Running title: CDKB1;1-CYCA2;3 suppresses endocycle onset

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CDKB1;1 forms a functional complex with CYCA2;3 to suppress endocycle onset."}

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Abstract

The mitosis-to-endocycle transition requires the controlled inactivation of M-phase-associated cyclin-dependent kinase (CDK) activity. Previously, the B-type CDKB1;1 has been identified as an important negative regulator of endocycle onset. Here, we demonstrate that CDKB1;1 co-purifies and associates with the A2-type cyclin CYCA2;3. Co-expression of CYCA2;3 with CDKB1;1 triggered ectopic cell divisions and inhibited endoreduplication. Moreover, the enhanced endoreduplication phenotype observed after overexpression of a dominant-negative allele of CDKB1;1 could be partially complemented by CYCA2;3 co-overexpression, illustrating that both subunits unite in vivo to form a functional complex. CYCA2;3 protein stability was found to be controlled by CCS52A1, an activator of the anaphase-promoting complex. We conclude that CCS52A1 participates in the endocycle onset by down-regulating CDKB1;1 activity through the destruction of CYCA2;3.
In all eukaryotes, oscillations in the phosphorylation status of key proteins control the cell cycle progression through the action of kinases and phosphatases. In particular, serine-threonine kinase activity of the various cyclin-dependent kinase (CDK) complexes is crucial in determining the cycling state of a cell (Fisher and Nurse, 1996; Inzé and De Veylder, 2006). In plants, as well as in mammals, various CDK proteins have been identified and grouped into different classes according to their sequences (Vandepoele et al., 2002). Plants possess a unique group of CDKs, of which the B1-type and B2-type CDKs display a maximum of kinase activity at the G2-to-M transition and during mitosis, respectively (Inzé and De Veylder, 2006). Recently, in Arabidopsis (Arabidopsis thaliana), the activity level of the CDKB1;1 was found to control whether cells will divide mitotically or will undergo repeated rounds of re-replication in absence of cytokinesis, a process known as endoreduplication. In cells competent for division, the presence of CDKB1;1 triggers cells to enter into mitosis. By contrast, in the absence of CDKB1;1 activity, cells endoreduplicate (Boudolf et al., 2004b). Hence, the control of CDKB1;1 activity plays a crucial role in determining the timing of the mitosis-to-endocycle transition. However, the mechanisms that control CDKB1;1 activity remain unclear.

One essential step in CDK activation involves the association of the kinase with a regulatory cyclin subunit. Cyclins of higher eukaryotes are generally divided into three groups: G1/S (D-type), S/M (A-type), and mitotic (B-type) cyclins. Plants hold multiple members of each cyclin class, but the CDK-binding partner and biological significance have been identified for only a few of them (Inzé and De Veylder, 2006). The abundance of A- and B-type cyclins is controlled by the combined transcriptional activation and proteolytic turnover through ubiquitination (Glotzer et al., 1991). Protein ubiquitination is a multistep process, requiring at least three different enzymes: the ubiquitin-activating enzyme (E1) that forms a high-energy bond with ubiquitin, which is subsequently transesterified to an ubiquitin-conjugating enzyme (E2), and, finally, the E3 enzyme that transfers the ubiquitin either directly to the substrate or indirectly by bringing the E2 enzyme near the substrate. E3 ubiquitin ligases determine the specificity of the target protein and timing of polyubiquitination. The anaphase-promoting complex/cyclosome (APC/C) is a highly conserved ubiquitin ligase (E3) formed by 11 subunits in vertebrates and plants (Peters, 2002; Capron et al., 2003) and 13 subunits in yeast (Yoon et al., 2002), although its minimal ubiquitin ligase module comprises only APC2 and APC11 (Gmachl et al., 2000; Tang et al., 2001). The two latter subunits interact with each other and with the E2 ubiquitin-conjugating enzymes and have been shown to be sufficient for ubiquitin transfer in vitro, without any substrate specificity (Gmachl et al., 2000; Tang et al., 2001). In vivo, substrates are selected through binding of the APC/C activator proteins: FZY/CDC20 from late G2 to late anaphase and FZR/CDH1/CCS52 from late mitosis to the G1-to-S transition (Harper et al., 2002). Proteins carrying characteristic degradation motifs, such as D box,
KEN, GXEN, A, C, O, and the recently identified TEK boxes, are recognized by these APC activators and brought to the core complex for ubiquitination (Burton and Solomon, 2001; Burton et al., 2005; Kraft et al., 2005).

