Integration of Transcriptional Repression and Polycomb-Mediated Silencing of WUSCHEL in Floral Meristems

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Arabidopsis (Arabidopsis thaliana) floral meristems terminate after the carpel primordia arise. This is achieved through the temporal repression of WUSCHEL (WUS), which is essential for stem cell maintenance. At floral stage 6, WUS is repressed by KNUCKLES (KNU), a repressor directly activated by AGAMOUS. KNU was suggested to repress WUS through histone deacetylation; however, how the changes in the chromatin state of WUS are initiated and maintained to terminate the floral meristem remains elusive. Here, we show that KNU integrates initial transcriptional repression with polycomb-mediated stable silencing of WUS. After KNU is induced, it binds to the WUS promoter and causes eviction of SPLAYED, which is a known activator of WUS and can oppose polycomb repression. KNU also physically interacts with FERTILIZATION-INDEPENDENT ENDOSPERM, a key polycomb repressive complex2 component, and mediates the subsequent deposition of the repressive histone H3 lysine 27 trimethylation for stable silencing of WUS. This multi-step silencing of WUS leads to the termination of floral stem cells, ensuring proper carpel development. Thus, our work describes a detailed mechanism for heritable floral stem cell termination in a precise spatiotemporal manner.

INTRODUCTION

In Arabidopsis (Arabidopsis thaliana), stem cells are confined to a specific domain called the meristem. In the shoot apical meristem (SAM), stem cells are constitutively active and contribute to continuous growth. However, in the floral meristem, stem cells are terminated after initiation of the full complement of floral organs to ensure proper differentiation of the reproductive organs of the flower. The homeobox gene WUSCHEL (WUS), which is expressed in the organizing center (OC) of the SAM and in the floral meristem, plays an important role in the maintenance of the stem cell pool (Mayer et al., 1998). In the SAM, WUS is a direct target of SPLAYED (SYD), an ATP-dependent SWItch/Sucrose Non-Fermentable (SWI/SNF) chromatin remodeling factor (Kwon et al., 2005), which utilizes the energy of ATP hydrolysis to alter the accessibility of cis-regulatory DNA regions for the transcriptional machinery (Cairns, 2005). WUS is transcriptionally activated by SYD, which is required for the proper maintenance of stem cells (Kwon et al., 2009), and this is accompanied by deposition of the histone trimethylation on lysine 4 of histone H3 (H3K4me3) activation mark (Berger et al., 2011). WUS is also a target of PRC2-mediated epigenetic repression via histone H3K27me3 (Zhang et al., 2007). H3K27me3 is catalyzed by the polycomb repressive complex2 (PRC2). During reproductive developmental, the PRC2 complex includes CURLY LEAF (CLF), which is an H3K27 methyltransferase (Goodrich et al., 1997). Another PRC2 component, FERTILIZATION-INDEPENDENT ENDOSPERM (FIE), is a homolog of the Dro sophila WD motif-containing protein extra sexcombs (Esc; Ohad et al., 1999). FIE can physically interact with CLF, and knockdown of FIE leads to strong morphological aberrations, suggesting that FIE plays an important role in the control of vegetative and reproductive development (Katz et al., 2004). In addition, EMBRYONIC FLOWER2 (EMF2) can also interact directly with CLF. Mutation of EMF2 results in drastic early flowering phenotypes (Yoshida et al., 2001). TERMINAL FLOWER2 (TFL2)/LIKE HETEROCROMATIN PROTEIN1 may be a functional component of PRC1 and localizes with the repressive mark H3K27me3 throughout the Arabidopsis genome (Turck et al., 2007).

In Arabidopsis, several factors are known to recruit PcG to individual genes. During vernalization, the noncoding RNA
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Background: During early flower development, self-renewing stem cells produce enough cells to be consumed for the formation of floral organs, including sepals, petals, stamens, and carpels, which are patterned in concentric rings. Floral stem cells are specified by the gene named WUSCHEL (WUS). At a certain stage of flower development, WUS is repressed and silenced; therefore, floral stem cell activity vanishes to ensure proper development of carpels. We previously found that a small protein named KNUCKLES (KNU) functions as an upstream repressor of WUS, with the result that floral stem cell activity is terminated.

Question: We wanted to understand how KNU represses and silences WUS in a detailed manner. Before this, little was known regarding the final events of floral stem cell termination at high resolution.

Findings: We found that KNU integrates initial transcriptional repression with epigenetic stable silencing of WUS. KNU protein directly binds to the WUS promoter and causes eviction of SPLAYED (SYD) protein from the WUS gene. SYD is a known activator of WUS and can act against the repressive chromatin status of WUS. KNU protein also physically interacts with FERTILIZATION-INDEPENDENT ENDOSPERM (FIE), which mediates the silencing of WUS at the chromatin level. These multi-step events lead to the termination of floral stem cells, thus ensuring proper carpel development.

Next steps: We are working on how the robust stem cell activity is fully shut off within a narrow time window to secure the proper timing of carpel differentiation.

RESULTS

Spatial and Temporal Association between KNU and WUS in the Floral Meristem

A plant line doubly transgenic for ProKNU:KNU-VENUS (Sun et al., 2014) and ProWUS:green fluorescent protein (GFP)-endoplasmic reticulum (ER; Gordon et al., 2007) was established to examine the spatiotemporal expression patterns of KNU and WUS. Prominent WUS expression was observed in the SAM and in the floral meristems of stages 2 to 6 flower buds (Smyth et al., 1990; Mayer et al., 1998), whereas KNU activity was only detected in flower buds from stage 6 onward (Figures 1A and 1C; Supplemental Figures 1A to 1C). KNU expression was initially detected in the central zone (Figure 1B; Supplemental Figures 1D to 1F), which later became broader, including the top three stem cell layers and OC (Supplemental Figures 1G to 1O). This transient overlap at floral stage 6 in the expression domains of KNU and WUS hints at cell-autonomous repression of WUS by KNU. In the ProWUS:β-glucuronidase (GUS) line (Baurle and Laux, 2005), WUS was detected in the SAM and in early stage 6 flower buds, but it was absent from late stage 6 flower buds (Figures 1D to 1F). By contrast, in the ProKNU:KNU-GUS line (Sun et al., 2009), KNU was detected in early stage 6 flower buds in the stem cell niche and in late stage 6 flower buds in developing carpels (Figures 1G to 1I). In floral stage 7, compared with silenced activity of WUS (Supplemental Figure 1P), KNU expression continues at the basal part of developing carpels and starts at the abaxial side of stamen primordia (Supplemental Figure 1Q). KNU expression later converged on the basal central cells of carpels (Figure 1C), which were previously described as silenced late OC cells (Liu et al., 2011), suggesting that KNU may be required in these cells for persistent silencing of WUS.

