Interaction of LEAFY, AGAMOUS and TERMINAL FLOWER1 in maintaining floral meristem identity in Arabidopsis

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Accepted 22 February 2002

SUMMARY

The Arabidopsis transcription factor LEAFY acts upstream of homeotic genes such as AGAMOUS to confer floral identity on meristems that arise after the transition to reproductive development. Compared to the genetic circuitry regulating the establishment of floral meristem identity, little is known about its maintenance. Previous experiments with leafy heterozygous plants and agamous mutants grown in conditions that reduce the floral inductive stimulus have shown that both genes are required to prevent reversion of floral to inflorescence meristems. Here, we present evidence that LEAFY maintains floral meristem identity independently of AGAMOUS, and that the primary role of LEAFY is either direct repression of shoot identity genes or repression of an intermediate factor that activates shoot identity genes. The latter conclusions were deduced from the phenotypes conferred by a gain-of-function transgene, LEAFY:VP16, that appears to act as a dominant negative, or antimorphic, allele during maintenance of floral meristem identity. These observations contrast with previous findings that LEAFY acts as a direct activator of floral homeotic genes, supporting the hypothesis that the transcriptional activity of LEAFY is dependent on specific co-regulators.

Key words: Arabidopsis thaliana, Flower development, Meristem identity, LEAFY, Floral reversion

INTRODUCTION

In flowering plants, almost the entire adult body derives from groups of undifferentiated cells called meristems, which include a small number of true stem cells. In the aerial portion of the plant, leaves and axillary shoots are formed during the initial, vegetative phase, and flowers after the plant has been induced to make the transition from vegetative to reproductive development. Several genes that are required to confer floral identity on newly arising meristems have been identified, including LEAFY (LFY) and APETALA2 (AP2), and the three closely related APETALA1 (AP1), CAULIFLOWER (CAL) and FRUITFULL (FUL) genes (Bowman et al., 1993; Ferrándiz et al., 2000; Huala and Sussex, 1992; Irish and Sussex, 1990; Schultz and Haughn, 1991; Schultz and Haughn, 1993; Shannon and Meeks-Wagner, 1993; Weigel et al., 1992). In the absence of these genes, all of which encode transcription factors (Gu et al., 1998; Kempin et al., 1995; Mandel et al., 1992; Okamura et al., 1997; Parcy et al., 1998), floral meristems are partially or completely replaced by shoot meristems, while ectopic overexpression of several of them causes an opposite phenotype, replacement of shoots with flowers (Liljegren et al., 1999; Mandel and Yanofsky, 1995; Weigel and Nilsson, 1995). The activity of the floral meristem-identity genes is counteracted by the shoot-identity gene TERMINAL FLOWER1 (TFL1), which encodes a protein that is likely involved in signal transduction (Alvarez et al., 1992; Bradley et al., 1997; Liljegren et al., 1999; Ratcliffe et al., 1998; Ratcliffe et al., 1999; Shannon and Meeks-Wagner, 1991; Shannon and Meeks-Wagner, 1993).

In many species, including Arabidopsis, a floral inductive stimulus is required only transiently to cause a stable transition from vegetative to reproductive development. In contrast, a floral inductive stimulus is required continuously in several other species, and its absence can cause either inflorescence or floral reversion. In inflorescence reversion, a shoot ceases to produce flowers and reverts to the formation of leaves with axillary vegetative shoots. In floral reversion, individual flowers stop producing floral organs and initiate vegetative organs (Anthony et al., 1996; Battey and Lyndon, 1984; Battey and Lyndon, 1986; Battey and Lyndon, 1988; Battey and Lyndon, 1990; Pouteau et al., 1997; Pouteau et al., 1998). The latter observation indicates that floral meristem identity not only needs to be established, but also maintained.

Both inflorescence and floral reversion are rare in wild-type Arabidopsis (Bowman, 1994; Laibach, 1951), but floral reversion has been described in several mutant backgrounds (e.g., Bowman et al., 1993; Clark et al., 1993; Mizukami and
Ma, 1997; Okamura et al., 1996). While these instances of floral reversion differ in details, they all have in common that the flowers do not revert to a leaf-producing vegetative shoot meristem, but to a flower-producing inflorescence meristem.