Recently, the APC/C activator genes CDH1, FZR, and CCS52A have been found to promote the endocycle onset and progression in human, fruit fly (Drosophila melanogaster), and the plants, Medicago truncatula and Arabidopsis, respectively (Sigrist and Lehner, 1997; Cebolla et al., 1999; Schaeffer et al., 2004; Lasorella et al., 2006; Binné et al. 2007; Lammens et al., 2008; Narbonne-Reveau; 2008; Larson-Rabin et al., 2009). In fruit fly and mammals, the mitotic cyclins degraded by APC/C^{FZR,CDH1} at the endocycle onset have been identified. However, in plants, this identification turned out to be difficult because of the enormously expanded number of cyclins. In vitro binding assays yielded a subset of potential cyclin-CCS52 interactions (Fülöp et al, 2005), but, unfortunately without placing them in a developmental context.

Here, we report on the interaction of CDKB1;1 with A2-type cyclins. Biochemical and genetic studies revealed that CDKB1;1 and CYCA2;3 form a functional complex whose activity drives the mitotic cell cycle progression and prevents cells to enter the endocycle program. Moreover, we identified CYCA2;3 as an in vivo substrate of APC/C^{CCS52A1}, but not of APC/C^{CCS52A2}. We conclude that the controlled inactivation of CDKB1;1-CYCA2;3 by APC/C^{CCS52A1} directs the endoreduplication process in Arabidopsis.

RESULTS

CYCA2;3 interacts with CDKB1;1

Previously, we have demonstrated that CDKB1;1 activity, together with the E2Fa-DPa transcription factor, controls the balance between proliferation and endoreduplication (Boudolf et al., 2004b). However, the regulatory cyclin subunit that interacts with CDKB1;1 in this defined developmental context remained to be identified. To find interaction partners of the mitotic CDKB1;1 kinase, a yeast two-hybrid screen was used with an Arabidopsis cell suspension cDNA library fused to the GAL4 sequence-encoding activation domain. The screening was carried out with a dominant negative allele of the CDKB1;1 gene (CDKB1;1.N161), because initially no cyclin interactors had been identified with the wild-type gene as bait. This strategy turned out to be successful, probably thanks to stabilization of the kinase-cyclin complex, and resulted in the identification of CYCA2;2 and CYCA2;3 as potential CDKB1;1 interactors (data not shown). To confirm these interactions, we applied the tandem affinity purification (TAP) technique that has been proven to be a powerful tool to characterize protein complexes in plants (Van Leene et al., 2007). CYCA2;2, and CYCA2;3 were fused with the TAP-tag, expressed in Arabidopsis.
cell cultures and the resulting immunological complexes were purified (Van Leene et al., 2007). Mass spectrometry driven peptide sequencing allowed the identification of the CDKB1;1 protein as part of the CYCA2;3, but not of the CYCA2;2, complexes (Table I; data not shown). As only the interaction of CYCA2;3 with CDKB1;1 was observed in both the yeast two-hybrid and TAP analyses, we decided to focus on this interaction.

**CDKB1;1 and CYCA2;3 co-localize in the nucleus**

To ascertain the interaction of CYCA2;3 and CDKB1;1 in planta, bimolecular fluorescence complementation (BiFC) was utilized. The sequences coding for CYCA2;3 and CDKB1;1 were fused in frame with the N-terminal and C-terminal fragments of the enhanced green fluorescent protein (eGFP), namely CYCA2;3-nGFP and CDKB1;1-cGFP, and CDKB1;1-nGFP and CYCA2;3-cGFP, respectively. The interaction between the different fusion proteins was tested by transient expression in leaf epidermal cells of tobacco (*Nicotiana benthamiana*). No fluorescence was detected when any combination with empty vectors was introduced into tobacco cells (CYCA2;3-nGFP and cGFP, nGFP and CDKB1;1-cGFP, CDKB1;1-nGFP and cGFP, and nGFP and CYCA2;3-cGFP) (data not show). By contrast, eGFP fluorescence was observed in the nuclei of cells transfected with CYCA2;3-nGFP and CDKB1;1-cGFP (Fig. 1A), or with CDKB1;1-nGFP and CYCA2;3-cGFP (data not shown) demonstrating that the CYCA2;3 protein interacted with CDKB1;1 in the plant nucleus. Fluorescence was most intense at localized foci, probably corresponding to the chromocenters. When the subcellular localization of CYCA2;3 and CDKB1;1 was examined in tobacco leaf epidermal cells, the fusion protein CDKB1;1-eGFP resided in both the nucleus and the cytoplasm, whereas the fusion protein CYCA2;3-eGFP was found exclusively in the nucleus (Fig. 1A).

