Environmental perception and epigenetic memory: mechanistic insight through \textit{FLC}

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SUMMARY

Chromatin plays a central role in orchestrating gene regulation at the transcriptional level. However, our understanding of how chromatin states are altered in response to environmental and developmental cues, and then maintained epigenetically over many cell divisions, remains poor. The floral repressor gene \textit{FLOWERING LOCUS C} (\textit{FLC}) in \textit{Arabidopsis thaliana} is a useful system to address these questions. \textit{FLC} is transcriptionally repressed during exposure to cold temperatures, allowing studies of how environmental conditions alter expression states at the chromatin level. \textit{FLC} repression is also epigenetically maintained during subsequent development in warm conditions, so that exposure to cold may be remembered. This memory depends on molecular complexes that are highly conserved among eukaryotes, making \textit{FLC} not only interesting as a paradigm for understanding biological decision-making in plants, but also an important system for elucidating chromatin-based gene regulation more generally. In this review, we summarize our understanding of how cold temperature induces a switch in the \textit{FLC} chromatin state, and how this state is epigenetically remembered. We also discuss how the epigenetic state of \textit{FLC} is reprogrammed in the seed to ensure a requirement for cold exposure in the next generation.

Keywords: \textit{Arabidopsis thaliana}, vernalization, chromatin, bistability, \textit{FLOWERING LOCUS C}, Polycomb, non-coding RNA.

INTRODUCTION

Many organisms align their behaviour, metabolism and development to specific external cues. Temperature is a major environmental cue, but how this is perceived is not well understood. Plants use continuous monitoring of long-term temperature signals to infer seasonal progression in order to align development with external conditions. Unlike some environmental signals (e.g. photoperiod), temperature signals are noisy. To be capable of inferring seasonal information, plants must have systems that are capable of averaging fluctuating temperature, and also ‘remembering’ previous temperature exposure. Our understanding of how seasonal changes in temperature influence plant development is most advanced for the process of vernalization: the acceleration of flowering through exposure to prolonged cold. A requirement for vernalization ensures that plants over-winter vegetatively and flower in the following spring. Central to this process in \textit{Arabidopsis thaliana} is regulation of the floral repressor locus \textit{FLOWERING LOCUS C} (\textit{FLC}) (Michaels and Amasino, 1999; Sheldon et al., 1999). In winter-annual \textit{Arabidopsis} accessions, \textit{FLC} is initially highly expressed and prevents transition to reproductive development before winter. \textit{FLC} expression is repressed by prolonged cold exposure, and this repression is then epigenetically maintained until embryo development after flowering (Figure 1a) (Michaels and Amasino, 1999; Sheldon et al., 2000). \textit{FLC} regulation therefore provides an excellent system by which to dissect the molecular mechanisms behind temperature perception, as well as epigenetic memory and reprogramming.

In this review, we describe the key regulators of \textit{FLC} and summarize the current understanding of \textit{FLC} chromatin regulation at various stages of the vernalization process, including how \textit{FLC} is repressed in response to cold exposure (cell-autonomous switching), how this cold exposure is maintained during subsequent growth in warm conditions.
conditions (epigenetic memory), and how FLC is reprogrammed during embryo development, with opposing functions of the autonomous and FRIGIDA pathways setting the FLC expression level and determining reproductive strategy.

**CELL-AUTONOMOUS SWITCHING UNDERLIES QUANTITATIVE SILENCING DURING COLD EXPOSURE**

A key feature of vernalization is its quantitative nature: flowering is progressively accelerated as plants are subjected to increasing cold exposure (weeks and months). This was elegantly explained when FLC expression was shown to progressively decrease with increasing weeks of cold exposure (Michaels and Amasino, 1999; Sheldon et al., 1999). This repression is then stably epigenetically maintained after plants are returned to warm conditions. Many studies in other systems have revealed that epigenetic gene regulation systems commonly have two expression states: 'ON' or 'OFF' (Ptashne, 2004; Dodd et al., 2007; Veening et al., 2008; Ferrell, 2012). Such a gene regulation system is said to be bistable: both states are self-perpetuating under the same external conditions (Ferrell, 2002). This is also true of FLC: after cold exposure, FLC expression is actually ON or OFF in individual cells (Angel et al., 2011; Berry et al., 2015). Rather than inducing a graded reduction of FLC expression in each cell, cold exposure instead increases the number of cells that have switched from an ON state to an OFF state (Figure 2a). When measured at the level of a tissue or whole plant, FLC expression appears quantitatively graded because of the large number of cells in the sample. The slow switching of cells from FLC-ON to FLC-OFF during cold exposure has been referred to as ‘digital repression’ by analogy with digital computers, which handle data as discrete ‘bits’ of information (0 or 1).

The decision to flower therefore seems to be distributed across many cells of the plant, with each cell responding independently (Angel et al., 2011). If all cells responded to cold exposure with an analogue (graded) FLC expression change, each cell would have to ‘remember’ a quantitative FLC expression level and pass this on through mitosis to ensure stability of epigenetic repression. Digital repression is an elegant mechanism by which
plants may respond quantitatively to cold exposure without the need for individual cells to store complex quantitative information.

Cell-autonomous FLC repression may be converted back to an analogue flowering-induction signal at the level of a whole plant by floral integrators regulated by FLC. For example, one of the genes directly repressed by FLC is FLOWERING LOCUS T (FT), which is expressed in the phloem companion cells in the vasculature, and subsequently moves from the leaves to the shoot apex to induce flowering (Wigge, 2011). Movement of FT throughout the plant may act to average expression between different parts of the plant and thereby provide an indicator of ‘readiness to flower’ at the whole-plant level.