To examine the detailed timing of WUS repression by KNU, a line with inducible KNU activity, apetala1 caulifower (ap1 cal) Pro35S:KNU-AR, was used for quantitative (q)PCR expression analysis (Figures 2A and 2B). In ap1 cal Pro35S:KNU-AR, the ap1
double mutant enriches for meristematic tissues (Alvarez-Buylla et al., 2006), while KNU-AR, a fusion protein between KNU and the steroid hormone ligand binding domain of the androgen receptor (AR), is sufficient to inducibly terminate the floral meristems upon continuous induction of the KNU activity (Sun et al., 2009). A single 5α-androstan-17β-ol-3-one (DHT) treatment lead to a 40% decrease in the WUS mRNA level at 4 h relative to the 0-h time point. At 8 h and 12 h after induction, we observed a trend toward an increase in WUS expression (Figure 2A), which could be explained by a CLAVATA (CLV)-dependent compensation mechanism (Müller et al., 2006). We also treated the ap1 cal Pro35S:KNU-AR plants with cycloheximide (CHX, a protein synthesis inhibitor) alone or with CHX together with DHT and found that WUS repression by KNU is independent of protein synthesis (Figure 2B). In addition, in ProWUS:GUS Pro35S:KNU-AR in response to continuous DHT treatment followed by staining at 1, 2, 3, and 5 d after the start of treatment, WUS expression remains repressed by KNU (Figure 2C). Thus, WUS may be directly

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**Figure 1.** KNU and WUS Expression Patterns.

(A) Confocal observation of the doubly transgenic inflorescence for ProWUS:GFP-ER (Gordon et al., 2007) (red) and ProKNU:KNU-VENUS (green), which was confirmed to rescue knu-1 (Sun et al., 2014). *, shoot apical meristem. Numbers, floral stages (Smyth et al., 1990).

(B) Higher magnification of the side view of a stage 6 floral bud of ProWUS:GFP-ER ProKNU:KNU-VENUS. The inset in (B) is the close-up of the central zone, showing WUS and KNU expression in meristematic cells.

(C) ProKNU:KNU-GUS (Sun et al., 2009) staining in a wild-type flower at stage 8. Bars = 50 μm for (A) to (C).

(D) to (I) GUS staining of ProWUS:GUS and ProKNU:KNU-GUS in the wild-type inflorescences, early stage 6 and stage 7 flowers.

(D) to (F) ProWUS:GUS staining in inflorescence (D), early stage 6 flower bud (E), and late stage 6 flower bud (F).

(G) to (J) ProKNU:KNU-GUS staining in inflorescence (G), early stage 6 flower bud (H), and late stage 6 flower bud (I). Bars = 100 μm for (D) to (I).
repression of KNU and the repression can be maintained, if KNU is continuously expressed. Because KNU is also expressed in stem cell layers (Figure 1B; Supplemental Figures 1M to 1Q), we monitored the expression of CLV genes as well. CLV1, CLV2, and CLV3 expression all show initial reduction by KNU at 4 h after DHT treatment but recovery later (Figure 2D), suggesting CLV genes may also be repressed by KNU.

To test whether and in what time course the KNU protein directly binds WUS, we performed chromatin immunoprecipitation (ChIP) in ap1 cal Pro35S:KNU-AR-myc using an antibody against c-Myc. Plants were treated with DHT at 0 and 24 h twice, and inflorescences were harvested at 4 and 48 h, respectively, after the start of initial treatment (Figures 3A and 3B; Supplemental Figures 2A and 2B). An approximate 1.8-fold moderate enrichment of KNU was detected at the WUS promoter in the region from −308 bp to −125 bp upstream of the ATG start codon (primer set W2, Supplemental Table) as early as 4 h (Supplemental Figures 2A and 2B). We also noticed that at 4 h, an approximate 1.6-fold moderate enrichment can be detected within the first intron of WUS (primer set W3, Supplemental Table). At 48 h, we detected stronger (up to twofold) enrichment of KNU binding at the W2 site of the WUS promoter (Figures 3A and 3B). The initial binding at 4 h of KNU at W3 is consistent with a report that KNU is within a histone deacetylation complex associated with the first intron of WUS (Bollier et al., 2018). Because histone acetylation is associated with transcriptional activity (Sawarkar and Paro, 2010), we monitored H3 acetylation level on WUS chromatin upon KNU activation. We found a 40% decrease of H3 acetylation level in the first intron of WUS (primer set W3, Supplemental Table) by 4 h, and no further reduction of H3 acetylation by 12 h (Figures 3A and 3C). This agrees with the recent finding that KNU affects WUS chromatin via H3 deacetylation (Bollier et al., 2018). By contrast, the binding of KNU on the first intron of WUS (W3 region) is not detectable at the 48-h time point (Figures 3A and 3B).

To verify the binding of KNU to the WUS promoter, we performed yeast one-hybrid assays. The result confirmed direct binding of KNU to the W2 region of the WUS proximal promoter (Figures 3A and 3D). The direct binding of KNU was further examined by electrophoretic mobility shift assays (EMSAs). Four fragments for the W2 region (W2-1 to W2-4) were biotin labeled and incubated with maltose binding protein (MBP)–tagged KNU protein. We also used two fragments for the W1 region (W1-1 and W1-2) as controls. W2-1 and W2-4 produced clear band shifts (Figures 3A and 3E), while W1-1 and W1-2 showed no band shifts (Figures 3A and 3F). Moreover, the addition of excess unlabeled competitor probes effectively reduced the amount of shifted bands (Supplemental Figure 3C), repressing the KNU bound cis-element, we first used 5’ upstream sequences of WUS to carry out phylogenetic shadowing with eight Brassicaceae species (O’Malley et al., 2016; Yamaguchi et al., 2018). Three conserved regulatory modules (CRMs) were identified and defined as CRM1, CRM2, and CRM3 (Supplemental Figure 3A). Because the W2 region is within the CRM3, CRM3 was further analyzed and we noticed there is a conserved core aatc motif (Supplemental Figure 3B), which is also found in both W2-1 and W2-4 fragments. Mutating aatc to gggg in W2-1– and W2-4–unlabeled competitor probes cannot reduce the amount of shifted bands (Supplemental Figure 3C),...
Figure 3. KNU Binds to the WUS Promoter.

(A) Schematic diagram showing the WUS locus and the promoter region used for ChIP assays, yeast one-hybrid assays, and EMSAs in (B) to (G). Black rectangles represent coding regions. Fragments: W1-1, −648 to −583; W1-2, −582 to −518; W2-1, −308 to −265; W2-2, −264 to −213; W2-3, −212 to −175; W2-4, −174 to −125 bp upstream from the ATG start codon.

(B) ChIP assay using ap1 cal 35S:KNU-AR-3myc inflorescences harvested 48 h after DHT treatment. Nuclear protein complexes were immunoprecipitatd with anti-c-Myc agarose beads, and the enriched DNA was used for qPCR analysis. The y axis shows relative enrichment using anti-HA agarose beads as a control. Mu-like transposons served as a negative control locus and were set to 1. Asterisks indicate significant differences between the control locus (MU) and different primer sets of WUS (*P < 0.05, Student’s t test).

