Chromatin assembly factor CAF-1 is required for cellular differentiation during plant development

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Chromatin assembly factor CAF-1 facilitates the formation of nucleosomes on newly replicated DNA in vitro. However, the role of CAF-1 in development is poorly understood because mutants are not available in most multicellular model organisms. Biochemical evidence suggests that FASCIATA1, FASCIATA2 and MSI1 form CAF-1 in Arabidopsis thaliana. Because fasciata mutants are viable, CAF-1 is not essential for cell division in plants. Arabidopsis CAF-1 mutants have defects in shoot apical meristems; in addition, CAF-1 is required to establish seedling architecture, leaf size and trichome differentiation. CAF-1 is needed to restrict branching of trichomes on rosette leaves. Increased trichome branching in CAF-1 mutants is not strictly correlated with increased nuclear DNA content. In addition, fas2 glabra3 double mutants show an additive genetic interaction, demonstrating that CAF-1 acts genetically parallel to the GLABRA3-containing, endoreduplication-coupled trichome branching pathway. However, CAF-1 is often needed to restrict endoreduplication, because seedlings of most CAF-1 mutants have increased ploidy. Notably, in the Landsberg erecta background, loss of CAF-1 does not affect ploidy, demonstrating that loss of CAF-1 can be compensated in some Arabidopsis accessions. These results reveal that the functions of FAS1, FAS2 and MSI1 are not restricted to meristems, but are also needed to control genome replication at multiple steps of development.

KEY WORDS: Arabidopsis, CAF-1, Chromatin, Endoreduplication, MSI1, Shoot apical meristem, Trichome

INTRODUCTION

During the cell cycle, nuclear DNA must be fully replicated and equally distributed to the daughter cells. The genetic information encoded in the DNA does not only consist of the primary nucleotide sequence along the chromosomes, but also has an important epigenetic component that is established by the chromatin state(s) across the regulated loci. Biochemical and genetic studies have identified many proteins that are involved in the establishment or maintenance of chromatin. One of the well-studied protein complexes involved in chromatin metabolism is chromatin assembly factor CAF-1 (for a review, see Krude and Keller, 2001; Mello and Almouzni, 2001; Loyola and Almouzni, 2004). This heterotrimeric complex is found in yeast, animals and plants, and facilitates nucleosome assembly on newly replicated DNA (Smith and Stillman, 1989; Bulger et al., 1995; Verreault et al., 1996; Kaufman et al., 1997; Kaya et al., 2001). Human CAF1 binds newly synthesized H3-H4 histone dimers and, because its largest subunit (p150) physically interacts with the proliferating cell nuclear antigen PCNA, these histones are targeted to regions of DNA synthesis during replication or repair (Gaillard et al., 1996; Verreault et al., 1996; Shibahara and Stillman, 1999; Moggs et al., 2000; Zhang et al., 2000; Krawitz et al., 2002). Importantly, all three CAF-1 subunits physically interact with other proteins as well: the smallest subunit, p48, is found in multiple complexes affecting chromatin dynamics (for a review, see Hennig et al., 2005); the second largest subunit, p60, interacts with the histone chaperone anti-silencing factor 1 (Mello et al., 2002); and p150 interacts with heterochromatin protein 1, methyl-binding protein 1 and the Bloom’s syndrome DNA-helicase BLM (Murzina et al., 1999; Reese et al., 2003; Jiao et al., 2004; Sarraf and Stancheva, 2004). However, it is unclear whether CAF-1 formation and the other interactions described above occur simultaneously, or whether they are exclusive, indicating CAF-1-independent functions of the subunits.

Yeast mutants deficient in CAF-1 subunits are viable but show enhanced sensitivity to UV light (Kaufman et al., 1997; Game et al., 1999). In addition, maintenance of silencing at mating type loci and near the telomeres is impaired (Enomoto et al., 1997; Kaufman et al., 1997; Monson et al., 1997; Enomoto and Berman, 1998; Smith et al., 1999; Taddei et al., 1999). Unlike in yeast, much less is known about the role of CAF-1 in the life cycle of multicellular organisms, mainly because mutants are not readily available. Transgenic approaches were therefore used to analyze CAF-1 function during the development of model organisms. For example, expression of a truncated version of human p150 interfered with the maintenance of transcriptional gene silencing in mammalian cells (Tchenio et al., 2001), and expression of a truncated version of p150 in Xenopus caused severe defects in embryo development, suggesting that CAF-1 is essential in vertebrates (Quivy et al., 2001). This hypothesis was strongly supported by RNAi knock-down experiments of p150 in human cell lines. Such cells showed delayed DNA replication and accumulated in S-phase (Hoek and Stillman, 2003). Similarly, silencing of p60 expression by RNAi caused apoptosis in dividing, but not in quiescent, human cells (Nabatiyan and Krude, 2004).