Figure 2. FLC expression and chromatin during vernalization.
(a) FLC expression is gradually repressed during vernalization at the tissue or whole-plant level. At the cellular level, this corresponds to a gradual switching of cells from an FLC ‘ON’ state to an FLC ‘OFF’ state. FLC repression is stable upon return to warm conditions.
(b) The high expression state of FLC chromatin is characterized by H3K4me3, H3K36me3, histone acetylation, and active transcription by polymerase II. During cold exposure, repression may be ‘nucleated’ by a PHD–PRC2 complex, which mediates a switch from H3K36me3-rich to H3K27me3-rich chromatin. At the same time, expression of COOLAIR is increased. For loci in the repressed state after cold exposure, H3K27me3 and PHD–PRC2 spread to cover the entire locus. In this repressed state, both FLC and COOLAIR transcription are reduced.
FLC chromatin during the switching process

Genetic screens have been fruitful in identifying factors required for FLC activation and repression. Many of these protein factors act directly at the FLC locus to modulate the local chromatin environment in order to either promote or repress FLC transcription (Crevillon and Dean, 2010). Although difficult to prove conclusively, it is widely believed that post-translational modifications of histones play important roles in maintenance of both active and repressed FLC expression states. This hypothesis comes from two main lines of evidence. The first line of evidence is correlation: tri-methylation of histone H3 at lysine 4 and lysine 36 (H3K4me3/H3K36me3) as well as histone acetylation and histone H2B ubiquitination (H2Bub1) are commonly associated with actively transcribed genes in species from yeast to mammals (Li et al., 2008). These histone marks are enriched on activated FLC loci (Figure 2b) (Yang et al., 2014). When FLC is repressed, these marks are replaced by tri-methylation at lysine 27 of histone H3 (H3K27me3) (Bastow et al., 2004; Sung and Amasino, 2004; De Lucia et al., 2008; Angel et al., 2011), which is a hallmark of repressed genes (Margueron and Reinberg, 2011) (Figure 2b). These observations indicate that FLC repression involves switching chromatin from an activated state (H3K4me3/H3K36me3/H2Bub1) to a repressed state (H3K27me3). The second line of evidence is genetic: Proteins responsible for placing activating histone marks such as H3K4me3 (ATX1 and SDG25) (He et al., 2004; Pien et al., 2008; Tamada et al., 2009; Shafiq et al., 2014) or H3K36me3 (EFS/SDG8) (Kim et al., 2005; Zhao et al., 2005; Shafiq et al., 2014; Yang et al., 2014) are required for generating activated FLC chromatin and high levels of FLC expression (Figure 2b). These proteins are homologous to the conserved Trithorax group of proteins required for maintenance of epigenetic active states in higher eukaryotes such as flies, nematodes and mammals (Steffen and Ringrose, 2014). For the repressive mark H3K27me3, genetic screens for components defective in maintenance of the repressed FLC state after vernalization led to isolation of a protein complex that is responsible for delivering H3K27me3 to FLC chromatin (Gendall et al., 2001; Sung and Amasino, 2004; Wood et al., 2006; Greb et al., 2007; De Lucia et al., 2008). Part of this complex is homologous to Polycomb repressive complex 2 (PRC2), which is also structurally and functionally conserved in higher eukaryotes. Core PRC2 components are estimated to be involved in maintenance of H3K27me3 at approximately 4000 genes in Arabidopsis (Zhang et al., 2007a; Deng et al., 2013). The specific PRC2 complex associated at FLC also includes components of the plant homeodomain (PHD) family (Sung and Amasino, 2004; Sung et al., 2006b; Greb et al., 2007; De Lucia et al., 2008). This PHD-PRC2 complex is physically located at FLC after vernalization, and is essential for maintenance of the repressed state after vernalization (Gendall et al., 2001; Greb et al., 2007) (Figure 2b). Thus, chromatin-based regulation of FLC via the coordinated switch of histone modifications from H3K4me3/H3K36me3/H2Bub1 to H3K27me3 has emerged as a key concept underlying the epigenetic activated and repressed FLC expression states.

The high degree of conservation of these histone modifications (and the protein complexes that deposit them) among eukaryotes suggests that they play important conserved roles in gene regulation. However, it has been difficult to prove conclusively that particular histone modifications are absolutely required for mediating the activating or repressive effects of Trithorax or Polycomb. The main reason for this is that model organisms with a functional Trithorax/Polycomb system also have many copies of histone H3 genes. Thus, it is difficult to create mutations to confirm that specific histone residues are the relevant physiological substrates of these complexes. Progress was made relatively recently through a set of experiments in Drosophila, in which the 23 copies of histone H3 were replaced with 12 copies of histone H3 with either wild-type lysine 27 or a mutant histone in which lysine 27 was replaced with arginine (H3-K27R) (Pengelly et al., 2013). Cells that only expressed H3-K27R histones and not wild-type histones failed to repress Polycomb target genes, demonstrating that PRC2 acts through histone modifications to maintain transcriptional repression of its targets.