Subsequently, we also tested whether the CDKB1;1-CYCA2;3 complex was formed in Arabidopsis plants. For this purpose, we supertransformed Arabidopsis plants carrying the CDKB1;1-cGFP gene construct with a T-DNA harboring the CYCA2;3-nGFP gene. Fifteen out of 20 double transformed lines showed detectable fluorescence and four of the most intense ones were selected for further analysis. The fluorescent signal of the complex was detected in the nucleus in roots and hypocotyls (Fig. 1B; data not shown).

**Co-overexpression of CDKB1;1 and CYCA2;3 induces ectopic cell divisions**

Interestingly, both the overexpression of *CDKB1;1.N161* and the knockout of CYCA2;3 result in an increased DNA ploidy level (Boudolf et al., 2004b; Imai et al., 2006), suggesting that they might operate together to suppress the endocycle onset. To test this hypothesis, we analyzed phenotypically the plants co-expressing the CDKB1;1-cGFP and
Microscopic analysis of the cotyledons revealed much smaller cells with newly formed cell walls in the plants co-expressing the
\textit{CDKB1;1-cGFP} and \textit{CYCA2;3-nGFP} constructs when compared to the wild-type (Columbia-0 [Col-0]) plants, indicating an important induction of ectopic cell divisions (Fig. 2, A and B). Furthermore, as seen by flow cytometry of the cotyledons, the pool of endoreduplicating cells had decreased, resulting in a 85% reduced endoreduplication index (EI), which is the mean number of endoreduplication cycles per nucleus (Fig. 2, C and D). Similar results were obtained for leaves and roots (Supplementary Figure S1).

To investigate whether the ectopic cell division and reduced endoreduplication phenotype was due to a specific action of the CDKB1;1-CYCA2;3 complex, plant overexpressing either \textit{CDKB1;1}, \textit{CDKB1;1.N161}, or \textit{CDKA;1} were crossed with lines harboring a \(\beta\)-estradiol-inducible construct overexpressing \textit{CYCA2;3-GFP} (Imai et al., 2006) and the F\(_1\) generation was characterized phenotypically. Cotyledons of seedlings grown for 7 days on agar medium with and without 10 \(\mu\)M \(\beta\)-estradiol were subjected to flow cytometry to analyze the DNA ploidy content (Fig. 3; Table II). Induction of \textit{CYCA2;3-GFP} expression in a wild-type or \textit{CDKA;1}-overexpressing background resulted in a similar, slightly reduced EI, representing the mean number of endoreduplication cycles per nucleus. By contrast, when \textit{CYCA2;3-GFP} expression was induced in a \textit{CDKB1;1}-overexpressing background, an important increase in the proportion of 2C cells (p<0.05 for proportion of 2C cells in \textit{CYCA2;3-GFP x CDKB1;1} versus in \textit{CYCA2;3-GFP}) and reduction of the EI were observed.

Overexpression of solely the wild-type \textit{CDKA;1} or \textit{CDKB1;1} genes does not affect the cell cycle (Hemerly et al, 1995; Boudolf et al., 2004a). Analogously induced \textit{CYCA2;3-GFP} expression in a wild type or \textit{CDKA;1} overexpressing background did not affect profoundly the cell division (Fig. 4). By contrast, microscopic analysis of mature cotyledons clearly showed the induction of ectopic cell divisions in plants co-expressing \textit{CDKB1;1} and \textit{CYCA2;3-GFP}, as illustrated by the occurrence of smaller cells and newly formed cell walls with a straight appearance (Fig. 4). Moreover, CYCA2;3-associated kinase activity was higher in plants co-expressing \textit{CDKB1;1} and \textit{CYCA2;3-GFP} than in plants expressing \textit{CYCA2;3-GFP} or co-expressing \textit{CYCA2;3-GFP} and \textit{CDKA;1} (Fig. 5). Taken together, these results imply that CDKB1;1 and CYCA2;3 might form a functional complex in planta.

Overexpression of the dominant negative \textit{CDKB1;1.N161} allele competes with its endogenous wild-type counterpart for regulatory proteins, resulting in a decrease in endogenous CDKB1;1 activity, increased DNA ploidy levels, and formation of aberrant stomata (Boudolf et al., 2004a, 2004b). Induction of \textit{CYCA2;3-GFP} in a \textit{CDKB1;1.N161}-overexpressing background partially complemented the endoreduplication phenotype (p<0.05, EI for \textit{CYCA2;3-GFP}_{induced} \times \textit{CDKB1;1.N161} versus EI for \textit{CYCA2;3-GFP}_{not-induced}
× CDKB1;1.N161) (Fig. 3; Table II), mainly as a consequence of the suppression of the 16C population, but could not restore the aberrant stomatal phenotype (Fig. 4).