The model plant Arabidopsis thaliana is currently the only multicellular organism for which mutants in all three CAF-1 subunits are available. Reconstitution experiments showed that FASCIATA 1 (FAS1, a homolog of p150), FAS2 (a homolog of p60) and Arabidopsis MSI1 (a homolog of p48) form a functional CAF-1 complex in vitro (Kaya et al., 2001). Mutants deficient in FAS1 and FAS2 were originally identified because of their fasciated phenotype (Reinholz, 1966; Leyser and Furner, 1992). Fasciation describes a set of developmental abnormalities...

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caused by defects of the shoot apical meristem (SAM) that includes altered phyllotaxis, broadening and bifurcation of the stem, and alterations in the number of floral organs (Wodzicki, 1905). The SAM contains slowly dividing stem cells that give rise to all cells in above-ground, post-embryonic plant organs (Scheres et al., 2004). Proper organization of the SAM depends on several proteins, including the key regulator SCARECROW (Laux et al., 1996). The fasciated phenotype of fas1 and fas2 is caused at least in part by loss of the restricted spatial expression pattern of SCARECROW (Kaya et al., 2001). In addition to SAM defects, fas1 and fas2 have defects in the root apical meristem (RAM), which produces the cells needed for post-embryonic root growth (Scheres et al., 2004). This is because the restricted spatial expression patterns of the RAM key regulator SCARECROW are partially lost in the fasciata mutants (Kaya et al., 2001). Surprisingly, plants lacking both FAS1 and FAS2 subunits of CAF-1 are viable and fertile, but express some silenced transposons or transgenes (Takeda et al., 2004; Ono et al., 2006). By contrast, msi1 null mutants are not viable and seeds abort early during embryo development (Köhler et al., 2003; Guitton et al., 2004). MS11 co-suppression (msi1-cs) plants with strongly reduced protein levels (>90% reduction) are viable but show severe developmental defects, including homeotic transformation of floral organs and sterility (Hennig et al., 2003). Because such defects were not observed in the fasciata mutants, it was concluded that they are caused by the reduced function of other MS11-containing complexes, such as the MEDEA (MEA) or CURLY LEAF Polycomb group complex (Hennig et al., 2003; Köhler et al., 2003; Hennig et al., 2005; Schönrock et al., 2006a).

Thus, CAF-1 is required for the execution of normal developmental programs in the apical meristems, but roles for CAF-1 in other tissues are much less understood. Here, we show that expression of FAS1 and FAS2 is high in actively dividing cells, and that several aspects of development, including seedling growth and leaf hair differentiation, are impaired in Arabidopsis mutants lacking CAF-1. Therefore, CAF-1 plays a more general role in plant development than has been previously appreciated.

MATERIALS AND METHODS

Plant material and growth conditions

Seeds of Columbia (Col), Landsberg erecta (Ler) and Enkheim (En) Arabidopsis thaliana wild-type accessions, and of fas1-1 (Reinholz, 1966; Kaya et al., 2001), fas2-1 (Leyser and Turner, 1992; Kaya et al., 2001) and gl3-1 (Koornneef et al., 1982; Payne et al., 2002) mutants were obtained from the Nottingham Arabidopsis Stock Centre. New fas1 and fas2 alleles were identified in T-DNA insertion mutant collections (Sessions et al., 2002; Alonso et al., 2003, and named fas1-4 and fas2-4 (see Figs S1, S2 in the supplementary material). Plants were kept in Conviron growth chambers on four layers of water-soaked filter paper, which were placed into clear plastic boxes. A 48-hour dark treatment at 4°C was followed by induction of germination by white light for 10 hours and further incubation of seedlings in the dark at 23°C or under LD photoperiods.