Polycomb complexes in Arabidopsis and their functional equivalents in Drosophila, Caenorhabditis elegans and mammals have been reviewed in detail elsewhere (Arabidopsis: Holec and Berger, 2012; Drosophila: Steffen and Ringrose, 2014; mammals: Margueron and Reinberg, 2011). The specific complex located at FLC that is important for the vernalization response comprises the core PRC2 components FIE, VRN2, MSI1 and SWN or CLF, as well as the PHD proteins VRN5, VIN3 and VEL1 (Sung and Amasino, 2004; Sung et al., 2006b; De Lucia et al., 2008). CLF and SWN are homologues of E(z) in Drosophila (EZH2 in mammals). This is the enzymatic subunit that catalyses H3K27me3 through its SET domain (Cao et al., 2002). FIE is homologous to Esc in Drosophila (EED in mammals), which has been shown to specifically recognize H3K27me3. In the context of PRC2, H3K27me3 binding by EED results in allosteric activation of PRC2 H3K27me3 methyltransferase activity (Margueron et al., 2009). The zinc finger protein VRN2 (Su(z)12) and the WD40-domain protein MSI1 (p55) are core complex components that make contacts with histones and enhance PRC2 catalytic activity. LHP1 is also physically located at FLC chromatin in the repressed state, and appears to be important in maintenance of repression (Mylne et al., 2006; Sung et al., 2006a; Turk et al., 2007). LHP1 is capable of binding H3K27me3.
when plants are exposed to cold, VIN3 expression is induced (Sung and Amasino, 2004), and VIN3 accumulates as part of a PHD–PRC2 complex downstream of the FLC transcription start site (De Lucia et al., 2008). This region is referred to as the nucleation region, and consists of approximately three nucleosomes centred over exon 1/the start of intron 1 (Figure 2b). This complex results in coordinated loss of H3K4me3/H3K36me3 and gain of H3K27me3 at the nucleation region (Yang et al., 2014). In parallel with this change in chromatin state, transcriptional down-regulation of FLC and up-regulation of COOLAIR antisense transcripts occur (Swiezewski et al., 2009). These transcriptional changes occur independently of VIN3 (Swiezewski et al., 2009; Helliwell et al., 2015). The down-regulation of FLC sense transcription early during cold exposure may be an important prerequisite for recruitment of Polycomb complexes to the nucleation region. Indeed, it was shown that H3K27me3 is effectively ‘wiped out’ when transcription across FLC intron 1 is driven by an artificial inducible promoter in transgene experiments (Buzas et al., 2011). Further support for the idea that PRC2 is capable of targeting transcriptionally repressed loci ‘by default’ has come from recent experiments in mammalian embryonic stem cells (Riising et al., 2014). In these experiments, it was found that global transcriptional inhibition was sufficient to induce ectopic PRC2 recruitment to Polycomb target genes that were not normally silenced in embryonic stem cells (Riising et al., 2014). This study also showed that PRC2 was dispensable for initial transcriptional shutdown of many genes that are switched off during in vitro differentiation of embryonic stem cells. It appears that PRC2 may act to sample permissive chromatin sites and to silence those that are not transcriptionally active (Klose et al., 2013). Thus, transcription itself may form a key component of the ‘activated state’, which antagonizes Polycomb silencing. An interesting finding relevant to this proposal is that PRC2 interacts with nascent RNA at both inactive and active loci across the mammalian genome (Kaneko et al., 2013, 2014).

Exactly how Polycomb complexes are targeted to specific genomic locations such as the FLC nucleation region remains the subject of intense research. Several studies have identified sequences in the first intron as being important for vernalization (Figure 1c) (Sheldon et al., 2002; Sung et al., 2006a; Angel et al., 2011). In Drosophila, the well-studied Hox loci contain specific DNA sequences that are recognized by sequence-specific DNA binding proteins. These proteins then provide a targeting platform for the Polycomb and Trithorax complexes. The DNA elements are called Polycomb response elements (Steffen and Ringrose, 2014). To date, specific sequences capable of acting as epigenetic memory elements in the same way as Drosophila Polycomb response elements have not been identified in plants or mammals. The discovery of long non-coding RNA and the RNA-binding ability of Polycomb complexes led to the hypothesis that long non-coding RNAs may act as ‘recruiters’ of PRC2 (Tsai et al., 2010). This is the proposed mechanism of action of a sense long non-coding RNA (COLDAIR) transcribed from FLC intron 1 (Heo and Sung, 2011). However, the COLDAIR sequence is not well conserved in FLC orthologues from close relatives of A. thaliana, such as Arabidopsis lyrata and Capsella rubella (Castaings et al., 2013).

The role of COOLAIR in vernalization. (a) Terminator exchange (TEX) lines have the COOLAIR promoter replaced with the RUBISCO (RBCS) terminator. FLC-TEX is not transcriptionally repressed as rapidly as the control (FLC). While H3K27me3 accumulation at the nucleation region of FLC appears unaffected in FLC-TEX, H3K36me3 is not removed from FLC chromatin during cold exposure. (b) Nucleation of H3K27me3 at FLC during cold exposure requires a PHD–PRC2 complex containing VIN3 and VRN5. COOLAIR does not affect H3K27me3 nucleation, but may act to stabilize an H3K36me3 demethylase at the nucleation region.

