDAC mutant. Histone acetylation, examined at mat2-P, was as expected increased in the clr3A drl6-1 mutant correlating with mat2-P expression (Figure 8). Whether increased acetylation was the sole cause for derepression of the mating-type region in the clr3A drl6-1 mutant is unclear since this mutant also lacked H3K9me at mat2-P (Figure 8D) leaving open the possibility that loss of silencing results from a combination of increased acetylation and reduced H3K9me. More generally full expression of mat2-P was observed only in mutants lacking both a H3K9me pathway component (Swi6, Clr3 or Clr4) and a component belonging to the REII/Clr6/Clr5 epistasis group (Figure 1, Figure 2, Figure 6, Figure 8) highlighting the redundancies and cross-talks which take place between deacetylation and H3K9me pathways to elicit full silencing in the mating-type region. Relatively little is known regarding the mechanisms by which histone modifications facilitate or inhibit gene expression in any eukaryote. In fission yeast, Clr3 preferentially deacetylates H3K14ac and Clr6 deacetylates several lysines of histone H3 and H4 [4]. Both enzymes repress transcription by limiting the access of Pol II to heterochromatin [14,27–30]. The H3K9 methyltransferase Clr4 has also been reported to restrict Pol II access to heterochromatin [34]. This might be through a direct effect of H3K9me, or it might be through the ability of Clr4 to indirectly recruit HDACs. Clr3 fails to associate with mat2-P in swi6 mutants [14] suggesting it also fails to associate with mat2-P in clr4A mutants. Other studies indicate the chromodomain protein Chp2 bound to H3K9me recruits the Clr3-containing complex SHREC while Swi6 recruits the Clr6-containing complex Clr6 CII [28–30]. HDACs and HMTs are found in complexes in higher eukaryotes and HP1, like Swi6 or Chp2 in S. pombe, can bridge H3K9me with HDACs [35,36] indicating transcriptional repression by H3K9me might generally occur through the action of HDACs. In the present case, the ability of Clr4 to indirectly recruit HDACs might account for its redundant effects with Clr5.

Genes placed in heterochromatic regions can remain sensitive to transcriptional activation. For example in S. cerevisiae, a URA3 gene inserted near a telomere is silenced by the Sir proteins and histone deacetylation but its expression can be stimulated by increased levels of Ppr1, a transcriptional activator of URA3 [37]. Similarly, lack of Ppr1 increases URA3 silencing at the silent mating-type loci in S. cerevisiae mutants partially deficient for silencing [38] By analogy, increased expression of the ste11 gene in clr3A mutants suggests a mechanism for the high haploid meiosis observed in for example clr3A clr4A mutants. Namely, the loss of H3K9 methylation combined with the presence of an activated transcription factor increases transcriptional activity at the normally-silent mating-type cassettes. Arguing against this simple model, we found that overexpressing ste11+ in swi6-115 cells starved for nitrogen does not lead to high levels of haploid meiosis (Figure 5C), indicating the effects of clr3A in the mating-type region are not solely due to increased ste11+ expression in this mutant. Our data do not exclude more complex models where down-regulation of the ste11+ gene or of the Ste11 protein activity by Clr5 would contribute to silencing in the mating-type region.