Generation of transgenic plants with reduced MS11 protein levels

In contrast to the viable fas1-1 and fas2-1 mutants, which have premature stop codons and are most likely null alleles (Kaya et al., 2001), loss of MS11 is lethal (Köhler et al., 2003; Guitton et al., 2004). Therefore, we constructed transgenic lines in which the level of MS11 was only moderately decreased by a MS11 antisense construct. A 532-bp ClaI/XhoI fragment of the MS11 coding sequence was fused in antisense orientation to the cauliflower mosaic virus (CaMV) 35S promoter in the binary vector pSALK2792 and transformed into Col wild-type plants. We selected the line 1ASB1 (msi1-as), which segregated a single transgene in a 1:3 ratio and had 30-50% of wild-type MS11 protein levels (see Fig. S3A in the supplementary material), for further characterization, but the phenotypes described below were observed for several independent lines. Similar to fas1-1 and fas2-1, but in contrast to msi1-cs and msi1-as plants were fertile and showed no seed abortion. Development of msi1-as plants was delayed, and plants had a reduced rosette size, a delayed flowering time and reduced growth of primary shoots, although more severe symptoms of fasciation, such as stem bifurcation, were not observed (see Fig. S3C in the supplementary material; data not shown). MS11 shares only 25-52% identity with the other MS11-like proteins in Arabidopsis, suggesting that expression of the MS11 antisense-RNA construct would not affect expression of MS12-5; and semi-quantitative RT-PCR did not reveal any changes in MS12-5 transcript levels in msi1-as plants (see Fig. S3B in the supplementary material). In addition, we could not detect elevated transcript levels for AGAMOUS (AG) or APETALA2 (AP2) in msi1-as leaves (see Fig. S3D in the supplementary material). AG and AP2 are floral homeotic genes that are ectopically expressed in non-floral tissues of msi1-cs plants, but not in fas1-1 or fas2-1 mutants (Hennig et al., 2003).

Protein gel blot analysis

Protein extracts and protein gel blots using a specific anti-MS11 antiserum were performed as described previously (Ach et al., 1997; Hennig et al., 2003).

DNA isolation and RT-PCR

DNA was extracted from leaves of plants as previously described (Hennig et al., 2003). For RT-PCR analysis, 0.4-1.0 µg total RNA was treated with DNase I. The DNA-free RNA (0.2-1.0 µg) was reverse-transcribed using an oligo(dT) primer and MMLV reverse transcriptase (Clonetech, Palo Alto, CA). Aliquots of the generated cDNA were used as template for PCR with gene-specific primers (Table 1).

Analysis of hypocotyl development

Dark-grown seedlings were mounted in water and observed with differential interference contrast (DIC) optics. Pictures were recorded with an AxioCam HRc CCD camera (Zeiss, Jena, Germany) and analyzed using ImageJ software, which is freely available at http://rsb.info.nih.gov/ij/index.html.

Ploidy analysis

Tissue was cut into small pieces in 400 µl nuclear extraction buffer (Partec, Münster, Germany), incubated for 30 minutes on ice, filtered through a 30 µm mesh, mixed with 1 ml nuclear staining buffer (Partec) and, after further

Table 1. Sequences of gene-specific primers used for RT-PCR

<table>
<thead>
<tr>
<th>Gene</th>
<th>Forward primer</th>
<th>Reverse primer</th>
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<tr>
<td>MS12</td>
<td>ATTTGCCCAACAGCTTCCTCAGA</td>
<td>TGGGAAGACCTCCTCCTCATGG</td>
</tr>
<tr>
<td>MS13</td>
<td>TGGCCGATTACATGTCCTGA</td>
<td>TCCCCAACCCTGTTGATACC</td>
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<tr>
<td>MS14</td>
<td>AGCAAGGTTGAAAAAGCGCA</td>
<td>CATCAAACAAAACCCGAGTG</td>
</tr>
<tr>
<td>MS15</td>
<td>GGACAAAGGTTGCGACTTCCA</td>
<td>GCCGCAATCTCATCAATGACC</td>
</tr>
<tr>
<td>AG</td>
<td>TGGGACAAATCTCAACCCGAGGA</td>
<td>CCCATCAATGCTGTGG</td>
</tr>
<tr>
<td>AP2</td>
<td>ATTTGCGGTTGTCGGACACC</td>
<td>ATGACCTCGGACTGATCC</td>
</tr>
<tr>
<td>GAPDHα</td>
<td>ATGGGCTTGGTACCTTCTTCG</td>
<td>TTCTTGGACACGCTTCAAT</td>
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<td>GAGAGGCTACATACTTTGTAAG</td>
</tr>
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<td>FAS1</td>
<td>CTTCACATCTTCTACATACATCAATC</td>
<td>TGTTTACGCAATGACACGCC</td>
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incubation on ice for 10 minutes, analyzed with a Partec Ploidy Analyzer. For quantification, the results of three to six independent preparations were averaged.