(C) ChIP assay using ap1 cal 35S:KNU-AR inflorescences harvested at 0, 4, and 12 h after a single 100 nM DHT treatment. The y axis shows the calibrated relative ratio of bound DNAs to input DNAs after IP. Mu-like transposons served as a negative control locus and were set to 1. Error bars represent the SD of three (B) and two (C) biological replicates with three technical replicates each. Asterisks indicate significant differences between different time points at certain primers sets of WUS (*P < 0.05, Student’s t test).

(D) Yeast one-hybrid assays demonstrate that KNU associates with the WUS promoter W2 region. AbA, Aureobasidin A.

(E) to (G) EMSAs confirm that KNU binds to the W2-1 and W2-4 fragments. The arrow indicates the DNA–protein complex. Nonlabeled oligonucleotides were used as competitors. MBP was used as a negative control.
indicating that the aact motif could be the putative KNU binding cis-element.

**Polycomb-Mediated Epigenetic Silencing of WUS Is Delayed Relative to WUS Repression**

To determine whether the transcriptional repression of WUS by KNU is associated with PcG-mediated silencing of the WUS locus, the H3K27me3 level on WUS was examined at different time points after the DHT treatment in ap1 cal Pro3SS;KNU-AR inflorescences. An increase in the H3K27me3 level at the WUS locus was observed at 8 and 12 h, but not at 4 h, after DHT treatment relative to that at the 0-h time point (Figures 4A and 4B; Supplemental Figures 4A and 4B). By contrast, WUS transcript was repressed by KNU within 4 h in the same inducible line (Figures 2A and 2B). Thus, transcriptional repression of WUS by KNU precedes deposition of the repressive mark H3K27me3, which may be required for heritable silencing of WUS at the chromatin level. We also examined dynamic FIE enrichment on WUS chromatin using ap1 cal Pro3SS;KNU-AR ProFIE:FIE-VENUS, a line generated by crossing ap1 cal Pro3SS;KNU-AR with ProFIE:FIE-VENUS (Sun et al., 2014). An increase in FIE enrichment at the WUS locus was observed at 4 h and 12 h (Figures 4A and 4C). These results suggest that H3K27me3 may be deposited in a KNU-dependent manner and that there are a few to several hours of time lag between PRC2 binding and H3K27me3 deposition.

The proximal promoter region (primer set W2, Supplemental Table), where KNU binds to the promoter within 4 h. The eviction of SYD from the proximal promoter (covering regions including both W1 and W2 primer sets, Supplemental Table) at 0 h. However, SYD binding became weaker (~40% decrease in occupancy at the W2 region, P < 0.05) at 4 h and even weaker at 12 h (~30% of the initial occupancy at W2, P < 0.01; Figures 4A and 4D). This suggests that binding of KNU leads to the eviction of SYD from the WUS promoter within 4 h. The eviction of SYD preceded the deposition of H3K27me3 (Figures 4B and 4D; Supplemental Figures 4A and 4B), suggesting that KNU triggers transcriptional repression at least partially by acting antagonistically with SYD.

By opening the WUS locus, SYD may contribute to higher DNA accessibility (Cairns, 2005) and deposition of H3K4me3 (Wu et al., 2012), a mark associated with actively transcribed chromatin (Sawarkar and Paro, 2010). To comprehensively understand the epigenetic events on the WUS chromatin upon KNU activation, the dynamic level of H3K4me3 and DNA accessibility at WUS was examined. At 0 h, in ap1 cal Pro3SS;KNU-AR inflorescences, high H3K4me3 levels were detected, which peaked at the proximal promoter of WUS (primer set W2, Supplemental Table). KNU activation resulted in a slight decrease of the H3K4me3 level at 4 h (~20% decrease at W2) and a further reduction by 12 h (~50% of initial level at W2; Figures 4A and 4E). To assess the dynamic accessibility of the WUS locus upon KNU activation, we used formaldehyde-assisted isolation of regulatory elements (FAIRE), a method that enriches accessible (nucleosome-depleted) genomic DNA from crosslinked chromatin (Simon et al., 2012). FAIRE revealed an ~50% decrease of the accessibility at the WUS locus, especially at the KNU-bound region (primer set W2, P < 0.01; Supplemental Table), within 4 h after KNU induction. Twelve hours after KNU induction, accessibility to the WUS locus decreased even further, to 24% of the initial levels (P < 0.01; Figures 4A and 4F). To check whether WUS locus accessibility disrupts RNA polymerase II (Pol II) function, we performed a ChIP assay to examine Pol II enrichment at the WUS locus. We noticed an ~50% decrease of Pol II enrichment on the proximal promoter of WUS (primer set W2, Supplemental Table) at 4 h and an ~70% decrease at 12 h (Figures 4A and 4G).

To assess the genetic interaction between KNU and SYD, we crossed a null mutant knu-2 (Sun et al., 2009) with a null allele of syd-5 (Bezhani et al., 2007). The double mutant flowers show a similar phenotype as syd-5 flowers, with defective stigma, while the bulged gynoecia harboring ectopic carpels normally observed in knu-2 flowers were not found in knu-2 syd-5 flowers (Figures 5A to 5F). We also checked WUS expression by in situ hybridization in knu-2, syd-5, and knu-2 syd-5 mutant flowers (Figures 5G to 5L). Consistent with our previous report, prolonged WUS expression was detected in stage 6 and stage 10 flowers of the knu-2 mutant (Figures 5G and 5J; Sun et al., 2009). However, prolonged WUS expression was not observed in stage 6 and stage 10 buds of syd-5 or knu-2 syd-5 mutant flowers (Figures 5H, 5I, 5K, and 5L). These data indicate that SYD function is required for the prolonged WUS activity in knu-2 flowers.

**Silencing of WUS Requires KNU-Dependent PcG Recruitment**

Next, to examine whether WUS chromatin changes are KNU-dependent during flower development, we examined WUS chromatin status using ap1 cal Pro3SS:AP1-GR inflorescences (GR is the steroid-binding domain of the rat glucocorticoid receptor; Wellmer et al., 2006). To avoid the noise generated by insect hybridization in knu-2, syd-5, and knu-2 syd-5 mutant flowers (Figures 5G and 5J; Sun et al., 2009). However, prolonged WUS expression was not observed in stage 6 and stage 10 buds of syd-5 or knu-2 syd-5 mutant flowers (Figures 5H, 5I, 5K, and 5L). These data indicate that SYD function is required for the prolonged WUS activity in knu-2 flowers.

We first assessed H3K4me3 and H3 acetylation levels on WUS chromatin on day 0 and day 4. The ChIP results demonstrate general decreases of H3K4me3 and H3 acetylation levels throughout the entire WUS locus on day 4 (as indicated by primer sets W1 to W5, Figures 6A and 6B; Supplemental Figures 5B and 5C; Supplemental Table). To test whether the decrease of H3K4me3 and H3 acetylation on WUS is dependent on KNU activity, the knu-2 mutation was introduced into ap1 cal Pro3SS:AP1-GR. In the knu-2 ap1 cal Pro3SS:AP1-GR inflorescences, we noticed the levels of H3K4me3 and H3 acetylation remains largely unchanged between day 0 and day 4 (Figure 6C; Supplemental Figure 5D). These results suggest that KNU activity is required for the removal of active histone marks of H3K4me3 and H3 acetylation on the WUS locus during flower development.