In contrast to the establishment of floral meristem identity, its maintenance has received relatively little attention. It is particularly intriguing that LFY, a cardinal factor in establishing floral meristem identity, is also required for its maintenance (Okamura et al., 1996). It is unclear how direct this effect of LFY is, especially since LFY is a direct activator of the homeotic gene AGAMOUS (AG), which itself is required for stable floral meristem identity (Busch et al., 1999; Mizukami and Ma, 1997; Okamura et al., 1996). Ify mutants are of limited use in studying this process, because, in these plants, floral meristem identity is not properly established in the first place. Here, we use a combination of mutants and transgenic plants to dissect the role of LFY in the maintenance of floral meristem identity. First, we show that LFY maintains floral meristem identity independently of homoeotic gene activation. Second, we provide evidence that LFY is likely to perform this function by acting as a transcriptional repressor of shoot identity genes.

MATERIALS AND METHODS

Plant material

Plants were grown under a 3:1 mixture of Cool White and Gro-Lux (wide spectrum) fluorescent lights at 23°C. Unless otherwise noted, plants were grown in long days (16 hours light, 8 hours darkness). Short day conditions were 8 hours light, 16 hours darkness.

Wild type was either Landsberg erecta (Ler) or Columbia (Col-0, Col-7). ag-1 and ify-6 mutants in Ler (Bowman et al., 1989; Weigel et al., 1992), and tfl1-1 and ify-12 mutants in Col-0 have been described previously (Huital and Sussex, 1992; Shannon and Meeks-Wagner, 1991). LFY:VP16 lines DW245.2.7 and DW245.2.25 (strong phenotype as homozygotes), and DW245.2.37 (weak phenotype) were in the Col-7 background (Parcy et al., 1998). Additional transgenic plants were generated by vacuum infiltration of Col-7, using vectors pDW245 (for LFY:VP16) and pFP17 (for LFY:mVP16) (Bechtold et al., 1993; Parcy et al., 1998). dCAPS genotyping of ag-1 heterozygotes has been described elsewhere (Neff et al., 1998). ify-6 and ify-12 heterozygous and homozygous plants were identified by CAPS genotyping (Konieczny and Ausibl, 1993) as described previously (Blázquez et al., 1997) (http://www.weigelworld.org).

Plant analysis

Methods for in situ hybridization, scanning electron microscopy and light microscopy were according to Parcy and colleagues (Parcy et al., 1998). The TFL1 probe was derived from p129D7 (Bradley et al., 1997).

Any flower that produced secondary flowers interior to the first whorl of organs was considered to be reverting. Partially reverted flowers continued to produce floral organs, while completely reverted flowers did not, and produced only secondary flowers.

RESULTS

AG and LFY have additive effects on floral reversion

Previous work has shown that both LFY and AG are required for the maintenance of floral meristem identity, as flowers of lfy/LFY heterozygous plants or ag homozygous mutants can revert to shoots under weak floral inductive conditions such as short days (Mizukami and Ma, 1997; Okamura et al., 1996). To determine whether reduction of LFY activity and loss of AG function affect reversion independently, we compared ag mutants that were either wild-type for LFY, or heterozygous for a ify null allele. Under our conditions, LFY/LFY ag/ag plants grown in short days reverted only rarely. In contrast, lfy/LFY ag/ag plants showed frequent floral reversion (Table 1, Fig. 1H), indicating that LFY prevents reversion even in the absence of AG.

Abnormal meristem development in LFY:VP16 flowers

LFY is a direct activator of homeotic genes such as AG and AP1 (Busch et al., 1999; Parcy et al., 1998; Wagner et al., 1999). The fact that LFY activates transcription in a heterologous system, yeast, only when fused to the VP16 transcriptional activation domain (Cousens et al., 1989; Triezenberg et al., 1988), or when co-expressed with another transcription factor, indicates that LFY has to interact with other proteins to regulate downstream targets (Busch et al., 1999).