Ploidy of trichome nuclei was determined as described (Walker et al., 2000). Briefly, young rosette leaves were fixed in FAA (50% ethanol, 5% glacial acetic, 10% formaldehyde). Staining was performed for 1.5 hours with 130 μg/ml DAPI in McIlvaines buffer (60 mM citric acid, 80 mM sodium phosphate, pH 4.1). Samples were washed once for 15 minutes and once for 1 hour with McIlvaines buffer, and mounted in McIlvaines buffer with 50% glycerol. Fluorescence was recorded with a MagnaFire CCD camera (Optronics, Goleta, CA), or with an Apogee Alta U32 CCD camera (Apogee Instruments, Roseville, CA). Images were quantified using ImageJ. Total fluorescence of at least 30 representative nuclei per experiment was determined and calibrated using guard cell nuclei (n>=30), which are considered to be strictly diploid (Walker et al., 2000).

Analysis of leaf histology
Plants were grown until bolting before leaves were harvested. Leaf area was determined by scanning the leaves and measuring their size with ImageJ. Leaves were then fixed in ethanol-acetic acid (9:1) at room temperature for 2.5 hours, dehydrated in 90% then 70% ethanol for 1 hour each, and cleared in clearing solution [66.7% (w/v) chloral hydrate, 8.3% (w/v) glycerol in water] at 4°C overnight. Samples were mounted in clearing solution and investigated with DIC optics. Images were recorded with an AxioCam HRc CCD camera and analyzed with ImageJ.

RESULTS
Lack of CAF-1 causes defects in seedling development
The current model proposes that CAF-1 facilitates nucleosome assembly during S-phase of the cell cycle (Loyola and Almouzni, 2004). Accordingly, the expression of the two large CAF-1 subunits increases in proliferating Arabidopsis cells, and is cell cycle regulated in Arabidopsis and yeast (Kaya et al., 2001) (see Fig. S4 in the supplementary material). By contrast, expression of the small subunit MSI1 does not strongly correlate with cell proliferation or cell cycle. These expression patterns reflect the more widespread role of MSI1 in other chromatin complexes (Hennig et al., 2005). The expression data suggest that CAF-1 is required in dividing cells. However, to date, only defects in meristem function have been studied in detail for fasciata mutants (Reinholz, 1966; Leyser and Furner, 1992; Kaya et al., 2001). To test whether CAF-1 function is required in other organs as well, we characterized meristem-independent cell proliferation and differentiation in CAF-1 mutants. fas1 and fas2 alleles have been previously characterized in Landsberg erecta, Enkheim or Nossen (Reinholz, 1966; Leyser et al., 1992; Kaya et al., 2001). To test whether any defects observed are genuine traits of CAF-1 loss or are caused by the genetic background of the different accessions, we identified novel fas1 and fas2 alleles in Columbia – fas1-4 and fas2-4 (see Figs S1, S2 in the supplementary material). The fas1-4 and fas2-4 phenotypes are similar to the phenotypes of other fasciata mutants: the plants are smaller than wild type and develop fasciation.

Seedling organs such as hypocotyl and cotyledons are not formed by the apical meristems, but are formed during embryogenesis. Therefore, we analyzed seedlings of CAF-1 mutants in more detail. General seedling morphology was not severely affected in fas1, fas2 or msi1-as seedlings grown in long-day photoperiods (Fig. 1A, see also Figs S1, S2 in the supplementary material), but msi1-as seedlings consistently showed cotyledon epinasty, i.e. a downward curling of the cotyledons. As this phenotype was not observed in fas1 or fas2 seedlings, but was sometimes apparent in msi1-cs lines (P. Taranto, PhD thesis, University of California, Berkeley, 1998), we conclude that it is not related to CAF-1 but rather to a different MSI1-function.

Dark-grown seedlings of all three CAF-1 mutants had shorter hypocotyls than did wild type (Fig. 1B); this phenotype was most pronounced for fas1-1, and weakest for fas1-4 and msi1-as. Note that some FAS1 transcript is made in the fas1-4 insertion mutant (see Fig. S1 in the supplementary material), demonstrating that fas1-1 but not fas1-4 is a null allele. By contrast, both fas2 alleles appear to be null (see Fig. S2 in the supplementary material). When seedlings were grown under continuous white light, all plants responded strongly with inhibition of hypocotyl elongation (data not shown). The short hypocotyls formed in the light precluded the detection of length differences between CAF-1 mutants and wild type.