To further investigate dynamic WUS chromatin status change including SYD binding, the DNA accessibility change, and H3K27me3 level during flower development, we also performed...
Figure 4. WUS Chromatin Dynamics after KNU Activation.

(A) Schematic diagram showing the WUS locus and the promoter region used for ChIP assays in (B) to (G).

(B) H3K27me3 analysis by ChIP assays using ap1 cal Pro35S::KNU-AR inflorescences harvested at 0, 4, and 12 h after a single 100 nM DHT treatment.

(C) FIE binding in ap1 cal Pro35S::KNU-AR inflorescences harvested at 0, 4, and 12 h.

(D) SYD binding analysis. Infl orescences were harvested at 0, 4, and 12 h. Error bars represent the SE of three biological replicates.

(E) H3K4me3 analysis by ChIP assays using ap1 cal Pro35S::KNU-AR inflorescences harvested at 0, 4, and 12 h after a single 100 nM DHT treatment.

(F) DNA accessibility at the WUS locus in the context of chromatin assayed by FAIRE upon KNU activation in ap1 cal Pro35S::KNU-AR. The Ta3 retrotransposon (At1g37110) was used as the negative control locus and was set to 1.
ChiP assays using day 0 and day 4 inflorescences of ap1 cal Pro35S:AP1-GR treated with dexamethasone (DEX). SYD enrichment decreases on the WUS promoter (including both W1 and W2 regions) by day 4 compared with day 0 (Supplemental Figure 5E). Similarly, DNA accessibility of the WUS locus also decreases to ~40% on W2 by day 4 compared with day 0 (Supplemental Figure 5G). By contrast, in knu-2 ap1 cal Pro3SS: AP1-GR, no obvious decreases were detected for SYD enrichment and WUS DNA accessibility (Supplemental Figures 5F and 5H). For H3K27me3 assays, the ChiP results showed background levels of H3K27me3 at the WUS locus at day 0, which could be due to the contribution of nonmeristematic cells, and an increase in the H3K27me3 levels throughout the entire WUS locus on day 4 (Figure 6D). The enrichment of H3K27me3 was strongest in the first intron (primer set W3, Supplemental Table), and on day 4 the repressive mark level was nearly twice that observed on day 0 (P < 0.05, Figure 6D). These results indicate that WUS repression at floral stage 6 → 7 is associated with the deposition of H3K27me3 on the WUS locus. While in knu-2 ap1 cal Pro3SS:AP1-GR, only a background level of the H3K27me3 repressive mark was observed at day 0 and day 4 on the WUS locus in the knu-2 ap1 cal Pro35S:AP1-GR plants (Figure 6E). Hence, deposition of the repressive mark H3K27me3 on WUS requires KNU activity.

Since the PRC2 complex is responsible for the deposition of H3K27me3 on WUS, the transgenic lines ap1 cal ProFIE:FIE-VENUS Pro35S:AP1-GR and ap1 cal ProEMF2:EMF2-VENUS Pro35S:AP1-GR (Wellmer et al., 2006; Sun et al., 2014) were used to examine the change in binding of PRC2 at the WUS locus. On day 0, only background levels of FIE binding were detected at WUS, whereas on day 4 there was a distinct enrichment of FIE (up to twofold) at the WUS proximal promoter region (P < 0.05, Figure 6F; primer set W2, Supplemental Table 1). Similarly, approximately a twofold enrichment of EMF2 was detected in the same region (P < 0.05; primer set W2, Supplemental Table) on day 4 compared with the background level on day 0 (Supplemental Figures 5B and 5I). In the knu-2 mutant background, enrichment of both FIE and EMF2 were detected at background levels at the WUS locus on days 0 and 4 (Figure 6G; Supplemental Figure 5J). These data show that recruitment of PRC2 to WUS is dependent on KNU activity during flower development.

**PcG Activity Is Required for the Stable Silencing of WUS**

To determine whether WUS expression during flower development is affected in PcG mutants, the floral phenotypes were examined in the following mutants: tfi2-1, emf2-1, cif-28, fie-11/+ (fie-11 homozygous is embryonically lethal and cannot germinate), and the transgenic cosuppression line Pro35S:GFPIE, with a mostly silenced FIE activity (Katz et al., 2004). Generally, mutants of each PcG component show distinct floral phenotypes. The tfi2-1 mutant displays fused terminal flowers with two carpels in each gynoeceum (Larsson et al., 1998). The emf2-1 flowers produce two fused infertile carpels surrounded by six small sessile leaves (Yoshida et al., 2001; Sung et al., 2003). The flower phenotypes of the cif-28 and fie-11/+ mutants are indistinguishable from the wild type (Guiltin et al., 2004; Doyle and Amasino, 2009; Deng et al., 2013). None of these mutants displayed an indeterminate floral phenotype, possibly due to heterozygosity (for fie-11/+) or due to the activity of redundantly acting PcG factors. By contrast, unlike the wild-type flowers with two fused carpels, more than half (57 of 100 plants) of the Pro35S:GFPIE cosuppression plants produced multiple fused carpels with ectopic carpel-like tissue inside (Figures 7A to 7C). In the wild-type flower buds, WUS mRNA was mostly undetectable from stage 6 onward (Figures 7D to 7F; Lenhard et al., 2001; Lohmann et al., 2001). On the contrary, WUS persisted in the stage 6 and stage 7 carpel primordia and even in carpels of stage 10 flowers of the FIE cosuppression line (Figures 7G to 7I). The ectopic WUS in FIE-silenced flowers provides genetic evidence that PcG-mediated H3K27me3 plays an essential role in stable silencing of WUS from stage 6 onward, which is required for termination of the floral stem cells.

We also tested the effect of ectopic KNU expression in the polycomb mutant background, and generated tfi2-1 Pro35S:KNU-AR and cif-28 Pro3SS:KNU-AR (Figures 8A to 8F). After KNU activation with continuous DHT treatment, the treated plants showed a similar floral phenotype as tfi2-1 and cif-28 flowers, respectively (Figures 8B, 8C, 8E, and 8F). This is in stark contrast with the premature termination of floral meristems observed in Pro35S:KNU-AR continuously treated with DHT (Figures 8A and D; Sun et al., 2009). These results demonstrate that repression of WUS by KNU requires PcG activity. By contrast, loss of cif or tfi2 activity in the knu mutant background revealed no or only a slight increase in indeterminacy (Supplemental Figures 6A to 6F). We further monitored time-course WUS expression in cif-28 Pro35S:KNU-AR upon DHT treatment. WUS is repressed to ~0.6-fold at 4 h upon KNU activation but recovered to ~1-fold at 8 h and later time points (Supplemental Figure 6G). In tfi2-1 Pro35S:KNU-AR with DHT treatment, WUS expression showed a similar trend as in cif-28 Pro35S:KNU-AR (Supplemental Figure 6H). These results suggest that in cif-28 or tfi2-1 mutant backgrounds, WUS is initially repressed by KNU, but the repression is not stable without PcG activity. In addition, we found that KNU can still bind to the WUS promoter in the cif-28 null mutant background (Supplemental Figures 6I and 6J), suggesting that PRC2 is not involved in the recruitment of KNU. Thus, KNU-dependent recruitment of PRC2 is necessary for stable silencing of WUS.
Figure 5. Genetic Interaction between knu-2 and syd-5.