Fig. 1. Floral reversion in ag-1 mutant backgrounds. (A) Wild-type flower with sepals (se), petals (pe), stamens (st) and carpels (ca) forming the central gynoecium. (B) LFY:VP16, intermediate phenotype. The outer whorl is occupied by carpelloid organs. Organs in whorl 2 are missing or replaced by stamens. (C) LFY:VP16, strong phenotype. The number of floral organs is reduced further. All of them are carpelloid, and no whorled structure is apparent. (D) ag-1. Stamens in whorl 3 are replaced by petals, and the central gynoecium by an internal flower that repeats the pattern of the primary flower. (E-G) LFY:VP16 ag-1, strong phenotype. Young flowers are similar to those of ag mutants and include petaloid sepals (E). In older flowers, a new inflorescence (inf) emerges from the center (F,G). (H) lfy-6/+ ag-1 flower from a plant grown in short days. After a few whorls of floral organs had formed, the flower reverted to an inflorescence. All plants were grown in long days except (H). Scale bars 1 mm.
Maintenance of floral meristem identity

1999; Lohmann et al., 2001; Parcy et al., 1998). Fusion to the VP16 activation domain also allows LFY to activate AG independently of other factors in planta (Busch et al., 1999; Parcy et al., 1998). Since LFY is normally an activator of AG, the more potent LFY:VP16 can be interpreted as a hypermorphic form of LFY. However, if LFY transcriptional activity is context dependent, LFY:VP16 might have a dominant-negative effect by activating target genes that are directly repressed by unmodified LFY. There are several examples for conversion of a transcriptional repressor into an activator by fusion to the VP16 domain (e.g., Conlon et al., 1996; Estes et al., 2001; Ferreiro et al., 1998; Waltzer et al., 1995; Zuber et al., 1999). A process during which LFY might normally act as a repressor could be maintenance of floral meristem identity, during which LFY prevents floral reversion, presumably by repressing the transcription of shoot identity genes. If this is the case, LFY:VP16 should have effects on floral reversion similar to those resulting from reduction of wild-type LFY activity.

The floral phenotype of LFY:VP16 plants is mostly due to ectopic AG expression and consists of reduced floral organs and conversion of petals to stamens and sepals to carpels (Fig. 1A-C) (Parcy et al., 1998). Because there are no obvious signs of floral reversion in mature LFY:VP16 flowers, we studied developing LFY:VP16 flowers using the scanning electron microscope. Initiation of floral meristems in LFY:VP16 plants was similar to wild type, but deviated from wild type subsequently. Instead of initiating four first-whorl organs in a cruciform manner, LFY:VP16 produced an irregular number of first-whorl organs, often more than four (Fig. 2A,B,F). In wild type, the formation of the first whorl is followed by the initiation of petal primordia in the second whorl and stamen primordia in the third whorl (Smyth et al., 1990). Between the stamen primordia, floral meristem development is terminated by formation of the domed gynoecium primordium, which gives rise to the congenitally fused carpels (Fig. 2E,I). In LFY:VP16, there was no evidence of second- or third-whorl primordia demarcating the gynoecial dome (Fig. 2F,J). Instead, the meristem continued to grow apically, and new, fused primordia were initiated in a pattern that was at least partially spiral (Fig. 2J). These primordia eventually fused to produce an abnormal gynoecium that had an excess of style tissue at the expense of valve tissue (Fig. 2M,N). The abnormal

| Plants | 19 | 13 |
| Plants examined per plant | 20 | 20 |
| Reverting flowers, range | 0-20 | 0-2 |
| Reverting flowers, average | 10.5 | 0.5 |
| Standard deviation | 8.9 | 0.8 |

Plants were grown in short days. Reversion was counted on the first 20 flowers produced by the primary inflorescence of each plant. lfy-6/LFY and LFY+/LFY+ are significantly different from each other (Student’s t-test, P<0.00015).