Our observations expand current models for silencing in the mating-type region (Figure 9). We propose that Clr5 and deacetylation – of histones and possibly other as-yet-undefined substrates of Clr3 or Clr6 – repress mat2-P via the REII element. Independently, deacetylation would proceed from Atf1-binding sites near mat3-M as proposed by others [12,13] and perhaps through some other DNA element in REII distinct from the Atf1-binding sites [16]. The effects of Clr5 and Atf1 would not be strictly local, however each factor would predominantly affect the REII/Clr6/Clr5 epistasis group (Figure 1, Figure 2, Figure 6, Figure 8) highlighting the redundancies and cross-talks which take place between deacetylation and H3K9me pathways to elicit full silencing in the mating-type region. Relatively little is known regarding the mechanisms by which histone modifications facilitate or inhibit gene expression in any eukaryote. In fission yeast, Clr3 preferentially deacetylates H3K14ac and Clr6 deacetylates several lysines of histone H3 and H4 [4]. Both enzymes repress transcription by limiting the access of Pol II to heterochromatin [14,27–30]. The H3K9 methyltransferase Clr4 has also been reported to restrict Pol II access to heterochromatin [34]. This might be through a direct effect of H3K9me, or it might be through the ability of Clr4 to indirectly recruit HDACs. Clr3 fails to associate with mat2-P in swi6 mutants [14] suggesting it also fails to associate with mat2-P in clr4A mutants. Other studies indicate the chromodomain protein Chp2 bound to H3K9me recruits the Clr3-containing complex SHREC while Swi6 recruits the Clr6-containing complex Clr6 CII [28–30]. HDACs and HMTs are found in complexes in higher eukaryotes and HP1, like Swi6 or Chp2 in S. pombe, can bridge H3K9me with HDACs [35,36] indicating transcriptional repression by H3K9me might generally occur through the action of HDACs. In the present case, the ability of Clr4 to indirectly recruit HDACs might account for its redundant effects with Clr5.

Figure 9. Model for gene silencing in the mating-type region. Both Clr5 and Atf1 repress gene expression by promoting deacetylation in their respective target regions, Clr5 directly or indirectly via the REII element (this study), and Atf1 via Atf1-binding sites near mat3-M [12,13]. The effects of Clr5 and Atf1 gradually decrease as the distance from their respective cis-acting element increases. An additional layer of silencing is orchestrated by Clr4. Clr4 can be recruited by direct binding to Atf1 [12] or through the RNAi-dependent cenH nucleation site [11]. H3K9me catalyzed by Clr4 permits binding of the chromodomain proteins Swi6 and Chp2 and spreading of histone deacetylation [14,28–30]. Inactivation of both the Clr4 and Clr5 pathways is required for mat2-P expression. While the clr4A clr5A combination derepresses mat2-P (this study), this is not the case for the clr4A clr6-1 combination [3]. To account for these different phenotypes, we suggest that Clr3 can partially substitute for Clr6 in a Clr5-dependent manner. doi:10.1371/journal.pgen.1001268.g009
for other chromatin-mediated effects unrelated to transcription for example effects on recombination and transposition [41,42]. Similarly, Clr5 has other functions than those described here such as a role in DNA repair suggested by the hypersensitivity of clb5Δ cells to DNA-damaging agents [43]. This role in the resistance to DNA damage might be performed together with Clr6, like gene repression, since clb6-1 mutants are also sensitive to DNA-damaging agents [44]. Clr5 might furthermore affect genome integrity through its control of a large region prone to neocentromere formation [20] (Figure 5). Unlike Atfl, Clr5 does not belong to a well-described family of transcription factors, however all known characteristics of Clr5 are compatible with a role in chromatin organization and transcription. For instance Clr5 localizes to the nucleus, the transcription profile of the clr5 mutant is consistent with Clr5 regulating transcription through deacetylation, and the predicted physical characteristics of Clr5 are also compatible with a role in transcription.

The Clr5 protein is predicted to contain a large disordered region. Intrinsically unstructured proteins (IUPs) are a large group of proteins that lack well-defined secondary and tertiary structures, (reviewed in [45,46]). Many IUPs interact with other proteins via their disordered region, which has been proposed to undergo induced folding upon interaction with a binding partner [46]. Transcription factors are abundant among IUPs for example Jun, p53, Myb, and CREB contain unstructured domains. Similar to histone tails, their disordered nature allows access for various covalent modifications such as phosphorylation, ubiquitination, and acetylation, facilitating the concomitant folding and interaction with binding partners.