Post-germination hypocotyl growth in the dark results mostly from cell elongation and only a few cell divisions occur (Gendreau et al., 1997). To determine whether the shorter hypocotyls in dark-grown CAF-1 mutant seedlings are caused by defects in cell division or elongation, we counted hypocotyl epidermal cell number and measured cell size (Fig. 2A,B). The results show that hypocotyl epidermal cells of both fas2 alleles are significantly shorter than in the wild-type, whereas cell size was not, or only weakly, affected in fas1-1, fas1-4 and msi1-as. These results suggest that the reduced size of hypocotyl epidermal cells is a genuine trait of fas2 mutants and is not caused by the genetic background. Moreover, loss of
CAF-1 does not necessarily cause size reductions for hypocotyl epidermal cells. By contrast, seedlings lacking any of the three CAF-1 subunits had reduced cell numbers in their hypocotyls. This reduction was strongest in fas1-1 and weakest in msi1-as. Only the weak fas1-4 allele had slightly increased cell numbers. Interestingly, hypocotyls of fas1, fas2 and msi1-as seedlings were significantly thicker than hypocotyls of wild-type plants (Fig. 2C). Notably, the increase in hypocotyl diameter was strongest in the weak fas1-4 allele, whereas changes in cell size and cell number were smallest in this allele. In summary, CAF-1 subunits are therefore not only required to control cell proliferation in the SAM and RAM, but also for normal cell proliferation in hypocotyls.

Hypocotyl cells of fas1-1 undergo increased DNA endoreduplication

Elongating hypocotyl cells endoreduplicate their DNA more in dark-grown than in light-grown seedlings (Gendreau et al., 1997), and cell elongation and endoreduplication are often tightly coupled. Because cell elongation is impaired in fas2 hypocotyls, we measured DNA endoreduplication in dark- and light-grown CAF-1 mutant seedlings. However, rather than a decrease in endoreduplication, seedlings grown in long-day photoperiods or in the dark showed increased DNA endoreduplication (Fig. 3A,B): the fraction of 2C nuclei decreased from 30-40% to 20-30%, whereas the fraction of 8C and 16C nuclei increased. This shift in ploidy was strongest for fas1-1, fas1-4 and fas2-4, but was less pronounced for msi1-as. We also measured ploidy directly in nuclei of fas1-1 and wild-type hypocotyl cells, and found that the increased DNA content was caused, at least partially, by higher ploidy in the hypocotyl (data not shown). Interestingly, ploidy patterns in fas2-1 did not differ from those of wild-type Landsberg erecta. Thus, CAF-1 deficiency does not generally affect DNA endoreduplication, and the reduced cell size in dark-grown fas2-1 and fas2-4 hypocotyls does not correlate with reduced endoreduplication.

Size of leaf epidermal cells is altered in CAF-1 mutants

The SAM produces leaf primordia, but the final leaf morphology is mostly independent of SAM function (Byrne, 2005; Fleming, 2005). The smaller rosette diameter and the serration of rosette leaves in fasciata mutants in the Col and En accessions (Reinholz, 1966; Leyser and Furner, 1992; Serrano-Cartagena et al., 1999; Kaya et al., 2001) suggested that cell proliferation and/or expansion was affected during leaf development. To test this hypothesis, the histology of rosette leaves was investigated. In addition to the fas1-1 allele in En, we included the novel fas1-4 allele in the Col background. The phenotype of fas1-4 plants was similar to that of other fasciata mutants, including alterations in phyllotaxis and reduced shoot height (see Fig. S1 in the supplementary material). Furthermore, fas1-4 rosette leaves were serrated, similar to the rosette leaves of fas1-1 and fas2-4 plants. Growth of rosette leaves occurs in two phases: outgrowth through cell division and enlargement of the blade through cell expansion (Beemster et al., 2005). Cross sections through the first or second rosette leaves of plants at bolting did not reveal any obvious differences in internal leaf histology between wild type and mutants (data not shown). By contrast, epidermal cells of these leaves were significantly larger in the CAF-1 mutants than in the wild type (Fig. 4A,B). This effect was much stronger in the fas1-4 and fas2-4 mutants (1.5 to 2-fold increase) than in the msi1-as plants (1.2-fold increase).

Next, we determined the number of leaf epidermal cells. Consistent with the observation that CAF-1 mutations interfere with regulation of cell division rates during hypocotyl development, the number of epidermal cells was reduced in rosette leaves of both fas1-4 and fas2-4 (Fig. 4C). By contrast, the number of epidermal cells was not significantly altered in msi1-as plants. Similar results were obtained when the third and fourth rosette leaves were analyzed (Fig. 4D,E). These results show that CAF-1 is required not only to control cell proliferation in the SAM, RAM and hypocotyls, but also for normal cell proliferation in expanding rosette leaves. In addition, these results suggest that the phenotype of fasciata mutants does not become more severe during plant development.