Table 1. Floral reversion in ag-1 background

![Fig. 2. Scanning electron micrographs of developing mutant and transgenic flowers. The top row shows inflorescence shoot apices (meristem indicated with an asterisk) surrounded by developing flowers. Numbers indicate floral stages (Smyth et al., 1990).](https://example.com/fig2)

(A,E,I,M) Wild type. (E) Stage 5 flower, with two sepals (se) dissected away to reveal the developing stamens (st) and the floral meristem (fm), which has begun to form the central gynoecium consisting of congenitally fused carpels. (I) Stage 7 flower, in which the floral meristem has terminated with the formation of carpels (ca). (M) Mature flower with four whorls or organs, including sepals, petals (pe), stamens and carpels. (B,F,J,N) Strong LFY:VP16 line. Note supernumerary organs in the first whorl (1st) of developing flowers (F). The floral meristem is enlarged compared to that of the wild type and is beginning to produce another set of four organ primordia. (J) Three partially fused carpels are found in the center, which appear to have almost spiral phyllotaxy. A floral meristem is still visible in the center. (N) A mature flower that consists of several carpels and carpelloid organs that lack a clear whorled arrangement. (C,G,K,O) ag-1. The floral meristem persists and produces many whorls of organs that develop into sepals and petals. The floral meristem is indicated by an asterisk in (O). (D,H,L,P) LFY:VP16 ag-1. After the meristem has produced several whorls of organs, it reverts to an inflorescence meristem (indicated by an asterisk) that produces secondary flowers (sf). Note the enlarged floral meristem in H. Scale bars 50 μm (A-D, I-L), 20 μm (E-H), and 500 μm (M-P).
early development of LFY:VP16 flowers, with continued proliferation of the floral meristem and partially spiral phyllotaxis, suggests a meristem defect in these flowers. Specifically, the floral meristem may have partial shoot identity.

**AG masks floral reversion induced by LFY:VP16**

One possibility for why LFY:VP16 flowers have initially abnormal floral meristem development, but ultimately do not revert into shoots is that the effects of LFY:VP16 on reversion are counterbalanced by the effects of AG, the expression of which is dramatically increased in LFY:VP16. Not only is AG required for maintenance of floral meristem identity, but overexpression of AG can also be sufficient to convert shoots into flowers (Mizukami and Ma, 1997; Okamuro et al., 1996).

To determine whether increased AG expression masks an effect of LFY:VP16 on floral reversion, we examined LFY:VP16 ag plants. As described previously, ag completely suppresses the homeotic conversions seen in LFY:VP16 (Fig. 1D,E) (Parcy et al., 1998). However, after a few whorls of floral organs were produced, LFY:VP16 ag-1 flowers became proliferous and reverted either partially or completely to shoots (Fig. 1F,G). Partially reverted flowers continued to produce both floral organs and secondary flowers, while completely reverted flowers produced only secondary flowers in a spiral phyllotaxy. In contrast to ag or ify/LFY flowers that revert only in short days, LFY:VP16 ag flowers reverted both in long and short days.

Scanning electron microscopy of developing LFY:VP16 ag flowers revealed that the number of first-whorl organs was irregular, as with LFY:VP16 AG+ flowers, and often greater than four (Fig. 2C,D). In contrast to LFY:VP16 AG+ or non-transgenic ag flowers, only a few whorls of floral organs were produced, before the floral meristem reverted to a shoot meristem and produced new floral primordia on its flanks (Fig. 2G,H,K,L). Second-order flowers repeated the pattern of the primary flowers, with a few whorls of floral organs followed by the production of higher-order floral primordia (Fig. 2L,P).