In addition to its large predicted disordered region the Clr5 protein contains a hitherto undescribed domain in its N-terminal region. This domain and its N-terminal location are conserved among a family of fungal proteins of currently unknown function. Many proteins in this family are in the same size-range as Clr5, some also share with Clr5 a predicted unstructured domain in their C-terminal portion. In others we identified 1 to >10 ankyrin repeats (AR) in the place of the predicted unstructured region. AR form flexible bundles of stacked helix-loop-helix units connected by β-hairpins that create an interaction interface with other proteins [47–51]. AR proteins and IUPs resemble each other in their interactive plasticity and some AR proteins contain partly unstructured ankyrin repeats that become structured upon binding to a target surface, as exemplified by the N_{Bb} repressor (reviewed in [48]). These shared properties of ARs and IUPs, and the fact that some members of the Clr5 protein family contain ARs while others contain unstructured regions, suggest that the predicted unstructured domain of Clr5 also mediates protein interactions. The predicted high flexibility of the unstructured domain is consistent with its relatively low sequence conservation between the Clr5 homologues in S. pombe, S. japonicus, and S. octosporus. Clr5 is the first member of its family with an assigned function. Its involvement in a well characterized biological process amenable to genetic analysis provides valuable tools to unravel questions relevant not only to the regulation of gene expression but also to the fields of structural biology and molecular evolution.

Methods

S. pombe strains and media

The strains used in this study and their genotypes are listed in Table S1. Some were published previously as indicated [15,16,18, 26,52,53,54]. The clc3 ORF was replaced with the hph1 gene, which confers resistance to hygromycin B, by transforming SPK29 with a PCR product amplified from pCR2.1-hph1 [55] with GTO-312 (TTACATGTTTCGGGGGTTGACCTTGGATCTGTCGCTGCTATTTAGTACATTTAACACCCTTGATTTTACGGCCTCCAACCAAGCAACATTAGCCACAGGAAAGTCTCTTACCGGATCCCCGGGGTTAATTTAA) and GTO-313 (TAGGCAAGGGCAATGGTGAGAGAAAAATTAAAAACATCTAAATGAATATAGAGACACCGAGAAAAAGGGATGGCCAGAAAGACCAACTAAAGATAGGTACTGATTATAAACGAGACCACTAGGAAATATTACGTTAAGATACAAAAAAGGAATGCTCGTGTATACAC). Strains were plated onto AA-leu plates and incubated 3–5 days at 33° C before being replicated onto MSA supplemented with adenine and uracil to induce meiosis in the Leu⁺ transformants.

Inversion PCR

Inversion PCR was performed as essentially described previously [59] using the Expand Long Template PCR System (Roche) and primers OKR78 (CTGTGGGATAGGGCCCCCTGTGTGGTCTC) and OKR79 (ACTACAGTTCCTAATTGGATATTGTGAGG) in the cases where the genomic DNA had been digested with HindIII; OKR83 (GGGAAAACACTTGGGAGGAAACCCTACATGAG) and OKR78, or OKR84 (GGGAAAACACTTGGGAGGAAACCCTACATGAG) and OKR79 for the EcoRI digests; and OKR82 (GGCCTACACTTCCTGAGGGGTTTCC) and OKR79 for the HinP1II digests (Figure S6).

RNA extraction and transcript analysis

Total RNA was extracted as described previously [60,61]. For the clc3 transcript analysis, the clc3 mRNA was reverse-transcribed using Superscript II (Qiagen) in a reaction containing OKR86 (GACTGAGATGAGAGCAGGGAGGGAGGCCCTGTGGGATGTCTC) to prime cDNA synthesis and 25 μg of total RNA produced from PG1789. Diluted cDNA was amplified with Expand High Fidelity Polymerase (Roche) using OKR86 and JPO998 (CATCGAGCTTCCAAAGGATCGATGGGTAGC) for the analysis of other transcripts, cultures of wild-type or mutant strains growing exponentially in YES medium were harvested and starved for nitrogen in PM medium for 5 hours at 32°C in a shaking incubator to induce sexual differentiation. RT-PCR was performed as described in [17], with OKR93 (CCCTGCTTATATGATTTTAATTTTATTTTATTTTATTTTGTTGTC) and OKR94 (CATCTGAGGATGAGAGCAGGGAGGCCCTGTGGGATGTCTC) and 24 PCR cycles to amplify the mat2-P transcript; GTO-353 (CTCTTTAGAAATGTCATGAGGAGGAGGCCCTGTGGGATGTCTC) and GTO-355 (CGTTCTGACACTCCTGTCACAAGCTTGGC) and 24 PCR cycles to amplify the mat3-Mc transcript; GTO-265 (GCTTTTACAGCTAGAGGTGAGG)
and GTO-266 (CTTCCGACACAGGATTACGACC) and 25 PCR cycles to amplify wra4 and wra4-DS/E transcripts; GTO-223 (GAAACAACATGTTGCTTCTCAGA) and GTO-226 (TCTGTCAGTGCTGATGTA) and 27 PCR cycles to amplify RNA originating from centromeric repeats or conH on OKR70 (GGCATGACCTTTCTCAAGC) and OKR71 (GAGTCCAAGACAGATCAGT) and 23 PCR cycles for actin. No RT controls were conducted with GTO-223 and GTO-226 and 27 PCR cycles for all RNA preparations used in RT-PCR. No products were observed in these reactions.