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tion on the behaviour of the TEX construct showed very low 
ator exchange or TEX lines. Transgenic plants carrying 
coding RNAs could provide the required specificity to 
Therefore, it is currently unclear exactly how long non-
et al., 2014), and PRC2 RNA binding appears to be quite pro-
marks and to mediate cold exposure to ensure removal of activating chromatin 
ments have uncovered a role for COOLAIR in the coordi-
nated switch between H3K27me3 and H3K36me3 at the 
nucleation region (Csorba et al., 2014) during cold expo-
This study used a transgenic FLC construct in which the 
loger complexes. This process was recently shown to be 
important for regulation of the chromatin state at a Poly-
role of non-coding transcription in evicting chromatin 
While COOLAIR promoters and first exon sequences 
are highly conserved in perennial relatives of A. thaliana, as 
is cold induction of COOLAIR expression (Castaings et al., 
2014), suggesting a potentially conserved function in ver-
ificantly, as these have opposing profiles in the FLC 
nucleation region (Yang et al., 2014). Other experiments 
also support mutual exclusion of H3K36me3 and H3K27me3: they rarely co-exist on the same histone tail 
Johnson et al., 2004; Voigt et al., 2012; Yang et al., 
2014), the antagonism is functionally important (Yuan et al., 2011; Yang et al., 2014), and lack of H3K36me3 
results in a fully silenced state at FLC even in the absence of cold exposure (Yang et al., 2014). However, 
the absence of an absolute mirror profile between H3K27me3 and H3K36me3 across the whole FLC locus, 
predicted from modelling, suggests their antagonistic roles are a necessary but not sufficient component of the 
mechanism enabling switching between, and inheritance of, epigenetic states (Yang et al., 2014). It is currently 
unknown whether H3K27me3 at the nucleation region 
during cold exposure occurs in all cells equally (ana-
logue) or in an all-or-nothing fashion (digital), i.e. does 
H3K27me3 at the nucleation region increase gradually at 
all FLC loci at similar rates, or does the proportion of 
cells that have a strong, persistent H3K27me3 nucleation 
peak increase gradually during cold exposure?
These two possibilities have recently been considered 
using mathematical modelling of FLC chromatin (Angel et al., 2015). In an analogue nucleation model, the proba-
bility of switching a locus from activated to repressed 
depends on the height of the nucleation peak, which 
increases during cold exposure at approximately the same 
rate in all cells. In the digital nucleation model, cells either 
have a nucleation peak or do not have a nucleation peak, 
with the fraction of ‘nucleated’ cells increasing for longer 
cold exposures. In the digital model, only cells with a 
nucleation peak make the switch to the silenced state (with 
high probability) after cold exposure. This study showed 
that FLC silencing with analogue nucleation is not sensitive 
to short periods of cold exposure because the small 
H3K27me3 peak generated in all cells is not sufficient to 
switch the overall chromatin state of the locus. Conversely, 
if temperature is registered using a digital nucleation peak, 
the peak can easily ‘flip’ the state of the gene after any 
length of cold exposure because the peak ‘height’ is the 
same in any nucleated cell, regardless of the duration of 
cold exposure (Angel et al., 2015). The finding that ana-
logue temperature registration does not perform well for 
short cold exposures has strong implications for how
plants perceive cold in fluctuating temperatures. Whereas digital temperature registration may function to switch states at a certain probability when plants are exposed to cold, analogue temperature registration requires longer periods of cold exposure to generate effective H3K27me3 peaks in all cells. It therefore follows that a digital nucleation mechanism is much better at buffering fluctuating temperature regimes such as those normally experienced in natural environments. The authors tested the response of FLC expression to a fluctuating temperature regime, with 4-day breaks between short cold spells. They found that plants respond similarly to interrupted and non-interrupted cold exposure. This strongly supports the hypothesis that plants register temperature signals in a digital manner, with all-or-nothing H3K27me3 peaks at the FLC nucleation region arising during cold exposure.

An experimental observation in support of digital nucleation is the physical clustering of FLC loci that occurs during cold exposure (Rosa et al., 2013). Live-cell imaging in an FLC-lacO/lacI system was used to monitor changes in the physical position of FLC loci within the nucleus during vernalization. FLC-lacO alleles were found to physically cluster during cold exposure, and generally remain clustered after plants are returned to warm conditions (Rosa et al., 2013). Clustering depends on the presence of PHD–PRC2 components necessary for switching FLC to the silenced state, but not on LHP1. The quantitative increase in clustering with cold exposure paralleled the quantitative increase in H3K27me3 at the nucleation site, suggesting a tight connection between the switching mechanism and changes in nuclear organization.

How fluctuating temperatures are translated into digital silencing is an important question that is currently being addressed. Temperature registration in a field environment was studied in a two-year census of natural populations of the perennial plant Arabidopsis halleri (Aikawa et al., 2010). Expression of flowering time genes was measured every week in plants growing in natural field conditions. FLC expression was found to decrease gradually as the winter progressed. The authors attempted to correlate FLC expression with the fluctuating temperature regime experienced by the plants, and found that FLC expression levels were best explained by the cumulative mean daily temperature over the preceding 6 weeks.

**EPIGENETIC MAINTENANCE OF THE SILENCED STATE**

The involvement of histone modifications in regulating expression of Polycomb target genes such as FLC has given rise to the hypothesis that histone modifications are not only important mechanistically for achieving transcriptional repression but may also be carriers of epigenetic memory (Kaufman and Rando, 2010; Moazed, 2011; Steffen and Ringrose, 2014). The idea is that once FLC chromatin is covered in histone modifications such as H3K27me3, these modifications are sufficient to recruit the machinery (such as PRC2) to ensure that they are maintained indefinitely at that locus despite the noisy processes of nucleosome turnover and H3K27me3 demethylation. The concept of histone modifications as carriers of epigenetic information has become so embedded in current thinking that histone modifications are commonly referred to as ‘epigenetic marks’, implying that a region of such marks has the intrinsic capacity to instruct its own maintenance and inheritance in daughter cells. The debate over whether histone modifications are the cause or consequence of epigenetically heritable transcriptional states is on-going (Ptashne, 2007; Kaufman and Rando, 2010; Henikoff and Shilatifard, 2011).