**LFY:VP16 is not a neomorphic allele**

A concern with any gain-of-function allele is that it has activity unrelated to the normal function of the gene, or neomorphic activity (Muller, 1932). This would be the case, for example, if LFY:VP16 interacted with promoters or proteins that are not targets of unmodified LFY. A hallmark of neomorphic mutations is that they are not affected by the dosage of the wild-type gene. We have previously shown that the homeotic organ conversions in LFY:VP16 flowers are strongly dependent on the copy number of endogenous wild-type LFY, indicating that this phenotype is not due to neomorphic activity of LFY:VP16 (Parcy et al., 1998). To confirm that LFY:VP16 similarly does not act as a neomorph with respect to floral reversion, but rather as an antimorph, we studied a weak LFY:VP16 line, which does not show any homeotic organ conversions in a wild-type background, but produces an intermediate phenotype when in a ify heterozygous background, and a strong phenotype when in a ify homozygous mutant background (Fig. 3B) (Parcy et al., 1998). When introduced into an ag mutant background, this LFY:VP16 line showed no evidence of reversion. However, when we reduced the copy number of wild-type LFY from two to one in the ag line carrying the weak LFY:VP16 insertion, frequent reversion was observed (Fig. 3C,D). An even more dramatic reversion was seen in a ify homozygous mutant background; the floral meristem stopped producing floral organs and gave rise only to new floral buds (Fig. 3E,F). This observation demonstrates that LFY:VP16 and endogenous LFY compete for the same targets in the reversion process, as they do in specifying floral organ identity. We also note that, in a ify mutant background, LFY:VP16 produces a phenotype that is very different from weak loss-of-function alleles, for which an extensive allelic series has been described (Huala and Sussex, 1992; Levin and Meyerowitz, 1995; Schultz and Haughn, 1991; Schultz and Haughn, 1993; Weigel et al., 1992).

The LFY:VP16 phenotype in an AG+ background is strongly transgene dosage-dependent, such that homozygous transgenic plants always show a considerably stronger phenotype than hemizygous plants (Parcy et al., 1998). A similar effect as on homeotic organ conversions was seen with floral reversion, when we examined three LFY:VP16 ag families that segregated for transgene insertions with intermediate phenotypes outside the ag background. Only a minority of plants in the three families showed reversion, consistent with only homozygous transgenic plants reverting. In contrast, in two LFY:VP16 ag families segregating for insertions with strong phenotypes outside the ag background, all plants showed reversion.

As a further test to determine whether the LFY:VP16 effect was indeed due to the altered transcriptional activation potential conferred by the VP16 fusion, we transformed ag heterozygotes with the LFY:VP16 construct, which carries a truncated and inactive variant of the VP16 activation domain (Parcy et al., 1998). None of 12 LFY:VP16 ag primary transformants showed any sign of reversion. In contrast, 3 out of 4 LFY:VP16 ag primary transformants showed complete or partial reversion. Fisher’s exact test shows the two genotypes...
to be significantly different regarding reversion with \( P=0.007 \), from which we conclude that the VP16 transcriptional activation potential is necessary to induce floral reversion. Taken together with the observation that reversion in an \( ag \) background is observed both in plants that are compromised in wild-type \( LFY \) function (in \( lfy \) heterozygotes) and in \( LFY:VP16 \) plants, we conclude that \( LFY:VP16 \) is a dominant-negative allele of \( LFY \) with respect to floral reversion.

Expression of floral markers in \( LFY:VP16 ag \)

We extended our morphological analysis of reverting flowers in \( LFY:VP16 ag \) by analyzing the expression of two floral marker genes, \( AP1 \) and \( AG \). \( AP1 \) is initially activated throughout floral meristems, but becomes confined to the two outer whorls of organs, sepals and petals, from stage 3 on (Fig. 4A) (Mandel et al., 1992). Repression of \( AP1 \) at this time is due to activation of \( AG \) in the center of the flowers (Fig. 5A) (Drews et al., 1991; Gustafson-Brown et al., 1994).