Trichome differentiation is altered in CAF-1 mutants

Trichomes are leaf hairs that originate from the leaf or stem epidermis. In Arabidopsis, each trichome consists of a single cell and therefore provides an ideal system with which to study cell differentiation. Lateral inhibition maintains a regular spacing of trichomes in wild-type leaves. After trichome fate commitment, cells
stop dividing but continue to synthesize DNA. The differentiating trichome cell extends out of the leaf surface, undergoes two branching events and finally elongates extensively (Schnittger and Hülskamp, 2002; Larkin et al., 2003). The majority of trichomes on Arabidopsis leaves have three branches (Fig. 5A). By contrast, CAF-1 mutants contain many trichomes that develop more than three branches (Fig. 5B, G). In general, only about 80% of trichomes in CAF-1 mutants have three branches, but up to 30% have four to six branches (Fig. 5G). Similar results were obtained when the third and fourth leaves were analyzed (data not shown), suggesting that this trichome phenotype is stable throughout development. The leaves of CAF-1 mutants did not contain clustered trichomes suggesting that regular trichome initiation does not require CAF-1.

In wild-type Arabidopsis plants, trichomes are single cells with only one nucleus (Larkin et al., 2003). Microscopic investigation of DAPI-stained trichomes revealed that trichomes of CAF-1 mutants are also single cells with one nucleus (Fig. 5C-F). During trichome differentiation, four rounds of DNA endoreduplication usually occur, which establish a relative DNA content of 32C instead of the usual 2C of diploid cells. Because increased trichome branching is often correlated with extra DNA endoreduplication, we measured the DNA content in trichomes of CAF-1 mutants (Fig. 5H). Only trichome nuclei of fas1-1 and fas1-4 consistently contained more DNA in all experiments, suggesting that many trichome cells undergo at least one extra round of DNA endoreduplication. Although fas2-4 had a non-significant tendency for increased ploidy, this was not evident in all experiments, despite consistently increased trichome branching. Because fas2-1, fas2-4 and msi1-as trichomes develop extra branches without significantly increased ploidy levels, we reasoned that CAF-1 controls trichome branching via a pathway that is independent of DNA endoreduplication.

**FAS1, FAS2 and MSI1 act together in trichome development**

Although the similar phenotypes of fas1, fas2 and msi1-as plants strongly suggest that FAS1, FAS2 and MSI1 function in CAF-1 during trichome development, the different effects on ploidy make...
it possible that they affect trichome development independently of CAF-1. To test this possibility genetically, we generated fas1-4 fas2-4, fas1-4 msi1-as and fas2-4 msi1-as double mutants. All of these double mutants were viable, similar to the previously described fas1-1 fas2-1 double mutant (Hennig et al., 2003), and no obvious synergistic effects were observed during development. In particular, quantification of trichome branching showed no additive or synergistic effects between fas1-4, fas2-4 and msi1-as (Fig. 6A). Similarly, fas1-1 fas2-1, fas1-1 msi1-as and fas2-1 msi1-as double mutants generated by inter-accession crossings did not show increased trichome branching (data not shown). These results demonstrate that FAS1, FAS2 and MSI1 function in the same genetic pathway to control trichome development, possibly by acting together in the CAF-1 complex.

**Discussion**

**CAF-1 is required for control of hypocotyl growth**

Previously, CAF-1 function in plants has been described mainly for the SAM and RAM (Reinholt, 1966; Leyser and Furner, 1992; Kaya et al., 2001). In particular, defects in the organization of the SAM were suggested to cause abnormal phyllotaxis and a thickening or even bifurcation of the stem. These defects, together with the reduced growth rate of the primary shoot, are most likely the consequence of disruptions in normal SAM function. However, the fasciata mutants...
the effects in hypocotyls, loss of CAF-1 interfered with cell proliferation in rosette leaves, where the number of adaxial epidermal cells was reduced by half. In addition, cells in the adaxial epidermis of rosette leaves were significantly enlarged in CAF-1 mutants. This increase in cell size might be caused by a compensatory mechanism for the reduced cell numbers (Tsukaya, 2005). This could explain why, despite the greatly reduced numbers of epidermal cells, the leaf area is often only mildly reduced in fas1-4 and fas2-4 mutants (data not shown). Furthermore, altered cell number and cell size could potentially account for the change in trichome numbers on rosette leaves of CAF-1 mutants, because it was primarily the trichome density relative to leaf size, rather than the trichome density relative to epidermal cell number, that was reduced (data not shown). Thus, CAF-1 is needed for efficient cell proliferation in developing hypocotyls and rosette leaves, and compensation by altered cell size might occur preferentially in leaves but not in hypocotyls.