While histone modifications may act as carriers of epigenetic memory at some loci, it is worth considering other possibilities for epigenetic gene regulation that are not dependent on histone modifications. We discuss two main classes of memory mechanisms: cis memory and trans memory (Bonasio et al., 2010). In cis memory, epigenetic information is physically located at chromatin, possibly in the form of DNA methylation or histone modifications. In trans memory, epigenetic information is stored in the concentration of a diffusible factor, such as a transcriptional repressor.

**Trans memory**

In principle, both cis and trans memory mechanisms are capable of generating heritable bistable gene expression states. Trans memory is commonly used in bacterial systems such as lambda phage (Oppenheim et al., 2005), the Escherichia coli lac operon (Vilar et al., 2003) and for bet-hedging in bacterial populations (Veenning et al., 2008). Trans memory uses trans-acting feedback loops to generate multiple stable expression states. A simplified trans memory network is shown in Figure 4(a). The system comprises two genes, A and B, that mutually repress each other’s transcription and also auto-activate. For simplicity, A and B may be thought of as transcription factors. If gene A is expressed highly, then gene B will be repressed, and vice versa, which leads to two (mutually exclusive) stable states (A high/B low or A low/B high) (Figure 4a). Furthermore, it is easy to see how such a trans memory system leads to inheritance of expression states in daughter cells. As the DNA is replicated in a ‘low A/high B’ cell, protein B continues to activate its own expression, maintaining a constant concentration as the cell grows. When the cell divides, molecules of B are divided roughly equally between daughter cells, where they continue to activate expression of gene B (and repress expression of gene A). Thus, the low A/high B state is inherited.

While this is an artificially simple example, a complex gene regulatory network with many components and feed-
backs may also generate epigenetically stable expression states by means of trans-regulation. Reference to sequence-specific DNA-binding proteins such as transcription factors is convenient for explaining the concept of trans memory; however, other more exotic gene regulation mechanisms such as those involving trans-acting small RNAs also function in conceptually similar ways (Stuwe et al., 2014).

**Cis memory**

Like trans memory, cis memory must be bistable, i.e. it must have two self-perpetuating alternative gene expression states. Each of the ‘A’ and ‘M’ marks may recruit more modifications of the same type to nearby nucleosomes. Stable states are encoded by the local proportion of ‘M’ and ‘A’ histone marks. Inheritance in cis memory occurs by passing on nucleosomes to daughter DNA strands at the replication fork. Newly incorporated (unmodified) nucleosomes may be modified in the same way as the parental DNA because the inherited modifications recruit the relevant modification complexes.

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**Figure 4.** Mechanisms of epigenetic memory.  
(a) Trans memory. A hypothetical gene regulatory network containing transcription factors A and B is shown. These mutually repress each other’s transcription. Stable states of this network are encoded by the global concentrations of these factors. Inheritance in trans memory occurs by passing on high concentrations of one of the diffusible factors to the daughter cells.  
(b) Cis memory. A hypothetical three-state model of modified histones is shown. Each of the ‘A’ and ‘M’ marks may recruit more modifications of the same type to nearby nucleosomes. Stable states are encoded by the local proportion of ‘M’ and ‘A’ histone marks. Inheritance in cis memory occurs by passing on nucleosomes to daughter DNA strands at the replication fork. Newly incorporated (unmodified) nucleosomes may be modified in the same way as the parental DNA because the inherited modifications recruit the relevant modification complexes.
tion states. However, the key difference compared with trans memory is that the information carriers are physically located at the gene itself. DNA methylation is a more well-established carrier of epigenetic memory in cis than histone modifications (Chan et al., 2005). However, DNA methylation does not appear to be involved in FLC regulation during vernalization (Finnegan et al., 2005). Whether histone modifications can act as heritable elements that ensure propagation of activated and repressed states is still an open question. A pioneering theoretical model based on this hypothesis was initially developed to describe epigenetic memory at the silent mating-type region of the yeast Schizosaccharomyces pombe (Dodd et al., 2007). A conceptually similar model was later applied to the study of FLC, and demonstrated quantitative agreement with experimental chromatin immunoprecipitation data regarding switching of bistable epigenetic states at FLC through vernalization (Angel et al., 2011).

The model postulates that nucleosomes exist in one of three states: M (methylated/repressive), U (unmodified) and A (activating) (Dodd et al., 2007). Like trans memory, bistability in the cis memory model requires feedback. The feedback is implemented in the model in the following manner: modified nucleosomes such as M (e.g. H3K27me3) have the ability to recruit protein complexes (such as PRC2) to similarly modify nearby nucleosomes. This positive feedback of histone modifications tends to cause the region of chromatin to be predominantly covered in either M or A nucleosomes. The model therefore generates two stable chromatin ‘states’. The underlying molecular explanation for this ‘M recuits more M’ feedback mechanism in the case of PRC2 is thought to be that PRC2 contains one subunit that binds to H3K27me3 and another subunit that adds H3K27me3 (Hansen et al., 2008; Margueron et al., 2009). The molecular basis of the other feedbacks in the model is less well understood, but nonetheless the theoretical requirement for these feedbacks suggests interesting directions for future experiments.