Real-time RT-PCR displayed in Figure 1 was performed as described [61] to detect mut2-Pt using JPO-976 (TTGTAATA-TAGTATGCGCTTCAACTTG) and JPO-977 (TGTGTTAG-CTTGCTCTGCTAACCATT). Real-time PCR displayed in Figure 8 was performed using a Qiagen Quantitect SYBR Green RT-PCR kit for the reactions and a BioRad CFX96 PCR machine and BioRad software for the analysis. Dilution series of RNA prepared from a h90 strain were used to determine the range of exponential amplification which was found to extend to at least 30 cycles. All reactions were set up in triplicate except for the no-RT controls for which only one reaction was set up per sample. The mut2-Pt transcript was amplified with JPO-976 and JPO-977 using 75 ng of total RNA as template for each sample. The actin transcript was amplified using JPO-793 (AACGTCAAGTTCGAGGAAGTCC) and JPO-794 (GGCATCAGCTTCTACAGTG) using 75 pg RNA as template.

**Micro-array analysis**

A clr5 (SPK10) and a clr5A (SPK573) strain were propagated in liquid EMM2 medium, and harvested at a cell density of ~5.0 × 10^6 cell/ml. RNA extraction and micro-array analysis were performed as described previously [62] in duplicate. The GeneSpring software package was used for data analysis and comparisons with previously published microarray experiments. The significance of gene list overlaps was calculated using a standard Fisher’s exact test, and the P-values were adjusted with a fold (Table S2). Use of either list produced essentially the same results.

**ChIP analyses**

Cells were grown overnight in YES in a 30°C shaking incubator, diluted to 3.5 × 10^6 cells/ml in malt extract medium (ME) and incubated for a further 5 hr to induce nitrogen starvation. Chromatin immunoprecipitation was performed as previously described [61], but using 1% fixation and antibodies that recognize H3K9me2 (Abcam) or H3K9Ac (Millipore). Briefly, 3 × 10^7 cells were fixed with 1% paraformaldehyde for 18 min at room temperature prior to washing with PBS, permeabilization of the cell wall with zymolase 100T (0.4 mg/ml in PEMS), and incubation at 36°C for 20 min. Following extensive washing with PEMS, cell pellets were resuspended in 400 μl ChiP lysis buffer and sonicated (3 x, 10 s each). After pre-clearing with Protein A-agarose beads, the lysates were used for immunoprecipitation overnight with each antibody. Antibody-protein complexes were purified using Protein A-agarose beads, washed, and reverse-crosslinking of PCR products from duplicate DNA samples from wild-type, esp1−, esp2−, esp3− and esp4− cells were TOPO-cloned and sequenced.

**DAPI staining and microscopy**

Cells propagated on ME plates for 3–4 days at 32°C were scraped, washed in 500 μl PBS, and incubated at room temperature for 10 min in 8 μg/ml DAPI/PBS solution. The suspension was diluted approximately 20 fold in PBS and 150 μl were spun (Cyto-Tek, Samura) onto poly-lysine coated slides (Sigma). The slides were air-dried and one drop of Vectashield (Vector Labs) was added before applying the cover slip. Images were obtained using a Zeiss AxioskopII microscope fitted with a DAPI filter wheel and chroma filters, and a Coolspap HQ camera. All images were taken at maximum resolution, using 100x objective and IPLab software (Scanalytics).