**APC/C^CCS52A1, but not APC/C^CCS52A2, determines CYCA2;3 stability in vivo**

One of the most defined characteristics of cyclins is their periodicity and concomitant instability. The CYCA2;3 protein contains a D box, which was demonstrated to determine the protein’s half-life (Capron et al., 2003; Imai et al., 2006). D box motifs have been shown to mediate interaction with the APC/C activators CDC20/FIZZY and CDH1/FZR/CCS52, that bring the substrate to the APC/C (Burton and Solomon, 2001; Burton et al., 2005; Kraft et al., 2005). The recent identification of CCS52A1 and CCS52A2 as essential regulators of the endoreduplication program in Arabidopsis (Lammens et al., 2008; Larson-Rabin et al., 2009) and the observed decrease in ploidy in CYCA2;3-GFP plants led us to investigate whether CYCA2;3 and each of these activators might interact. Plants, with a homozygous mutation for CCS52A1 (ccs52a1-1) or CCS52A2 (ccs52a2-1) (Lammens et al., 2008), were crossed with plants harboring a β-estradiol-inducible CYCA3;2-GFP construct or a similar construct with a non-functional D-box sequence, designated mDB-CYCA2;3-GFP (Imai et al., 2006). The intensity of the nucleus-localized GFP signal was stronger than that of the control (CYCA2;3-GFP) when CYCA2;3-GFP was induced in a ccs52a1-1 background (ccs52a1-1 x CYCA2;3-GFP) (Fig. 6), indicative for an increase in CYCA2;3 stability upon loss of CCS52A1. The fluorescence intensity resembled that of plants expressing mDB-CYCA2;3-GFP, in both Col-0 and ccs52a1-1 background (Fig. 6). Remarkably, no change in CYCA2;3 stability could be observed in roots when CYCA2;3-GFP expression was induced in a ccs52a2-1 background (Fig. 6), suggesting that CYCA2;3 degradation in roots is specifically achieved by CCS52A1-, and not by CCS52A2-activated APC/C. CYCA2;3 stabilization in CCS52A1 was most clear in the columella cells and around the transition zone, marking the transition of mitotic division to endoreduplication (Fig. 7). No difference in GFP fluorescence could be observed at the meristematic zone (Fig. 7).

Next, it was tested whether the observed stabilization of CYCA2;3 in the ccs52a1-1 genotype had any effect on the endoreduplication levels. Although the induction of CYCA2;3-GFP reduces the endoreduplication levels both in roots and cotyledons (Imai et al., 2006), under our experimental conditions, this effect was more pronounced in cotyledons (Fig. 8). When induced in a ccs52a1-1 background, the stabilization of CYCA2;3-GFP further decreased the endoreduplication levels (Fig. 8A; Table III) (p<0.005, EI CYCA2;3-GFP_{induced} × ccs52a1-1 versus EI CYCA2;3-GFP_{induced}). The important increase in the proportion of 2C cells in 7-day-old cotyledons of the induced CYCA2;3-GFP plants suggested a CYCA2;3-dependent induction of ectopic cell divisions.
Indeed, microscopic analysis of cotyledons grown for 14 days after germination (DAG) on β-estradiol indicated ectopic cell divisions, as illustrated by the presence of smaller less differentiated cells (Fig. 9). In agreement with the decrease in endoreduplication, this ectopic cell division phenotype was enhanced upon induction of CYCA2;3 in the ccs52a1-1 background (Fig. 9).

**DISCUSSION**

**CDKB1;1 and CYCA2;3 control the mitotic-to-endocycle transition**

The regulated synthesis and destruction of cyclins provides waves of CDK activity, governing two crucial transitions within the cell cycle program, the entry into S-phase from G1 and into M-phase from G2. Because no M-phase is seen within the endoreduplication program, entrance into and maintenance of the endoreduplication cycle are thought to require the elimination of M-phase-associated kinase activity, which has been identified as the plant-specific mitotic CDKB1;1 (Boudolf et al., 2004b). Plants overproducing a dominant negative form of this CDK have increased endoreduplication levels and aberrant stomatal morphology (Boudolf et al., 2004a, 2004b). Although cyclins affecting endoreduplication levels in plants have been identified (Schnittger et al., 2002; Imai et al., 2006), no consensus exists on which cyclin(s) interact(s) with CDKB1;1, and constitute(s) an integral part of the M-phase CDK activity, which inhibits endoreduplication. By combining yeast two-hybrid, TAP purification, and BIFC, we showed that CYCA2;3 interacts with CDKB1;1. The enhanced endoreduplication phenotype induced by overexpression of CDKB1;1.N161 could be partially complemented by overexpression of CYCA2;3, demonstrating that CYCA2;3 and CDKB1;1 form a functional complex, whose activity inhibits endoreduplication. By combining yeast two-hybrid, TAP purification, and BIFC, we showed that CYCA2;3 interacts with CDKB1;1. The enhanced endoreduplication phenotype induced by overexpression of CDKB1;1.N161 could be partially complemented by overexpression of CYCA2;3, demonstrating that CYCA2;3 and CDKB1;1 form a functional complex, whose activity inhibits the endoreduplication program. Interestingly, the stomatal phenotypic trait of the CDKB1;1.N161-overexpressing plants could not be complemented by induced expression of CYCA2;3, indicating that during stomatal development other cyclins than CYCA2;3 might form active complexes with CDKB1;1. Alternatively, the levels of CYCA2;3 induction obtained in these experiments might be sufficient to trigger pavement cell divisions, but insufficient to compete with the dominant negative CDKB1;1 to drive stomatal divisions. This hypothesis would imply that the required dose of CDKB1;1 activity would be higher for a stomatal lineage than that for a normal proliferative division. Similarly, in fruit fly, levels of CDK activity necessary for asymmetric divisions of neuroblast cells are higher than those for symmetric divisions (Chia et al., 2008).