Why does the model need so many feedbacks? The key problem with storing epigenetic information in histone modifications is that the nucleosomes may be removed and replaced over time scales of hours (Jamai et al., 2007; Deal et al., 2010). If the marks are not re-written on a shorter time scale than this, chromatin states are not maintained, even within a cell cycle. The second major hurdle that a model of histone modification-based memory must overcome is inheritance through cell division. How is it that this model ensures inheritance of the ‘high M’ and ‘high A’ chromatin states? It is well known from many experiments (mainly in yeast and Drosophila) that nucleosomes are inherited semi-conservatively as DNA is replicated (Anunziato, 2005), i.e. nucleosomes are shared between daughter strands (Figure 4b). The hypothesis is that the histone modifications are also shared equally between daughter strands. If the spaces between the inherited nucleosomes are filled with new unmodified nucleosomes, a newly replicated DNA strand will have approximately half as many histone modifications as the original region of chromatin. The feedbacks in the model ensure that these modifications are sufficient to recruit the required protein complexes to ‘fill in the gaps’, and thus propagate the epigenetic state (Dodd et al., 2007) (Figure 4b). While inheritance of nucleosomes during DNA replication is well established, recent experiments in C. elegans have shown that histone modifications (H3K27me3) may also be passed on to daughter chromosomes in the absence of PRC2 (Gaydos et al., 2014), supporting the hypothesis that inherited histone marks may underlie epigenetic memory. In addition, it has been proposed that Polycomb and Trithorax proteins themselves are passed on locally at the DNA replication fork (Francis et al., 2009; Petruk et al., 2012), which may further contribute to the epigenetic stability of chromatin domains in a cis memory mechanism.

Memory is stored in cis at FLC

The components required for switching and maintenance of FLC expression states that were isolated using unbiased genetic screens suggest the existence of a chromatin-based mechanism for epigenetic memory. However, until recently, it remained difficult to exclude the existence of trans factor-based memory because FLC protein (a MADS-box transcriptional repressor) or non-coding RNA produced at the FLC locus could feed into a bistable trans-regulatory network. A recent study used two distinguishable fluorescent reporters of FLC expression in the same cells to investigate the cis-memory storage capability of FLC chromatin (Berry et al., 2015). It was shown that, after vernalization, two copies of FLC in the same cell may be in different expression states, i.e. one of the FLC reporters may be repressed in the same cell as the other reporter is active. Furthermore, the authors found that this ‘mixed’ expression state is stably inherited through several cell divisions. This indicates that the epigenetic memory of FLC expression is physically located in the local chromatin environment (Berry et al., 2015). It is therefore the chromatin state, rather than concentrations of diffusible trans factors, that dictates FLC transcription after vernalization. Together with previous results, this finding supports the hypothesis that histone modifications such as H3K27me3 are important components of epigenetic memory.

Instructive and responsive chromatin

In the case of cis memory, the chromatin state is responsible for instructing its own inheritance, and may therefore be referred to as ‘instructive’. In the case of trans memory, chromatin may still play a vital role in mediating the effects of trans factor binding events to orchestrate gene regula-
tion. However, in this case, chromatin is ‘responsive’ to trans factors rather than being the key epigenetic memory element.

*FT* is an example of Polycomb-repressed chromatin in *Arabidopsis* that may be ‘responsive’ rather than ‘instructive’. The *FT* locus is covered in high levels of H3K27me3 in the repressed state (Adrian *et al.* 2010), and repression depends partly on LHP1, which binds *FT* chromatin (Takada and Goto, 2003). However, the memory of repression is at least partly maintained by high concentrations of repressive trans factors, including *FLC* and SHORT VEGETATIVE PHASE (SVP) (Hepworth *et al.* 2002; Li *et al.*, 2008).

**Natural variation in epigenetic memory**

DNA sequence variation at *FLC* influences epigenetic silencing, and is likely to be very useful in elucidating chromatin switching and maintenance mechanisms (Li *et al.*, 2014). Genomic sequence analysis of >1000 accessions identified 20 *FLC* haplotypes that are defined only by non-coding polymorphisms. There were five high-frequency groups in the worldwide population. These multiple, functionally distinct *FLC* haplotypes appear to have been maintained in the population, and probably contribute to the broad geographical and niche ranges of *A. thaliana* accessions. The various groups had distinct epigenetic silencing characteristics. Two vernalized quickly, with a relatively short period of cold exposure (4–6 weeks) being sufficient for full epigenetic silencing. The remaining three vernalized slowly, with a longer period of cold exposure (10–12 weeks) required for silencing (Shindo *et al.*, 2006; Li *et al.*, 2014). When transgenes containing the various *FLC* haplotypes were transformed into a common genetic background, the same differences in regulation remained, demonstrating that the non-coding sequence polymorphisms influenced the rate of *FLC* epigenetic silencing (Li *et al.*, 2014). Detailed analysis of which sequence polymorphisms affect epigenetic memory was performed for the Northern Swedish accession Lov-1 (Coustham *et al.*, 2012). The Lov-1 accession is particularly unresponsive to short cold periods: 4 weeks is not sufficient to stimulate flowering, and seedlings need 12 weeks of cold exposure to fully saturate the vernalization requirement (Shindo *et al.*, 2006; Strange *et al.*, 2011). Transgenic studies analysing *FLC* constructs with different combinations of polymorphisms from the Lov-1 and Col-0 alleles showed that four distinct single nucleotide polymorphisms in the nucleation region of Lov-1 *FLC* accounted for a large proportion of the requirement for extended cold exposure (Coustham *et al.*, 2012).