**DNA and protein sequence analyses**

Sequence analyses were performed using online available BLAST [63], ClustalW (www.ebi.ac.uk/clustalw/), IUPred (http://iupred.enzim.hu/), and services from the Sanger Institute (www.sanger.ac.uk) and Broad Institute (www.broad.mit.edu).

**Localization of Clr5**

Clr5 tagged at its C terminus with GFP [52] was expressed from the endogenous clr5 locus and used for localization studies. Cells were propagated to early log phase in supplemented EMM2 medium. Images were obtained using the 100x objective of a Zeiss Axioskop fluorescence microscope equipped with a Hamamatsu Orca-ER digital camera and Volocity 5.0.

**Cloning and sequencing of clr5 cDNA and clr5 mutant alleles**

cDNA from exponentially growing wild-type cells [PG1789] was amplified using OKR86 and JPO998 as described above. A PCR product of approximately 600 bp was gel purified (Qiagen) and cloned into pCRII-TOPO (Invitrogen). The cloned cDNA was sequenced to identify the exon boundaries of clr5. To identify possible mutations within clr5 in the esp mutants [16], full-length genomic clr5 was amplified using primers OKR-95 (ATTCCGGGGATGCAAGAGAATTCCTAGC) and OKR-96 (CTTGAGGCTGACCTAAAGCAAGAATCTACATC) 18 PCR cycles and the Phusion polymerase (Finnzymes). PCR products from duplicate DNA samples from wild-type, esp1−, esp2−, esp3− and esp4− cells were TOPO-cloned and sequenced.
were JPO-976 and JPO-977. Data were normalized to the ch4A strain for the K9Me ChIPs, and to wild type for the K9Ac ChIPs.

Supporting Information

Figure S1  LEU2 insertions at the ch5 locus mapped by inverse PCR, and phenotypes of ch5A strains. (A) Position of LEU2 insertions relative to ch5 ORF in SPK129, SPK137, and SPK142. JPO998 and OKR 86 are primers used for the ch5 transcript analysis in C. The white lollipop indicates SPAC29B12.08 ORF start site proposed in databases (NCBI; Sanger Center); the black lollipop the start site suggested by our experiments. Black flowers show the location of the three LEU2 insertions. Genetic analysis of the previously isolated esp1 and esp2 mutants [24] demonstrated that these contained mutations tightly linked to esp5. Sequencing of ch5 in these mutants revealed single base pair mutations leading to an amino acid change in esp1 (R45A; allele renamed ch5-1059) or W50stop in esp2 (allele renamed ch5-1058). Similarly, sequencing the hitherto unpublished esp4 allele obtained in a similar screen found a short array of mutations leading to a frameshift in the beginning of the Clr5 unstructured domain. (B) Sequence of the three ch5:LEU2 insertion sites. Bases are numbered as in cosmids SPAC29B12. In each case, as seen from the alignments, a few nucleotides of ch5 were deleted by the integration event. (C) A size difference of about 600 bp between the PCR products obtained from cDNA or genomic DNA (gDNA) demonstrates mRNA splicing of ch5 transcript. (D) The ch5 intron introns conserved 5′ and 3′ splice motifs. Consensus splice motifs [66] are indicated in the shaded boxes. The nucleotide position refers to the position in SPAC29B12. W = T or A, Y = T or C (pyrimidines), and N = any base. (E) RT-PCR was performed using primers JPO-998 and OKR86 to examine ch5 transcript in wild-type and ch5-142 cells. (F) Analysis of mat2-Px transcript in wild-type (PG1789), ch5A (SPK464), swi6-115 (SPK29), and ch5A swi6-115 (SPK458) cells was performed as in Figure 1. (G) Tetrad dissection of a heterozygous diploid ch5+/ch5A on YES medium. The ch5A progeny form smaller colonies than the ch5+ progeny.

Found at: doi:10.1371/journal.pgen.1001268.s001 (0.98 MB TIF)

Figure S2  ch5A coding and predicted protein sequence. An intron in the ch5A gene is indicated in red.

Found at: doi:10.1371/journal.pgen.1001268.s002 (0.87 MB TIF)

Figure S3  Effect of ch5A on the expression of genes in the pheromone-response pathway. Expression ratios obtained in two micro-array experiments comparing ch5A to wild type are presented. Ratios greater than 2-fold are indicated in red. Pheromone induced genes controlled by the master regulator Ste11 and their relationships are depicted as described [67–71]. Clr5 regulates many genes in that pathway either directly or indirectly via Ste11 regulation.