Notably, the coexpression of CYCA2;3 and wild-type CDKB1;1 triggered more ectopic cell divisions than observed after overexpression of CYCA2;3 alone. As no effect on cell division is seen in CDKB1;1-overexpressing plants, these observations indicate that
CYCA2;3 is the rate-limiting factor in determining the level of CDKB1;1-CYCA2;3 activity. By contrast, no ectopic divisions were seen upon the coexpression of CYCA2;3 and CDKA;1, although both proteins have been reported to form a complex (Imai et al., 2006). These data suggest that the CDKA;1-CYCA2;3 complex is inactive or, alternatively, that CDKA;1 and CDKB1;1 are controlled differently at the posttranscriptional level. A-type CDK activity is regulated negatively by inhibitory phosphorylation (Da Costa et al., 2006; Harashima et al., 2007) and association with inhibitory proteins, such as Kip-related proteins (KRP)s (Schnittger et al., 2003; Verkest et al., 2005) and SIAMESE (Churchmann et al., 2006). By contrast, no such regulatory mechanisms have been demonstrated convincingly for CDKB1;1, indicating that cyclin binding might be the only requirement to activate it, whereas additional steps might be needed for CDKA;1 activation.

Generally, CDKs fulfill three major roles during mitotic cell cycle progression: entry into S phase, promotion of mitosis, and prevention of DNA re-replication (Porter, 2008). In fission yeast (Schizosaccharomyces pombe), the mitotic CDK complex hinders relicensing of replicated DNA by its association with the replication complex during chromosome duplication and prevents re-initiation of DNA synthesis (Wuarin et al., 2002). Similarly, CDKB1;1 might negatively regulate pre-replication complex (pre-RC) assembly and, thereby, repress the endocycle. Because CDKB1;1 activity peaks at the G2-to-M transition, it presumably plays a role only during this transition point. However, CDKB1;1 transcription is regulated through E2Fa and E2Fb transcription factors (Boudolf et al., 2004b; Magyar et al., 2005; Sozanni et al., 2006). Accordingly, CDKB1;1 transcript levels increase from the G1-to-S transition onward, followed by an increase in CDKB1;1 activity during S phase (Porceddu et al., 2001; Sorrell et al., 2001; Breyne et al., 2002; Menges et al., 2002). These data indicate that CDKB1;1 might already be functional before its observed expression peak at the G2-to-M transition. In yeast that has only one single CDK to control the cell cycle, a quantitative model describes three levels of CDK activity: low that allows licensing of DNA replication; intermediate that initiates DNA replication, but prevents relicensing; and high that enables mitosis (Stern and Nurse, 1996; Porter, 2008). Although cell cycle regulation is more complex in higher eukaryotes, a quantitative model for CDK action is still partially applicable (Porter, 2008; Krasinska et al., 2008). From this point of view, an intermediate CDKB activity during the S phase could be a working mechanism that represses relicensing.