Because \( AG \) activity is absent in \( ag \) mutants, \( AP1 \) continues to be expressed in the meristem of \( ag \) flowers (Fig. 4C,D) (Gustafson-Brown et al., 1994). In contrast to the persisting

\( AP1 \) expression in the center of \( ag \) flowers, we found that \( AP1 \) RNA disappeared from the center of \( LFY:VP16 \) \( ag \) interior flowers even before the meristem had completely reverted to an inflorescence meristem (Fig. 4E). \( AP1 \) RNA was already repressed in the center of \( LFY:VP16 ag \) flowers (arrowheads). (H) Mutant \( AG \) RNA disappears from the center of \( LFY:VP16 ag \) flowers only at a late stage, after the reverted meristem has begun to produce secondary flowers (inset in H, compare with inset in F, arrows). Scale bar in H represents 50 \( \mu \)m for all panels, except for insets in F and H (24 \( \mu \)m).
Fig. 6. Expression of *TFL1* RNA in wild type (A-C) and strong *LFY:VP16* (D-F) plants. Left column shows sections of shoot apices with inflorescence meristems (indicated by asterisks). Middle and right columns show sections of individual flowers. Numbers indicate floral stages (Smyth et al., 1990). In wild type, *TFL1* RNA is restricted to a group of subapical cells in the inflorescence meristem, and absent from flowers (arrowhead in A). In *LFY:VP16* flowers, there is ectopic *TFL1* expression, initially in a pattern similar to that in the shoot apical meristem (arrowheads in D,E). In the more advanced flower in (F), there is weak *TFL1* expression at the tip of the gynoecium (arrow). Occasionally, as in this flower, there is also a small group of *TFL1*-expressing cells at the base of the central gynoecium (arrowhead), possibly indicating a group of persisting meristematic cells. Scale bar in F represents 50 μm (A,C,D,F), and 24 μm (B,E).

meristems of *ag* flowers, mutant *AG* RNA continues to be expressed (Fig. 5E,F) (Gustafson-Brown et al., 1994). Initially, a similar pattern was seen in *LFY:VP16* ag flowers, but in older flowers, mutant *AG* RNA disappeared from the central meristem (Fig. 5H inset), indicating that it had lost floral identity. The disappearance of *AG* RNA from the center of flowers, however, appeared to be delayed relatively to that of *API*.

**Role of TFL1 in LFY:VP16-induced floral reversion**

One of the few cloned genes known to promote shoot meristem identity (or repress floral meristem identity) is *TFL1* (Bradley et al., 1997; Ratcliffe et al., 1998; Ratcliffe et al., 1999). Having shown that *LFY:VP16* has a dominant-negative effect on the maintenance of floral meristem identity, we wondered whether *TFL1* might mediate this effect. In wild type, *TFL1* is expressed in inflorescence meristems, but not developing flowers (Fig. 6A-C) (Bradley et al., 1997). Surprisingly, we found that *TFL1* was activated in *LFY:VP16* floral primordia, even though there was little morphological evidence for reversion in these flowers (Fig. 6D,E). In older flowers, weak ectopic *TFL1* expression was observed near the tip of the gynoecium, and, less often, in a group of cells at the base of the abnormal gynoecium (Fig. 6F).

To examine whether ectopic activation of *TFL1* is responsible for *LFY:VP16*-induced floral reversion, we generated *LFY:VP16 ag tfl1* plants. In contrast to *LFY:VP16 ag*, the flowers produced by *LFY:VP16 ag tfl1* plants never showed complete reversion to inflorescence shoots (Fig. 7C-G). Although the flowers on the main shoot produced a large number of secondary flowers, they did not stop producing floral organs, and secondary flowers remained interspersed with floral organs (Fig. 7F,G). That reversion was reduced, but not abolished, in *LFY:VP16 ag tfl1* indicates that ectopic activation of *TFL1* is partially responsible for floral reversion of *LFY:VP16* flowers. However, *TFL1* does not appear to be sufficient to trigger overt reversion, since *LFY:VP16 AG*+ flowers do not revert, despite ectopic *TFL1* activation. Similarly, expressing *TFL1* under the control of *AG* regulatory sequences in the center of *ag* mutant flowers is not sufficient to cause reversion (R. Hong, M. Busch and D. W., unpublished results).