**REPROGRAMMING *FLC* EXPRESSION IN THE SEED**

As the germ line in plants arises from the somatic tissues, extensive epigenetic reprogramming occurs prior to the next generation. This includes *FLC*, whose expression needs to be ‘reset’ at some stage after the floral transition to ensure a vernalization requirement in each generation. Unlike the slow quantitative switching from the ‘ON’ to ‘OFF’ state during cold exposure, the reprogramming occurs relatively synchronously in the developing seeds. *FLC* expression increases throughout embryogenesis, and reaches a maximum when the seed has fully formed (Sheldon *et al.*, 2008; Choi *et al.*, 2009). The activation in the early multicellular embryo occurs independently of *FRI* and autonomous pathway genes, which have major effects from late embryogenesis onwards (Choi *et al.*, 2009). While *FLC* expression is cell-autonomous after vernalization, it is currently not clear whether this is also true during resetting of *FLC* expression during embryogenesis and then during subsequent development in the next generation.

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Figure 5. *FLC* resetting.
(a) *FLC* expression is reset during embryogenesis. *FLC* expression increases from silique stage 17a (early globular embryo) until stage 19 (mature seed) (Roeder and Yanofsky, 2006). Resetting after vernalization is disrupted in the H3K27me3 demethylase mutant elf6-5.
(b) Perennials such as *Arabidopsis halleri* and *Arabis alpina* show down-regulated *FLC* expression each winter; *FLC* expression is then reset in all meristems, preventing flowering in those that have not yet expressed floral activators.
A genetic screen for mutants that fail to fully reset $FLC$ expression in the generation after vernalization revealed a role for *EARLY FLOWERING 6* (*ELF6*) (Crevillen et al., 2014) in epigenetic reprogramming (Figure 5a). $FLC$ expression was only slightly lower in *elf6*-5 than the wild-type if plants were not subjected to cold exposure (provided the previous generation was not vernalized). However, the increase in $FLC$ expression normally observed during resetting was much lower in *elf6*-5. This reduced expression and early flowering was inherited over subsequent generations, thus the *elf6*-5 mutation caused partial trans generational inheritance of vernalization-induced $FLC$ repression (Crevillen et al., 2014).

*ELF6* encodes a jumonji domain-containing protein with H3K27me3 demethylase activity that is highly expressed in flowers and embryos (Crevillen et al., 2014). This suggests that the hypomorphic mutation in *elf6*-5 leads to failure to fully remove the H3K27me3 modifications induced through vernalization. Inheritance of this repressed state in the germ line supports the role of H3K27me3 as a carrier of epigenetic information.

The timing of resetting differs in annual plants compared to perennial relatives (Wang et al., 2009). In perennials, only a subset of meristems switch to reproductive development at any one time. This appears to be achieved through combination of a requirement for specific environmental conditions with variation in meristem reproductive competence (Turck and Coupland, 2014). A homologue of $FLC$, *PERPETUAL FLOWERING 1* (*PEP1*), is needed in *Arabidopsis alpina* for perennial flowering (Wang et al., 2009). Like *FLC* in the annual *A. thaliana*, *PEP1* expression in *Arabis alpina* decreases during cold exposure in all meristems. In reproductive-competent meristems, this is sufficient to induce expression of downstream floral activators. However, unlike *A. thaliana*, there is only transient epigenetic memory of prolonged cold exposure (Figure 5b). On return to warm conditions, *PEP1* expression is reset, preventing flowering in those meristems that are not yet expressing floral activators. Mathematical modelling has suggested that the relative rates of addition/removal of activating and repressive histone modifications at $FLC$/$PEP1$ after cold exposure may account for differences in stability of the repressed epigenetic states (Satake and Iwasa, 2012). The genetic determinants of earlier resetting in *Arabis alpina* compared to *A. thaliana* are yet to be fully determined, but
appear to involve both cis regulatory sequence variation and differences in trans factors (Castaings et al., 2014).

**Opposing functions of FRIGIDA and autonomous pathways set the FLC expression level**

The expression level to which FLC is reset in the seed has significant consequences on the reproductive strategy of the plant. High FLC expression leads to a strong vernalization requirement, requiring over-wintering of plants before flowering. Low FLC expression relaxes the requirement for vernalization, and leads to the potential for rapid cycling, thus achieving multiple generations per year. The expression level of FLC is set by the opposing activities of the FRIGIDA (FRI) pathway (activating) and the autonomous pathway (repressive) (Koornneef et al., 1998). These participate in a ‘tug-of-war’ to set and maintain the FLC expression from late embryogenesis and into vegetative growth (Figure 6). The genetic and molecular analyses of the autonomous and FRIGIDA pathways have been reviewed previously (Crevillen and Dean, 2010; Letswaart et al., 2012). Here, we focus on how opposing FLC chromatin states are established by the two pathways to set the transcription level of FLC. This occurs in the developing embryo and is maintained through vegetative development, unless cold-induced silencing occurs.

The autonomous pathway represses FLC expression, resulting in early flowering (Koornneef et al., 1991). Components that function in this pathway include the RNA-binding proteins FCA (Macknight et al., 1997; Quesada, 2003) and FPA (Schomburg et al., 2001), the 3′ processing factors FY (Simpson et al., 2003) and Cstf77/Cstf64 (Liu et al., 2010), the core spliceosome subunit PRP8 (Marquardt et al., 2007, 2014), the chromatin regulators FLD (Liu et al., 2007), pTEFb (Wang et al., 2014) and LD (Lee et al., 1994). Low FLC expression is associated with a specific chromatin state: low acetylation, H3K4me2, H3K36me3 and high H3K27me3 (He et al., 2003; Yang et al., 2014) (Figure 6a). Conversely, high FLC expression requires FRIGIDA complex components: Trithorax-like SET-domain proteins ATX1 (Pien et al., 2008), SDG25 (Berr et al., 2009; Tamada et al., 2009), SDG7 (Lee et al., 2015) and SDG8 (Yang et al., 2014), and the WD40-domain protein AtWDR5a (Jiang et al., 2009) (Crevillen and Dean, 2010). The activated chromatin state is characterized by high acetylation, low H3K27me3, high H3K4me3/H3K36me3 in the nucleation region, and accumulation of H3K4me2 in the gene body (Figure 6b) (He et al., 2003; Liu et al., 2007; Yang et al., 2014). At elevated temperature, the H3K27 demethylase JMJD30 is also required for high FLC expression (Gan et al., 2014).