In synchronized cell cultures the expression of CYCA2;3 is restricted to the G2-to-M transition (Menges et al., 2005), which could argue against a possible function during S phase. However, the promoter of CYCA2;3 is not only active in proliferating tissue, but also in differentiated cells, such as stomatal guard cells and endoreduplicating cells, such as trichomes (Imai et al., 2006), suggesting a broader expression profile. In endoreduplicating cells, the CDKA;1-CYCA2;3 complex might negatively regulate the endocycle succession
through downregulation of pre-RC function (Imai et al., 2006). In vitro interaction of CYCA2;2 and chromatin licensing and DNA replication factor 1 (CDT1) supports this working mechanism (Castellano et al., 2004). Moreover, E2F transcription factors have been found to interact with A2-type cyclins (J.B., L.D.V, and E.R., unpublished results), another indication that A2-type cyclins might play a role during the S phase itself. In mammals, E2F activity is regulated by CDK2-cyclinA phosphorylation (Krek et al., 1994; Xu et al., 1994; Kitagawa et al., 1995; Hayashi and Yamaguchi, 1999; Morris et al., 2000). Inactivation of E2Fs by CDK2 phosphorylation promotes the mitotic cell cycle by driving cells into the G2 phase. We have shown that E2Fa-DPa regulates both the mitotic and endoreduplicating cycles in Arabidopsis (De Veylder et al., 2002) and that the decision to divide mitotically or to undergo endoreduplication depends on the presence of CDKB1;1 (Boudolf et al., 2004). Thus, CDKB1;1-CYCA2;3 might regulate the E2F-DP transcription factor in mitotically dividing cells, which might explain why CDKB1;1-CYCA2;3 overexpression triggers ectopic cell divisions.

Another possible working mechanism of the CDKB1;1-CYCA2;3 complex might be that it is directly responsible for the activation of CDKA;1 activity. A model in which CDKB1;1 controls the levels of CDKA;1 activity by phosphorylation has been proposed (Verkest et al., 2005) and, as a consequence, proteasomal degradation of the CDKA;1 inhibitor ICK2/KRP2. The overexpression of the CDKB1;1-CYCA2;3 complex might inhibit the action of ICK2/KRP2 and allow the cells to enter mitosis.

**CDKB1;1-CYCA2;3 abundance is controlled by APC/C**

The CYCA2;3 protein contains a clear D box, which has been demonstrated to be essential to the protein's half-life (Capron et al., 2003; Imai et al., 2006). D-box motifs occur in many proteins targeted for destruction by the APC/C and are thought to mediate target binding by APC/C activator proteins, such as CDC20/FZY and CDH1/FZR/CCS52 (Burton and Solomon, 2001; Burton et al., 2005; Kraft et al., 2005). The stabilization of CYCA2;3-GFP in CCS52A1 loss-of-function plants clearly indicates that CYCA2;3 is a CCS52A1 substrate. Moreover, the same stabilization could be observed upon mutation of the D box of CYCA2;3, indicating that CCS52A1-mediated destruction of CYCA2;3 happens in a D-box-dependent manner. Both CYCA2;3 and CCS52A1 have been linked before to the control of the endoreduplication program (Imai et al., 2006; Lammens et al., 2008; Larson-Rabin et al., 2009). Thus, our observations suggest that CYCA2;3 stabilization, at least partially, contributes to the decreased endoreduplication levels observed upon loss of CCS52A1. Interestingly, CYCA2;3-GFP was not stabilized in the roots of CCS52A2 knockout plants, although both CSS52A1 and CSS52A2 regulate the DNA ploidy level of leaf cells (Lammens et al., 2008).
The control of the APC/C activity plays an important role in the correct progression through the cell cycle (Acquaviva and Pines, 2006; Peters, 2006). In mammals, the APC/C complex inhibits CDK activity during late M and G1 phase, allowing licensing. During the remainder of the cell cycle, the APC/C must be inactivated for mitotic cyclins to accumulate. Inactivation of APC/C is achieved in part by the CDK-dependent phosphorylation of the APC/C activator CDH1 (the mammalian counterpart of CCS52A). The CDK-dependent inhibition of CDH1 seems to be conserved in plants, because mutations mimicking phosphorylation of the CDK phosphorylation sites in the Medicago CCS52A inhibits the interaction with the APC/C (Tarayre et al., 2004). Both in animals and plants, the APC/C activator genes CDH1, FZR, and CCS52A have been found to promote endocycle onset (Sigrist and Lehner, 1997; Cebolla et al., 1999; Schaeffer et al., 2004; Lasorella et al., 2006; Binné et al., 2007; Lammens et al., 2008; Narbonne-Reveau et al., 2008; Larson-Rabin et al., 2009). In plants, no data are available on the timing of APC/C activation by CCS52A, but the expression of CCS52A1 and CCS52A2 is known to be transcriptionally regulated with expression levels peaking between late M and early G2 (Fülöp et al., 2005). Previously, we have found CCS52A2, but not CCS52A1, transcription, is regulated by the E2Fe/DEL1 transcription factor (Lammens et al., 2008), indicating that both CCS52A genes are under a different genetic control. Moreover, in roots, CCS52A1 rather than CCS52A2, has been found to control endocycle onset (M. Vanstraelen and E.K., unpublished observations). Furthermore, stabilization of CYCA2;3-GFP within a ccs52a1-1 context is most evident in the transition zone, a region with high CCS52A1 expression (M. Vanstraelen and E.K., unpublished observations), and probably marks the site of endoreduplication onset in Arabidopsis roots. All together, these data indicate that CCS52A1 and CCS52A2 might operate in a tissue-specific manner, rather than being redundant. Unfortunately, the low levels of CYCA2;3-GFP did not allow us to test the effects of CCS52A1 and CCS52A2 knockout on CYCA2;3-GFP expression in leaves.