**DISCUSSION**

One of the main differences between shoot and floral meristems is that the central stem cell population in shoot meristems persists, whereas it is only transiently maintained in flowers. However, persisting stem cell proliferation in, for
example, clv1 or ag mutants, does not normally lead to floral reversion, but rather to the continued production of more floral organs (Bowman et al., 1989; Bowman et al., 1991; Clark et al., 1993; Mizukami and Ma, 1995; Sieburth et al., 1995). That floral reversion can be induced in some of these mutants, either by combining them with other mutants or by reducing floral inductive cues, suggests that the central stem cell population does not become irreversibly specified as floral, but rather that maintenance of floral meristem identity requires the continued activity of genes such as LFY. The results presented in this study support this hypothesis.

**Floral reversion in Arabidopsis**

Two types of situations in which floral meristems behave as inflorescence meristems have been described in *Arabidopsis*. One example is provided by ap1 cal double mutants, or even more strikingly, ap1 cal ful triple mutants, in which the inflorescence shoot meristem produces primordia that often behave very similarly to secondary inflorescence meristems (Bowman et al., 1993; Ferrándiz et al., 2000). This phenotype is reminiscent of floral reversion in many other species, typically induced by the removal of floral inductive cues (Battey and Lyndon, 1990). The *ap1 cal* and *ap1 cal ful* phenotypes are characterized by a failure to establish robust LFY expression, with concomitant ectopic TFL1 expression in lateral meristems. That changes in LFY and TFL1 expression are responsible for the *ap1 cal* and *ap1 cal ful* defects has been confirmed by demonstrating that overexpression of *LFY* or inactivation of *TFL1* strongly suppresses meristem proliferation in *ap1 cal* and *ap1 cal ful* mutants (Bowman et al., 1993; Ferrándiz et al., 2000). On the other hand, overexpression of AG, which acts downstream of LFY, is insufficient to suppress any aspect of the *ap1 cal ful* phenotype (Ferrándiz et al., 2000).

In contrast to *ap1 cal* or *ap1 cal ful* mutants, other mutants produce floral primordia that revert to an inflorescence shoot meristem only after several whorls of floral organs have been produced. This group of mutants includes *ag* mutants and *lfy* heterozygotes grown under short days, and *ap1 clv1* mutants (Clark et al., 1993; Okamura et al., 1996). Similarly, *LFY:VP16* *ag* floral meristems produce at least two whorls of organs before reverting to an inflorescence meristem. Also in contrast to *ap1 cal* or *ap1 cal ful*, inactivation of *TFL1* has only modest effects on floral reversion of *LFY:VP16*. Together, these observations indicate that the *LFY:VP16* allele uncouples the role of LFY in establishing and maintaining floral meristem identity.

**Role of LFY in maintaining floral meristem identity**

How does LFY contribute to the maintenance of floral meristem identity? LFY is a DNA-binding protein that directly regulates transcription of downstream genes (Busch et al., 1999; Parcy et al., 1998; Wagner et al., 1999). One of these targets is AG, which represses floral reversion (Mizukami and Ma, 1997; Okamura et al., 1996). The additive effects of reducing LFY copy number and inactivating AG on floral reversion indicate that LFY does not maintain floral meristem identity solely by ensuring a sufficient level of AG expression. This result is consistent with the finding that AG RNA expression is not obviously altered in young flowers of *lfy/LFY* plants grown in short days (Okamura et al., 1996).

There are two alternative explanations for the increased floral reversion in *ag/ag lfy/LFY* or *ag/ag LFY:VP16* plants. One possibility is that LFY and AG act entirely independently on floral reversion. Another possibility is that LFY acts as an AG substitute to maintain floral meristem identity in *ag* mutants. Indeed, LFY continues to be expressed in the center of (long-day grown) *ag* floral meristems (D. W., unpublished results). If maintenance of high levels of LFY expression in these meristems is compromised in short days, this could cause floral reversion in *ag* mutants, further exacerbated when LFY copy number is reduced.