Central to the autonomous pathway function is a co-transcriptional coupling between COOLAIR processing and the chromatin state at FLC (Figure 6a). COOLAIR is alternatively spliced and polyadenylated (Liu et al., 2007, 2010; Hornyik et al., 2010; Marquardt et al., 2014; Wang et al., 2014). Autonomous pathway components promote use of both the proximal COOLAIR splice acceptor site and the proximal polyadenylation site, and result in FLD-dependent H3K4me2 demethylation in the FLC gene body. This particular chromatin state then reinforces choice of the proximal splice site and polyadenylation site (Marquardt et al., 2014), possibly via a kinetic coupling mechanism (Allo et al., 2009). Slow transcription has been linked to proximal splice site choice and early termination (de la Mata et al., 2003; Hazelaiker et al., 2013).

High expression of FLC is promoted by FRIGIDA function through a Trithorax-like mechanism (Figure 6b). FRIGIDA associates with components of the RNA 5′ cap-binding complex for the nascent transcript, and leads to a higher proportion of the FLC transcripts containing a 5′ cap. Natural polymorphisms that alter splicing of distally polyadenylated COOLAIR promote FLC transcription, also via an influence on the capping of the nascent transcript (Li et al., 2015). The directly opposing functions of the autonomous and FRIGIDA pathways therefore mechanistically converge on the co-transcriptional link between COOLAIR processing and recruitment of chromatin regulators. Natural non-coding polymorphisms that define the functionally distinct FLC haplotypes (Li et al., 2014) may alter one of these opposing pathways, with small changes in either being magnified by the opposing effect of the other.

Given the central role of COOLAIR in regulation of FLC in both warm and cold conditions, it is interesting to consider specific regulators of COOLAIR expression. COOLAIR transcription is initiated from a non-canonical promoter within a genomic region carrying termination sequences for the sense transcript, a feature that is frequently found in yeast (Murray et al., 2012). Small RNAs (24- and 30-mers) homologous to the COOLAIR promoter have been detected, and these are required for maintenance of a small patch of H3K9me2-modified chromatin just upstream of the major COOLAIR start site in reproductive tissues (Swiezewski et al., 2007). To enable genetic screens for specific COOLAIR regulators, the COOLAIR transcript was modified to contain a luciferase-coding sequence (Swiezewski et al., 2009). These studies identified a homeodomain protein (AtNDX1) that binds to single-stranded DNA in a non-sequence-specific manner (Sun et al., 2013). This homeodomain protein stabilizes an RNA-DNA heteroduplex structure (called an R-loop) that extends from 200 bp upstream of the COOLAIR promoter for 300–700 nucleotides, sometimes reaching the COOLAIR proximal polyadenylation site. The R-loop suppresses COOLAIR transcription, probably through prevention of RNA polymerase II elongation (Sun et al., 2013). COOLAIR transcription through the R-loop is promoted by the P-TEFb transcription elongation complex (Wang et al., 2014). Although it was isolated specifically as a COOLAIR regulator, a mutation in the gene encoding AtNDX1 increased
both COOLAIR and FLC expression in the endogenous gene context (Sun et al., 2013), demonstrating the tight link between sense and antisense transcription. Such sense/antisense coordination may be aided by the presence of an FLC gene loop, which involves physical interaction of the 5’ and 3’ regions (Crevillen et al., 2012), and/or the antisense transcription unit fully encompassing the sense transcription unit (Szwiezewski et al., 2009). Another possibility is that sense or antisense transcription may influence the likelihood of a subsequent transcriptional event through modulation of the FLC chromatin environment.

CONCLUSION

The many regulatory inputs make FLC appear a very complex locus. However, as our understanding progresses, a conceptually simple mechanism is emerging. We see FLC regulation as a chromatin state switching system. FLC chromatin has an ON state, is switched to an OFF state by the environment (over-wintering) or through genotype, and is then switched back to the ON state by reprogramming (reversing the switch). Both the maintenance of states and switching between states involves an intimate connection between chromatin regulators and sense/antisense RNA transcription and processing – a mechanism that has yet to be fully elaborated. Nuclear organization is an additional layer of regulation.

Cell-autonomous epigenetic switching performs the biological function of registering and remembering unpredictable and noisy temperature signals. An emerging theme is that the relative stabilities of activated and repressed epigenetic states appear to have been subtly modulated in natural accessions by cis sequence variation to generate a range of FLC haplotypes with characteristic responses to cold exposure. This may be because many of the regulators of FLC (such as Polycomb/Trithorax and the RNA 3’ processing machinery) are not specific to FLC regulation but instead perform more general tasks all over the genome. FLC is unlikely to be exceptional with respect to gene regulation; it has just been studied in more detail than most genes. Whenever an adaptive trait depends so closely on quantitative gene expression levels, subtle changes in regulation have strong consequences on fitness. In these cases, we may expect a similar level of complexity in gene regulation. As such, FLC continues to provide a valuable paradigm for studies of chromatin-based gene regulation, environmental perception and decision making.

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