In conclusion, CDKB1;1 complexed with CYCA2;3 prevents cells from exiting the mitotic cell cycle, probably by repressing relicensing of DNA replication during S-to-G2 and boosting CDK activity at the G2-to-M transition. Further, we demonstrated that CDKB1;1-CYCA2;3 complex activity is mainly determined by the availability of the CYCA2;3 protein, whose abundance is controlled by APC/C<sub>CCS52A1</sub>.

**MATERIALS AND METHODS**

**Plant material and culture conditions**

*Arabidopsis thaliana* (L.) Heyhn plants (ecotype Col-0) were grown at 22°C and a 16-h photoperiod (65 μE m<sup>-2</sup> s<sup>-1</sup>) on half-strength Murashige and Skoog medium containing...
0.5 g L\(^{-1}\) MES, 10 g L\(^{-1}\) sucrose, and 0.8% plant tissue culture agar, unless noted otherwise. The \(CDKB1;1\) and \(CDKB1;1.N161\) lines (Boudolf et al., 2004a), \(ccs52a1-1\) and \(ccs52a2-1\) (Lammens et al., 2008), and \(CYCA2;3-GFP\) and \(mdb-CYCA2;3-GFP\) lines (Imai et al., 2006) have been described elsewhere.

**Yeast two-hybrid**

For a yeast two-hybrid screening, a fusion between the GAL4 DNA-binding domain and \(CDKB1;1.N161\) was used as bait. The cDNA for \(CDKB1;1.N161\) was obtained by mutation of the codon GAT (Asp161) for AAT (Asn161) by in vitro mutagenesis (Porceddu et al., 1999). Vectors and strains used were provided with the Matchmaker Two-Hybrid System (Clontech, Palo Alto, CA). The baits were constructed by inserting the \(CDKB1;1.N161\) PCR fragment into the pGBT9 vector. The \(CDKB1;1.N161\) PCR fragment was created from the cDNA using primers to incorporate EcoRI restriction enzyme sites (5'-CGGATCCGAATTCATGGAGAACGAG-3' and 5'-CGGATCCGAATTCTCAGAACTGAGA-3'). The \(CDKB1;1.N161\) PCR fragment was cut with EcoRI and cloned into the EcoRI site of pGBT9, resulting in the plasmid pGBTCDKBDN. The GAL4 activation domain cDNA fusion library was obtained from Clontech from mRNA of Arabidopsis cell suspensions harvested at various growing stages: early exponential, exponential, early stationary, and stationary phases (De Veylder et al., 1999). For the screening, a 500-mL culture of the \(Saccharomyces cerevisiae\) strain HF7c (\(MATa\  ura3-52\  his3-200\  ade2-101\  lys2-801\  trp1-901\  leu2-3,112\  gal4-542\  gal80-538\  LYS2::GAL1\ UAS\-\ GAL1\ TATA\-\ HIS3\  URA3::GAL4\ 17mers(3x)\-\ CyC1\ TATA\-\ LacZ) was cotransformed with 250 μg pGBTCDKBDN, 500 μg DNA of the library, and 20 μg herring testes carrier DNA according to the lithium acetate method (Gietz et al., 1992). To estimate the number of independent cotransformants, 1/1000 of the transformation mix was plated on Leu and Trp medium. The rest of the transformation mix was plated on medium to select for histidine prototrophy (Trp, Leu, and His). After 4 days of growth at 30°C, the colonies larger than 2 mm were streaked on histidine-lacking medium. Of the His\(^+\) colonies, the activation domain of the plasmids was isolated as described (Hoffman and Winston, 1987). The pGAD10 inserts were amplified by PCR using the primers 5'-ATACCACTACAATGGATG-3' and 5'-AGTTGAAGTGAACTTGCGGG-3'. Plasmid DNA was electroporated into \(Escherichia coli\) XL1-Blue and the DNA sequence of the inserts was determined. Extracted DNA was also used to retransform HF7c to test the specificity of the interaction.