Found at: doi:10.1371/journal.pgen.1001268.s003 (1.26 MB TIF)

Figure S4  Expression of ura4+ in the mating-type region. Northern blot of ura4 transcripts originating from the mating-type region (mat2-P:XbaI::ura4+) or euchromatic ura4 locus (ura4-DS/E) in ch5+ (ch5+; PG1210) or ch5 mutant (ch5-1058; PG1214; ch5-1059; PG1179) cells. All cells are swi6-115. Each ch5 mutation has a cumulative effect with the mutation in swi6, increasing the expression of mat2-P:XbaI::ura4 relative to ura4-DS/E.

Found at: doi:10.1371/journal.pgen.1001268.s004 (4.70 MB TIF)

Figure S5  Cumulative gene silencing by the RNAi pathway and Clr5. Ten-fold serial dilutions of unswitchable mat1-Msm10 mat2-P:XbaI::ura4+ cells mutated in the RNAi pathway (dcr1Δ) or ch5 (ch5-142) were spotted on TSA sporulation medium. (A) No sporulation was observed on uracil-containing medium, a medium supporting growth of all cells plated independent of the expression state of their mating-type region. This indicates that mat2-P can be repressed in all mutants examined. (B) and (C) Variegated sporulation was observed in some of the mutants on uracil-free medium. Uracil-free medium selects for cells with a partially or totally derepressed mating-type region. Haploid meioses were not detected in wild-type or dcr1Δ cells on uracil-free medium indicating mat2-P remains silent in these cells. Very low levels of haploid meiosis were detected in ch5-142 mutant and higher levels in the dcr1Δ ch5-142 double mutant. These observations are consistent with Clr5 repressing the mating-type region in a pathway different from the RNAi pathway. wt: PG1789; dcr1Δ: SPK425; ch5-142: SPK368; dcr1Δ ch5-142: SPK423; dcr1Δ ch5-142: SPK424.

Found at: doi:10.1371/journal.pgen.1001268.s005 (3.91 MB TIF)

Figure S6  Inverse PCR design. Primers and restriction sites used for the amplification of LEU2-containing DNA for mutagenesis, or for the subsequent inverse PCR reactions.

Found at: doi:10.1371/journal.pgen.1001268.s006 (3.39 MB TIF)

Figure S7  Statistical analysis for data presented in Figure 5E. The proportions of genes upregulated >2-fold in the ch5A mutant were determined along each chromosome in a sliding window of 20 consecutive genes and the probability of the observed proportions being due to chance was estimated and plotted for each window as detailed in Materials and Methods. The orange line represents a P value of 0.05 while the red line represents a P value of 0.001. The region on chromosome 1 (shown in Figure 5E) is significant for both lists. (A) A list of genes whose averaged expression between the duplicate microarrays was increased >2 fold in ch5A compared to wild-type. The peak in chromosome 1 is a 20-gene window centered around SPAP695.01c (P = 1.05 e-6). (B) A list of genes whose expression was increased >2 fold in both microarrays. The peak in chromosome 1 is centered on SPAP695.01c (P = 7.44 e-3). The peak in chromosome 2 is a 20-gene window centered on SPBC23G7.12c at the mating-type region (P = 2.46 e-3). Both gene lists are in Table S2.

Found at: doi:10.1371/journal.pgen.1001268.s007 (9.08 MB PDF)

Table S1  List of strains and their genotypes.

Found at: doi:10.1371/journal.pgen.1001268.s008 (0.09 MB DOC)

Table S2  Lists of genes used in Figure 5E and Figure S2.

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Author Contributions

Conceived and designed the experiments: KRH IH SS AC GT. Performed the experiments: KRH IH SS JWVJH AC GT. Analyzed the data: KRH IH SS JW JRAM JFP AC GT. Contributed reagents/materials/analysis tools: KRH IH SS JW JRAM JFP AC GT. Wrote the paper: KRH JRAM JFP AC GT.

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