(A) to (C) Mutation of syd-5 rescues the knu-2 meristem indeterminate phenotype (30 flowers each from knu-2, syd-5, and knu-2 syd-5 were observed, respectively). Flowers at stage 15 of knu-2 (A) have bulged pistils, while the pistils of syd-5 (B) and knu-2 syd-5 (C) flowers at stage 15 were not bulged.

(D) to (F) Cross sections of knu-2 (D), syd-5 (E), and knu-2 syd-5 (F) siliques stained with 0.1% toluidine blue in 0.02% sodium carbonate solution. Within the knu-2 mutant siliques, there are three reiterative ectopic carpels, as shown by red asterisks. Bar, 1 mm for (A) to (C).

(G) to (L) WUS expression is prolonged at stage 6 (G) and stage 10 (J) in knu-2 flower buds, but not in stage 6 and stage 10 flower buds of syd-5 (see [H] and [K]) and knu-2 syd-5 (see [I] and [L]). Arrowheads show ectopic WUS expression in meristematic cells. Bar = 100 μm for (G) to (L).
KNU Recruits PcG to WUS through Physical Interaction with FIE

To examine the molecular basis of KNU-dependent PcG recruitment, we tested for a physical interaction between KNU and PcG factors, including FIE, CLF, SWINGER, EMF2, and TFL2 by yeast two-hybrid analysis. The use of the KNU full-length coding sequence as bait revealed an interaction between KNU and the WD repeat domain of FIE (Payne et al., 2004) negated the interaction (Supplemental Figures 7A and 7B). To verify the yeast result,
bimolecular fluorescence complementation (BiFC) analysis was performed in tobacco (*Nicotiana tabacum*) leaves (Ohad et al., 2007). BiFC revealed an in vivo interaction between KNU and FIE in the nucleus (Figure 9A). By contrast, another C2H2 zinc finger protein, ZFP11, does not show in vivo interaction with FIE in the nucleus of tobacco leaves (Supplemental Figure 7C). Furthermore, coimmunoprecipitation (co-IP) analysis of nuclear extracts from stage 6 flower buds of *ap1 cal Pro35S:AP1-GR ProKNU:KNU-VENUS ProFIE:FIE-myc* confirmed the in vivo interaction of KNU and FIE in Arabidopsis (Figure 9B; Supplemental Figures 7D and 7E). Overall, these results provide evidence that KNU physically interacts with FIE in the nucleus and may recruit PcG.

**DISCUSSION**

**KNU Mediates Multi-Step Silencing of WUS in the Floral Meristem**

Here, we show that the C2H2 zinc finger protein KNU binding site (W2) on the *WUS* promoter overlaps with the region occupied by
the SWI/SNF chromatin remodeling factor SYD, which is required for the maintenance of WUS transcription (Kwon et al., 2005). Our ChIP assay showed that SYD binds to both W1 and W2 in vivo, and in our model, SYD binding is prevented by KNU. We also performed an EMSA experiment to test KNU binding to the W1 region of the WUS promoter. The result suggests that KNU does not bind to W1 (Figure 3F), at least in vitro. The W1 and W2 sites are less than 200 bp apart and SYD is a component of a protein complex (Bezhani et al., 2007); hence, the KNU and SYD binding sites likely partially overlap. Our findings also agree with the reported SYD binding region (Kwon et al., 2005). Besides, W3 also contains one atac sequence. KNU may initially bind to the core sequence in W3 to deacetylate the WUS locus (Bollier et al., 2018).

Our genetic analyses confirmed that meristem indeterminacy in knu is dependent on SYD activity (Figures 5A to 5F). KNU induction causes the rapid eviction of SYD protein (Figure 4D). We also show that recruitment of PcG on the WUS locus is KNU dependent and that PcG activity is necessary for stable silencing of WUS by KNU (Figures 6F and 6G; Figure 8; Supplemental Figures 5I and 5 J). KNU physically interacts with the key PRC2 component FIE and recruits PRC2 to the WUS promoter to silence WUS via H3K27me3 (Figures 4B, 4C, 6F, 6G, 9A, and 9B). WUS repression was initiated prior to H3K27me3 accumulation (Figures 2A and 4B; Supplemental Figures 4A and 4B). Therefore, the termination of floral stem cells may occur in sequential steps: initial transcriptional repression of WUS associated with rapid eviction of active chromatin remodelers, loss of DNA accessibility, loss of active histone marks, and subsequent PcG-mediated silencing of the WUS chromatin (Figure 10A). These multi-steps are integrated by KNU, which plays an important role in the programmed termination of the floral stem cells.

In human cells, nuclear hormone receptors require SWI/SNF chromatin remodeling factors at each successive round of transcription initiation at the promoter in vivo through maintaining open chromatin structures and active H3K4me3 marks (McNally et al., 2000; Nagaich et al., 2004). KNU induction also caused rapid reduction of DNA accessibility and H3K4me3 marks (Figures 4E and 4F). Furthermore, we show that H3 acetylation on the WUS locus decreased after KNU activation (Figure 3C). This is consistent with a recent finding that KNU recruits a histone deacetylase–containing complex to the WUS locus (Bollier et al., 2018). In vitro, PcG and SWI/SNF factors have mutually exclusive activities (Bar-Ziv et al., 2016). Thus, KNU causes H3 deacetylation, H3K4 demethylation, and SYD dissociation simultaneously, which would be prerequisite steps prior to H3K27me3-mediated epigenetic silencing of the WUS locus. One possibility is that the KNU-PcG complex forms first and acts together to remove SYD and then trigger the H3K27me3 deposition on WUS. Deposition of H3K27me3 on WUS may require reduced transcription, which was also implicated at the FLC locus, where H3K27me3 deposition on the gene body occurs only after transcription is decreased (Buzas et al., 2011). In animal cells, reduced transcriptional activity and

Figure 8. Repression of WUS by KNU Requires PcG Activity.

(A) to (F) Flowers of Pro35S:KNU-AR (see [A] and [D]), tfl2-1 Pro35S:KNU-AR (see [B] and [E]), and clf-28 Pro35S:KNU-AR (see [C] and [F]) after mock (see [A], [B], and [C]) or continuous DHT treatments (once a day for five continuous days; see [D] to [F]). After continuous induction of KNU, carpels were lost in the wild-type background (D), but not in the tfl2-1 or clf-28 mutant backgrounds (see [E] and [F]). Bar, 1 mm.
histone deacetylation also occur prior to H3K27me3 accumulation on gene body (Kehle et al., 1998). Persistent silencing of WUS beyond floral stage 6 may still require KNU, as KNU-GUS activity can still be observed in the late OC cells (Figure 1C; Liu et al., 2011). In those cells, the silenced status of WUS chromatin may be stably maintained by KNU through the continuous recruitment of PcG as well as histone deacetylase and through the prevention of SYD binding.