**CAF-1 is required for trichome differentiation**

Trichome morphogenesis is a well-studied developmental process, and many mutants with altered trichomes have been identified (Oppenheimer, 1998; Schnittger and Hülskamp, 2002; Larkin et al., 2003). The genetic analysis of branching mutants suggests that several redundant pathways control branch formation (Luo and Oppenheimer, 1999). One group of genes affecting trichome branching primarily controls the number of DNA endoreduplication cycles, which in turn determines branch number (Hülskamp et al., 1994; Perazza et al., 1999; Kirik et al., 2001). GL3 is one member of this group and encodes a bHLH protein that positively regulates endoreduplication and branching events in trichomes (Payne et al., 2000). A second group of branching mutants affects branch number independently of DNA endoreduplication (Folkers et al., 1997; Luo and Oppenheimer, 1999; Qiu et al., 2002). In all CAF-1 mutants, trichome patterning was maintained and no trichome clusters were observed, indicating that CAF-1 is not required for commitment to the trichome cell fate. Similarly, trichomes in fas1, fas2 and msi1-as, and in the double mutants we investigated, were single cells containing one nucleus, suggesting that most steps in trichome differentiation are completed normally even in the absence of CAF-1. However, all CAF-1 mutants had increased branch numbers. Interestingly, increased trichome branching was also observed in Hosoba toge toge, a deletion mutant lacking a 75.8-kb region encompassing 15 genes, including FAS1 (Kaya et al., 2000). Because only fas1 trichomes had a consistently increased DNA content, the increased branching is not strictly correlated with DNA endoreduplication. Therefore, CAF-1 functions either in a DNA endoreduplication-independent pathway or downstream of DNA endoreduplication to control trichome branching. This hypothesis is also supported by the fact that the gl3-1 fas2-1 double mutants analysed have intermediate branch numbers and none of the two alleles was epistatic over the other. Most likely, CAF-1 functions in a DNA endoreduplication-independent pathway for trichome branching. In summary, CAF-1 is not generally needed for cell fate determination, but it is needed for normal cell proliferation and, in trichomes, even for proper differentiation.

**CAF-1-independent functions of CAF-1 subunits**

Mutants lacking any one of the three subunits of *Arabidopsis* CAF-1 display a range of similar phenotypes that is consistent with the loss of CAF-1 activity. Similarly, CAC1, CAC2 and CAC3 are all required for CAF-1 function in yeast (Game and Kaufman, 1999). However, some phenotypes caused by reduced FAS1, FAS2 or MSI1...
levels differ, suggesting that CAF-1 subunits can function independently of CAF-1. For instance, only the loss of FAS2 led to smaller hypocotyl epidermal cells independent of the genetic background. Likewise, msi1-as plants show unique features, in particular they often develop cotyledon epinasty. Because this trait was never observed in fas1 or fas2, it most likely resulted from the lack of a CAF-1-independent MS11 function. In addition, the previously described msi1-cs plants develop severe phenotypic defects, including homeotic changes of floral organ identity, which are not present in fas1, fas2 and msi1-as (Hennig et al., 2003). Embryos of the msi1-1 mutant abort early in development, but embryos of fas1, fas2 and msi1-as show no obvious developmental defects (Kaya et al., 2001; Köhler et al., 2003; Guittion et al., 2004). Biochemical analyses suggest that MSI1-like proteins participate in several protein complexes acting on chromatin, including histone deacetylases, chromatin remodeling factors and Polycomb Group protein complexes (for a review, see Hennig et al., 2005). We found that Arabidopsis MSI11, in addition to FAS1, also interacts with fertilization-independent endosperm (FIE), histone deacetylase, and the retinoblastoma-related RBR protein (Ach et al., 1997; Hennig et al., 2003; Köhler et al., 2003) (data not shown). Further studies will reveal which of these partners participate(s) in CAF-1 complex-independent functions of MS11 during plant development.