LFY:VP16 is an activated version of LFY that can activate targets such as AG and *API* more strongly than wild-type LFY and that can therefore be classified as a hypomorphic allele with respect to activation of these targets (Parcy et al., 1998). In contrast, *LFY:VP16* appears to be an antimorphic allele with respect to maintenance of floral meristem identity, because it acts in a manner opposite to that of wild-type LFY.

Considering the evidence for LFY:VP16 being a transcriptional activator and the fact that at least one shoot identity gene, *TFL1*, is derepressed in *LFY:VP16* floral meristems, we postulate that transcriptional repression by LFY is involved in preventing reversion of a floral to an inflorescence meristem. If we assume further that floral reversion involves the activation of a hypothetical set of shoot identity genes, we can envision two scenarios through which LFY affects these genes (Fig. 8). In the first scenario, LFY negatively regulates shoot identity genes indirectly by activating a transcriptional repressor that downregulates or represses shoot identity genes. In the second scenario, LFY’s primary effect is transcriptional repression, either through
direct repression of shoot identity genes, or though repression of a positive regulator of shoot identity genes. In both cases, reducing LFY activity in ify heterozygotes would lead to floral reversion because of increased activity of shoot identity genes. However, if LFY’s primary effect was transcriptional activation of a hypothetical reversion repressor, LFY:VP16 should be even more effective than wild-type LFY in activating this repressor, and we would not expect reversion. In contrast, if LFY’s primary effect were repression of a hypothetical reversion activator, LFY:VP16 would have an opposite effect from wild-type LFY. Because LFY:VP16 acts in a dominant-negative fashion – floral reversion is observed both when wild-type LFY is reduced (in ify heterozygous plants) and in LFY:VP16 plants – we believe it most plausible that LFY’s primary effect in maintaining floral meristem identity is transcriptional repression.

It is unknown whether LFY has some intrinsic repression potential. We have shown previously that LFY is able to bind to AG and API regulatory sequences, but LFY on its own is not sufficient for transcriptional activation in a heterologous system, yeast (Busch et al., 1999; Lohmann et al., 2001; Parcy et al., 1998). We therefore proposed that LFY interacts with other factors to differentially affect the expression of downstream targets, a hypothesis that we recently confirmed by demonstrating that LFY directly interacts in activation of AG with another transcription factor, the homeo domain protein WUSCHEL (Lohmann et al., 2001). By analogy, we hypothesize that LFY interacts with an unknown co-repressor in preventing floral meristem reversion. Little is known about transcriptional repression in plants, but the Arabidopsis genome encodes putative co-repressors such as LEUNIG (Conner and Liu, 2000).

Which are the genes repressed by LFY to prevent floral reversion? TFL1 is derepressed both in ify mutants (Ratcliffe et al., 1999) and in LFY:VP16 plants (this work). However, although the TFL1 promoter contains putative LFY binding sites, these are not bound by LFY in vitro (M. A. Busch and D. W., unpublished data), suggesting either that TFL1 is not a direct target of LFY, or that other proteins are required for interaction of LFY with TFL1 regulatory sequences. To further understand the interaction of LFY and TFL1, it will be necessary to define the regulatory sequences sufficient for normal TFL1 expression.

We thank Jérôme Giraudat for allowing some of the experiments to be performed in his lab at Gif. We thank Charles Graham for help with scanning electron microscopy; Nicole Dagenais for performing in situ hybridizations; Nathalie Mansion for photographic work; Miguel Blázquez, Ilha Lee, Jan Lohmann and Ove Nilsson for discussions; Max Busch and Ray Hong for communicating unpublished results; José Dinnehy, Ray Hong and Xuelin Wu for critical reading of the manuscript; and an anonymous reviewer for suggesting alternative scenarios that explain the effects of LFY and AG on floral reversion. This work was supported by a fellowship from Human Frontiers Science Program Organization (F. P.), and grants from NIH (GM62932) and US Department of Energy (DE-FG03-98ER20317) to D. W. D. W. is a Director of the Max Planck Institute.

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