Our early work has shown that KNU, a repressor activated by AG, plays a critical role in the termination of WUS (Sun et al., 2009). Hereby in this study, we provide a precise mechanism toward understanding the nature of events in WUS repression during floral meristem termination. Although studies show that WUS may be mildly but directly repressed by AG from floral stage 3 onward through chromatin looping as an early event (Liu et al., 2011; Guo et al., 2018), our work unveils the final concrete events at floral stage 6 for WUS termination, especially the sequential epigenetic changes on WUS chromatin. Furthermore, our work not only agrees with a recent report that WUS could be initially repressed through histone deacetylation (Bollier et al., 2018) but also introduces a player, SYD, into the complex regulatory network, whose displacement from the WUS promoter is a critical initial step in repression of WUS expression. Furthermore, stable silencing of WUS is achieved by the recruitment of PcG and following deposition of H3K27me3. Thus, our study demonstrates the final details for stem cell termination with high resolution in plants during floral organ differentiation.

**Continuous Activity of KNU Is Required for WUS Silencing**

We noticed that KNU binds the WUS proximal promoter region (W2) for PRC2 recruitment (Figure 3; Supplemental Figures 2A and 2B), while H3K27me3 peaks on the first intron (W3) and 3′ untranslated region (W4) of WUS (Figures 4A and 4B; Supplemental Figures 4A and 4B). This suggests that recruitment of PRC2 and deposition of H3K27me3 are not always at the same location. For instance, FIE binds to the −1-kb upstream promoter region of the KNU transcriptional start site (Sun et al., 2014), while H3K27me3 can only be detected on KNU coding sequences (CDS; Sun et al., 2009). Another example is that the AS1–AS2 complex recruits PRC2 at promoter regions of BREVIPEDICELLUS and KNOTTED-LIKE FROM ARABIDOPSIS THALIANA2, while H3K27me3 peaks at transcribed regions or at the CDS of the two genes (Lodha et al., 2013).

For H3K27me3-mediated silencing of WUS, we noticed only continuous KNU activity (continuous DHT treatments on ap1 cal Prom35S::AP1-GR and ap1 cal Prom35S::AP1-GR ProKNU::KNU-VENUS ProFIE::FIE-myc) resulted in stable repression of WUS (Figure 2C), while single induction of KNU activity (single DHT treatment on ap1 cal Prom35S::KNU-AR) led to a transient decrease of WUS mRNA due to transcriptional repression (Figure 2A). We also observed a similar transient repression in PcG mutant backgrounds (Supplemental Figures 6G and 6H). Epigenetic silencing memory may not be successfully established by transient KNU activity since H3K27me3 deposition happens later than transcriptional repression. After WUS expression is initially repressed by transient KNU activity, a compensatory mechanism for WUS recovery by a CLV3-dependent mechanism may exist (Figures 2A and 2D; Müller et al., 2006). Furthermore, we show that CLV3 is repressed by KNU within 4 h (Figure 2D). These may hint at a tight repressive mechanism to terminate stem cell activity within a narrow time window. After WUS is fully silenced in the presumptive floral meristems, WUS starts to be induced in emerging ovule and stamen primordia. How this spatial and temporal specific reactivation of WUS is regulated is an interesting topic for further study.
Conserved Mechanism for PcG Recruitment to Target Genes via C2H2 Zinc Finger Proteins

Here, we show that in Arabidopsis, the C2H2 zinc finger protein KNU recruits PcG to WUS via physical interaction with the WD motif-containing protein FIE. There is also another C2H2 zinc finger protein SUPERMAN, which directly interacts with CLF, a histone methyltransferase and key component of PRC2, and negatively regulates the expression of auxin biosynthesis genes YUCCA1/4 (Xu et al., 2018). In Drosophila, the C2H2 zinc finger protein Hunchback, which forms a complex with the FIE putative ortholog Esc, recruits PcG to homeotic Hox genes in cells outside the Hox expression domain throughout development (Kehle et al., 1998). In human cells, the C2H2 zinc finger protein Zfp277 binds to the Ink4a/Arf locus, directly interacts with Bmi1, a PRC1 factor for PcG recruitment to Ink4a/Arf. (For simplicity, gene size and structures are not to scale.)

Figure 10. Models.

(A) Working model on how KNU represses WUS. Before stage 6, when the active histone marks H3K4me3 and H3 acetylation on WUS are detected, the active transcription of WUS is maintained by the SWI/SNF ATPase SYD. During the early floral stage 6, the KNU protein, which is induced by AG, may associate with PRC2 and the KNU-PRC2 complex directly binds to the WUS promoter by competing with SYD. That leads to eviction of SYD from the WUS promoter and a decrease in the active marks H3K4me3 and H3 acetylation. Both the repressor activity of KNU (mediated by histone deacetylation) and the eviction of SYD simultaneously lead to transcriptional repression of WUS. Subsequently, the KNU-PRC2 complex deposits the repressive mark H3K27me3 onto WUS, which is maintained by continuous expression of KNU after stage 6.

(B) A conserved mechanism for the recruitment of PcG to target genes by C2H2 zinc finger proteins in plants and animals. In Arabidopsis, the C2H2 zinc finger protein KNU binds to the WUS promoter and recruits PcG to WUS via direct interaction with FIE, a homolog of Esc of Drosophila. In Drosophila, the C2H2 zinc finger protein Hunchback (Hb), which binds the Uthalithorax (Ubx) promoter, together with dMi-2 recruits PcG to UBX via interaction with Esc. In human cells, the C2H2 zinc finger protein Zfp277, which binds the Ink4a/Arf locus, directly interacts with Bmi1, a PRC1 factor for PcG recruitment to Ink4a/Arf. (For simplicity, gene size and structures are not to scale.)

Drosophila, quiescent stem cells can be activated in adult tissues for homeostasis or repair upon tissue damage (Otsuki and Brand, 2018). After damaged tissue has regenerated, the stem cell activity should be repressed. However, the mechanism underlying the precise temporal control of stem cell activity during regeneration is largely unknown both in plants and in animals (Takemura and Nakato, 2017). It would be interesting to establish whether epigenetic-mediated multi-step termination of key stemness gene(s), as we show here in flower development, is conserved in animals, and to further assess whether C2H2 zinc finger proteins have a central role in this multi-step silencing of their target loci in both the plant and animal kingdoms.

METHODS

Plant Materials and Chemical Treatments

Except for tfi2-1, emf2-1, and the Pro35S:GFP-FIE cosuppression line (Colombia background), all plants were of the Landsberg erecta background and all were grown at 22°C under continuous light conditions. The spectrum contains equal levels of blue light (430 to 460 nm) and red light.
(630 to 660 nm). The light intensity was ~100 μmol m⁻² s⁻¹ at the soil surface level. Plants were photographed using a stereomicroscope (Carl Zeiss Micro-Imaging). Scanning electron microscopy images were acquired using an electron microscope (JSM-6360LV, JEOL).