**CAF-1 is needed for normal cell cycle progression during endoreduplication**

The DNA content of CAF-1 mutant cells was increased in light- and dark-grown seedlings. In both cases, DNA endoreduplication occurs during normal development, but many mutant cells continued DNA endoreduplication for on average one extra round. This observation was surprising considering that RNAi knock-down of human p150 causes an accumulation of cells in S-phase (Hoek and Stillman, 2003). Because Arabidopsis CAF-1 mutants are viable, plant cells appear to be less dependent on CAF-1 function, thus revealing an additional role of CAF-1, i.e. to prevent excessive rounds of DNA endoreduplication. In yeast and humans, CAF-1 appears to be required for kinetochore formation (Sharp et al., 2002; Sharp et al., 2003). Interfering with kinetochore formation could potentially bypass mitosis and cause an increased DNA content. Alternatively, failure to exit the G2 phase of the cell cycle could cause an accumulation of cells with increased DNA content. Because the effects on DNA content were similar in the strong fas1-1 and fas2-4 alleles and in the weak fas1-4 and msi1-as alleles, even a partial loss of CAF-1 activity can considerably affect cellular DNA content. However, CAF-1 is not absolutely essential for normal cell cycle progression in Arabidopsis, as the fas2-1 allele in Ler had a largely unchanged DNA content. This suggests that the Ler accession contains genetic determinants that make CAF-1 largely dispensable for normal cell cycle progression. Because the developmental phenotypes of the two fas2 null alleles fas2-1 and fas2-4 were similar in Ler and Col, only the cell cycle function but not the developmental function of CAF-1 can be compensated in Ler. In addition, this suggests that the developmental defects of CAF-1 mutants are not a direct consequence of defective cell cycle progression.

**A role of CAF-1 in duplication of epigenetic information**

CAF-1 has nucleosome assembly activity and functions by depositing histone H3-H4 dimers onto newly synthesized DNA, as it is recruited to places of DNA synthesis by PCNA (for a review see, Loyola and Almouzni, 2004). As CAF-1 facilitates replication-coupled chromatin assembly, it may be needed to faithfully duplicate epigenetic information in chromatin during mitosis (Enomoto and Berman, 1998; Ridgway and Almouzni, 2000; van Nocker, 2003; Henikoff et al., 2004). Indeed, CAF-1 is needed for the maintenance of gene silencing in yeast, mammals and plants (Enomoto and Berman, 1998; Hennig et al., 2003; Tchenio et al., 2001; Takeda et al., 2004; Ono et al., 2006; Schönrock et al., 2006b). In Arabidopsis, CAF-1 contributes to the compaction of heterochromatin but is not essential for the silencing of most heterochromatic genes (Schönrock et al., 2006b). Nevertheless, several silent heterochromatic loci become stochastically activated in some cells in a fraction of fas2 plants (Ono et al., 2006). In addition, the euchromatic GLABRA2 gene has a cell-type-specific chromatin environment, which is lost in fas2 mutants (Costa and Shaw, 2006). Interestingly, plants containing greatly reduced MS11 levels suffer from a progressive loss of floral morphology, whereas none of the analyzed fas1 or fas2 mutant alleles showed a similar increase in phenotype severity (Hennig et al., 2003). In contrast to the morphological phenotype, the molecular phenotype of fas2 mutants increased with plant age as the expression of SCR::GFP was disturbed more in older than in younger roots (Kaya et al., 2001), and the percentage of plants with de-repressed CACTA transposons increased from 20% to 65% (Ono et al., 2006). Some of the pleiotropic phenotypes of CAF-1 mutants occur stochastically (Leyser and Furner, 1992; Kaya et al., 2001) and are most likely caused by stochastic defects in the expression of developmental regulators. Thus, CAF-1 might be needed for normal development because it facilitates the faithful duplication of epigenetic information in chromatin during mitosis.

**CAF-1 is required for the control of multiple developmental processes in plants**

In yeast, double mutants defective in CAF-1 and HIR or ASF1 cause defects in cell proliferation (Tyler et al., 1999; Sharp et al., 2001; Sharp et al., 2002), and CAF-1 mutants in higher eukaryotes, including Arabidopsis, most likely suffer from delayed cell division as well (Hoek and Stillman, 2003; Schönrock et al., 2006b). Several of the less stochastic phenotypes of Arabidopsis CAF-1 mutants, including changes in embryonic and post-embryonic organ size (e.g. hypocotyl, rosette), and reduced growth rates, could be caused by defects in cell proliferation. Because CAF-1 is needed for both efficient S-phase progression (Hoek and Stillman, 2003) and mitosis (Sharp et al., 2002; Sharp et al., 2003), absence of CAF-1 activity can interfere with steps in development that are based on a sensitive balance between cell cycle progression, cell division and differentiation. In meristems, this balance is particularly important, and mutant phenotypes arising from imbalances in meristems are therefore very obvious. Our results demonstrate, however, that the function of CAF-1 is not restricted to meristems, but is also required during many other differentiation and developmental processes. Most strikingly, even the differentiation of single-celled trichomes, which is independent of cell division, depends on CAF-1 activity.

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**Supplementary material**

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/133/21/4163/DC1

**References**