DEX (D4902, Sigma-Aldrich), DHT (A8380, Sigma-Aldrich), and CHX (01,810, Sigma-Aldrich) treatments were performed by inverting the plants and submerging the inflorescences for 1 min in a solution containing either 1 μM DEX (for Pro35S::AP1-GR) or 100 nM DHT (for Pro35S::KNL-AR) or 10 μM CHX (for Pro35S::KNL-AR) together with 0.015% (w/v) Silwet L-77. The time of initial DEX or DHT treatment was defined as day 0 or 0 h. For the continuous treatment, the inflorescences were submersed more than 2 min in the solution repeatedly at 1-d intervals.

RNA Extraction and Expression Analyses

Total RNA was isolated from inflorescences using the RNaseasy Plant Mini Kit (Qiagen). RT was performed using the ThermoScript III RT-PCR system (Invitrogen). Quantitative real-time PCR assays were performed in triplicate using the 7900HT fast real-time PCR system (Applied Biosystems) and the KAPA SYBR FAST ABI Prism qPCR Kit (KAPA Biosystems). Expression assays were performed using RNAs from different batches of independently prepared plant inflorescences (biological replicates using different plants), and each was run in triplicate (technical replicates). Tbp41-like (Asgd43270) served as the internal reference gene (Czechowski et al., 2005).

Phylogenetic Shadowing and cis-Element Identification

Phylogenetic shadowing was performed as described previously (Yamaguchi et al., 2018). The 5’ intergenic sequence of the Arabidopsis (Arabidopsis thaliana) WUS promoter was obtained from the The Arabidopsis Information Resource website. Using the Arabidopsis WUS promoter sequence as a query, similar sequences from eight Brassicaceae were obtained through National Center for Biotechnology Information BLASTn. The resulting eight promoter sequences were aligned by mVISTA (http://genome.lbl.gov/vista/mvista/submit.shtml). Three CRM3s were identified and defined as CRM1, CRM2, and CRM3. Because KNU bound to the CRM3 region, CRM3 was characterized in detail by ClusterW (https://www.genome.jp/tools-bin/cluster) and a conserved and putative aatc KNU cis-element was identified.

In Situ Hybridization

Nonradioactive in situ hybridizations were performed as described previously (Carles et al., 2009). To produce a WUS-specific antisense probe, a pMHw16 clone carrying WUS cDNA was used as a template for in vitro transcription.

GUS Staining

GUS staining was performed as described previously (Ito et al., 2003) and observed on paraffin sections or plastic sections (Yamaguchi et al., 2018). Photographs were taken using a stereomicroscope (Carl Zeiss Micro-Imaging).

Vector Construction and Plant Transformation

ProFIE::FIE-myc was prepared as follows. First, the pENTR-D (Invitrogen)-based ProFIE::FIE-VENUS-myc (Sun et al., 2014) was digested with SfoI to release the VENUS fragment. Subsequently, the digested vector was self-ligated to generate ProFIE::FIE-myc. Finally, the pENTR-D-based ProFIE::FIE-myc was recombined into pKGW (Invitrogen) using LR-recombinase (Invitrogen). ProFIE::FIE-myc was introduced into ap1 cal Pro35S::AP1-GR ProKW::KNL-VENUS. The transformation was performed using the Agrobacterium tumefaciens-mediated floral dipping method (Clough and Bent, 1998).

ChIP Assays

ChIP experiments were performed as described previously (Ito et al., 1997), with slight modifications. Inflorescences were ground in liquid nitrogen and postfixed with 1% (w/v) formaldehyde for 10 min. Chromatin was isolated and solubilized by sonication to generate DNA fragments with an average length of 400 bp. After incubation with salmon sperm DNA/protein-A agarose beads (Millipore), the solubilized chromatin was incubated overnight with anti-H3K27me3 antibody (07-449, Millipore), anti-H4K4me3 antibody (07-473, Millipore), or anti–acetyl-H3 antibody (06-599, Millipore; 1:200 dilution used for all histone modification ChIP experiments), or the solution containing sonicated DNA fragments was incubated overnight with anti–c-Myc-Agarose beads (A2470; Sigma-Aldrich; 1:20 dilution used) or anti–hemagglutinin (HA)-Agarose beads as a control (A2095, Sigma-Aldrich; 1:20 dilution used, for KNU ChIP). The relative enrichment for KNU on the WUS locus was taken as the ratio between Myc and HA. For Pol II ChiP Pol II antibody (ab817, Abcam; 1:200 dilution used) was used, and for FIE ChiP and EMF2 ChiP GFP-Trap beads (gta-20, Chromotek; 1:20 dilution used) were used. DNA fragments were recovered from the purified DNA–protein complexes and then used for enrichment tests by real-time PCR analysis in triplicates. The primary ratio between the bound DNA after IP and the input DNA before IP was calculated for all the representative primer sets spanning the WUS genomic region, and the ratios were plotted to show the relative changes in the levels of the H3K27me3 mark, H3K4me3 mark, and H3 acetylation. For SYD Chip, ChiP was performed as described previously (Wu et al., 2015), with minor modifications. The SYD antibody was used as in a previous publication (Kwon et al., 2005). For the SYD ChiP result in the supplemental data (Supplemental Figures 5E and 5F), due to a lack of SYD antibody, we generated a tagging line of knu-2/+ ap1 cal Pro35S::AP1-GR ProSYD:SYD-GFP and used GFP-Trap beads (gta-20, Chromotek; 1:20 dilution used). ChiP sample was normalized to the related input sample. The percent input data were converted to enrichment rate and plotted to facilitate comparison of time-course occupancy levels. For all ChiP experiments, Mu-like transposons (Supplemental Table) served as a negative control locus and the relative enrichment rate was set to 1. ChiP assays were performed using inflorescences from different batches of independently prepared plant materials (biological replicates with using different plants), each run in triplicate (technical replicates).

Formaldehyde-Assisted Isolation of Regulatory Elements

FAIRE was performed as described previously (Wu et al., 2015), with minor modifications. Inflorescence tissues (0.5 g) were harvested after 1-min treatments in a solution containing 100 nM DHT at 22°C. Tissues were crosslinked with 1% (w/v) formaldehyde under vacuum for 10 min, replaced by 125 mM Gly in buffer 1 (Omidbakhshfard et al., 2014) for 5 min at room temperature, and rinsed with ice-cold water three times. Chromatin was isolated by blending in buffer 1, filtered through four layers of miracloth, washed with buffers (Omidbakhshfard et al., 2014), and sonicated to produce DNA fragment shorter than 500 bp. One volume of phenol:chloroform:isoamyl alcohol (25:24:1) was added to extract the chromatin, and samples were mixed for 2 min by vortex. After ethanol precipitation, DNA was purified again using a QiAquick DNA Purification Kit (Qiagen). DNA was determined for crosslinked and noncrosslinked FAIRE samples with a Light Cycler 480 (Roche) and Light Cycler 480 release 1.5.1.62 SP software (Roche) using FastStart DNA essential DNA Green Master (Roche). The Taq retrotransposon (A1f13110, Supplemental Table, Johnson et al., 2002) was used as the negative control locus for FAIRE experiments. FAIRE experiments were repeated twice, and the combined data are shown.

Yeast One-Hybrid Assays

Yeast one-hybrid assays were performed as described previously (Sparkes et al., 2006). WUS-W2 (~308 to ~125 bp upstream of the ATG start codon)
fragment was cloned into the pAbAi vector digested with SmaI and XhoI, creating WUS-W2-AbAi. WUS-W2-AbAi was linearized by digestion with BstBI prior to transformation of the yeast strain Y1H Gold. The full-length cDNA of KNU was isolated and cloned into the pGADT7 activation domain (AD) vector, creating the pAD-KNU plasmid. The pAD-KNU vector was subsequently transformed into the yeast strain containing the WUS-W2-AbAi constructs. Activation of the yeast was observed after 3 d on selection plates (synthetic dextrose/ 2% Ura) containing 200 ng mL−1 aureobasidin A.

Yeast Two-Hybrid Assay

To construct the vectors for yeast two-hybrid assays, the full-length and truncated versions of KNU as well as the WD repeat domain of FIE were amplified and cloned into pGADT7 or pGBKT7 (Clontech). The yeast two-hybrid assay was performed using the Yeastmaker Yeast Transformation System 2 (Clontech) according to the manufacturer’s instructions.

BiFC Assay

The full-length coding sequences of KNU and FIE were cloned into pGreen vectors and transformed into Agrobacterium. The Agrobacteria were co-infiltrated into tobacco (Nicotiana benthamiana) leaves of 3-week-old plants as described previously (Sparkes et al., 2006).

Co-IP Experiment

The flower buds at stage 6 from ap1 cal Pro35S:AP1-GR and ap1 cal Pro35S:AP1-GR ProKNU-KNU-VENUS ProFIE-FIE-myc were ground with a mortar and pestle in liquid nitrogen, and proteins were prepared in IP buffer (10 mM Tris-HCl, pH 7.4, 150 mM NaCl, 0.5 mM EDTA, 0.5% (v/v) Nonidet P-40, 5% (v/v) glycerol, 1 mM dithiobisulfoxide, and 1× Complete Protease Inhibitor Cocktail) and then incubated with anti-c-Myc agarose beads (Sigma-Aldrich) for 4 h at 4°C on a rotator. After incubation, the beads were washed four times with ice-cold Dulbecco’s PBS buffer and then eluted by boiling in SDS sample buffer. Samples were separated on 10% (v/v) SDS-PAGE gels, transferred to a nitrocellulose membrane, and then probed with anti-GFP antibody (Cell Signaling Technology). Detection was according to the procedures in the Clarity Western ECL Substrate Kit (Bio-Rad). Images showing immunoblot results were taken using the Chemi Doc XR+. Imaging System (Bio-Rad). Co-IP experiments were repeated twice, and representative data are shown.

Confocal Microscopy Imaging

To observe the reporter lines in Arabidopsis inflorescences, the transgenic seeds were sown in soil and the inflorescences were plucked and mounted on slides. The older floral buds were then carefully removed or spaced out to expose the SAM and early-stage floral buds. Dissected inflorescences were incubated with FM4-64 dye (50 μg/mL) for 45 min on slides. Plants were imaged using a Zeiss LSM 510 upright (with motorized stage) confocal microscope using an EC Plan-Neofluar 40×/1.30 Oil differential interference contrast or a Plan-Apochromat 20×/0.8 objective lens. GFP was stimulated with an argon laser at 488 nm at 60 to 70% of its output with emission filtered with a 505 to 530 nm band-pass filter. VENUS was stimulated with an argon laser at 514 nm at 65 to 80% of its output with emission filtered with a 530 to 600 nm band-pass filter. FM4-64 dye emission was filtered with a 585 nm long-pass filter. The z-stack was acquired using a 512 × 512 pixel frame, and the three-dimensional projections of the obtained z-stacks were generated with Zeiss LSM Image Browser version 4 and adjusted with Adobe Photoshop.

Electrophoretic Mobility Shift Assay

The DNA fragment of KNU CDS was inserted into the pMAL-c5G vector digested with Ndel and BamHI, which was expressed in Transetta (DE3) Chemically Competent Cells (TransGen Biotech) to produce MBP-tagged KNU protein. The recombinant fusion protein was purified using Amylose Resin (NEB) following the manufacturer’s instructions. The probes were labeled with biotin and annealed before use. The EMSA kit (Thermo Fisher Scientific) was used for binding reactions and detection of biotin-labeled probe. The nonlabeled probes were used as competitors at 50 times the concentration of labeled probes. For individual probes, the detailed length information is provided in the Figure 3A legend.

Statistical Analyses

Student’s t tests were performed using SPSS version 21 software to determine significance, whenever groups were compared, and are described in the corresponding figures (Figures 2B, 4B to 4G, and 6B to 6G; Supplemental Figures 2B, 4B, and 5C to 5J). Statistical significance was suggested at the indicated P-values. Detailed results of statistical analyses are available in Supplemental File.

Accession Numbers

Sequence data from this article can be found in the Arabidopsis Genome Initiative under the following accession numbers: KNU (At1g14010), WUS (At2g17950), AP1 (At1g69120), CAL (At1g26310), SYD (At2g28290), FIE (At3g20740), TFL2 (At5g17690), CLF (At2g23380), CLV1 (At1g75820), CLV2 (At1g65380), CLV3 (At1g69970), EMF2 (At5g1230), ZFP11 (At2g42410).

Supplemental Data

Supplemental Figure 1. Confocal observation of the doubly transgenic inflorescence for ProWUS:GFP-ER (red) and ProKNU:KNU-VENUS (green) in stage 6 flower buds, together with KNU and WUS expression patterns in stage 7 flower buds.

Supplemental Figure 2. ChiP assay for KNU binding on WUS.

Supplemental Figure 3. KNU binds conserved core sequence attc on WUS promoter.

Supplemental Figure 4. H3K27me3 analysis of WUS chromatin upon KNU activation.

Supplemental Figure 5. Change of WUS chromatin status is KNU-dependent.

Supplemental Figure 6. Genetic interaction between KNU with PcG factors, WUS expression in PcG mutants, and KNU binding on WUS in clf-28 mutant background.

Supplemental Figure 7. KNU physically interacts with FIE in yeast and co-immunoprecipitation of KNU and FIE.

Supplemental Table. List of primer sequences used in this study; primer names are followed by their sequences (5’ to 3’).

Supplemental File. Statistical analysis.

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AUTHOR CONTRIBUTIONS

B.S. and T.I. designed research; B.S., Y.Z., J.C., E.S., N.Y., J.X., L.-S.L., W.-Y.W., and X.G. performed research; D.W. revised the article; and T.I. and B.S. wrote the article.

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Integration of Transcriptional Repression and Polycomb-Mediated Silencing of WUSCHEL in Floral Meristems
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