**Tandem affinity purification and analysis**
Essentially, all steps were as described (Van Leene et al., 2007), including the Arabidopsis cell suspension cultivation, transformation and selection, protein extraction, and subsequent TAP. In short, the sequences coding for CYCA2;2 and CYCA2;3 were cloned by recombination into the pKNTAP vector, generating a Pro35S:TAP-CYCA2;2 and Pro35S:TAP-CYCA2;3 cassettes (pKNTAPCYCA2;2 and pKNTAPCYCA2;3). Arabidopsis cell suspension cultures were stably transformed by Agrobacterium-mediated cocultivation with pKNTAPCYCA2;2 and pKNTAPCYCA2;3. Transformed Arabidopsis cells were selected and transferred to a liquid medium for upscaling. Expression levels of TAP-tagged proteins were checked by protein blotting with an anti-calmodulin-binding protein antibody (data not shown). In the first round of affinity purification, protein extracts of 15 g plant material were incubated with an IgG resin. Bound complexes were released and eluted from the resin by tag cleavage with tobacco etch virus (TEV) protease. In the second affinity step on a calmodulin agarose column, co-eluting non-interacting proteins and the TEV protease were removed with the flow-through. Finally, both the CYCA2;2 and CYCA2;3 baits and interacting proteins were eluted from the calmodulin agarose through EGTA-mediated calcium removal. Eluted proteins were separated on 4–12% NuPAGE gels, excised, and analyzed by MALDI-TOF-TOF-MS as described (Van Leene et al., 2007). To increase the stringency of the data set, contaminating proteins due to experimental background as determined by Van Leene et al. (2007), were systematically subtracted from the lists of co-purified proteins.

**BiFC constructs cloning**

The BiFC constructs were obtained through recombinational Gateway cloning (Invitrogen). The GFP moieties were created by a PCR for N- and C-terminal parts of the fluorescent molecule. DNA sequences were generated that encoded an N-terminal part of the enhanced GFP, designated nGFP (base pairs 1-465, amino acids 1–155) and a C-terminal part, cGFP (base pairs 466-717, amino acids 156–239). No linker sequence was included. All full-length open reading frames (ORFs) of the cell cycle proteins of interest were recombined into the pDONR221 entry vector (Invitrogen) by a BP reaction. A multisite Gateway reaction resulted in translational fusions between the cell cycle ORFs and the moieties of GFP driven by the 35S promoter. The expression clones were generated in the pH7m34GW and pK7m34GW destination vectors (for the ORF::cGFP and ORF::nGFP fusions, respectively).

**Tobacco infiltration**

Wild-type tobacco (*Nicotiana benthamiana* L.) plants were grown under a normal
light regime (14 h of light, 10 h of darkness) at 25 °C and 70% relative humidity. All BiFC constructs were transferred into the *Agrobacterium tumefaciens* LBA4404 strain harboring the VirG plasmid. The obtained *Agrobacterium* strains were used to infiltrate tobacco leaves. The transient expression assay on tobacco leaves was done according to Batoko et al. (2000) with minor modifications. The transformed agrobacteria harboring the constructs of interest were grown for 2 days in a shaking incubator (200 rpm) at 28 °C in 5 mL of yeast extract broth medium supplemented with appropriate antibiotics (100 μg/ml spectinomycin and 40 μg/ml gentamycin). After incubation, 2 mL of well-grown bacterial culture was transferred to Eppendorf tubes and centrifuged (10 min, 5200g). The pellets were washed twice with 1 mL of infiltration buffer (50 mM MES, 2 mM Na$_3$PO$_4$, and 0.5% glucose, pH 5.6). The final pellet was resuspended in the infiltration buffer supplemented with 100 μM acetosyringone. The bacterial suspension was diluted with the same supplemented buffer to adjust the inoculum concentration to the final OD$_{600}$ value (dilution series from 0.5 to 0.1). For co-expression experiments, 500 mL of each bacterial culture was mixed prior to the leaf infiltration, with the inoculum of each construct adjusted to the required final OD$_{600}$. The inoculum was delivered to tobacco leaves by gentle pressure infiltration of the lower epidermis with a 1mL syringe without needle. The infiltrated area of the leaf was delimited and labeled with an indelible pen. The plant was incubated under normal growing conditions and results were analyzed 3-5 days after infiltration.

**Confocal microscopy**

Transgenic Arabidopsis plants and transfected tobacco leaves were assayed for fluorescence with a confocal microscope 100M with software package LSM 510 version 3.2 (Zeiss, Jena, Germany) and a confocal microscope (Olympus FluoView FV1000) equipped with a 63x water-corrected objective (numerical aperture of 1.2) to scan the cells. Emission fluorescence was captured in the frame-scanning mode alternating GFP fluorescence via a 500-550-nm band pass emission filter.

**Flow cytometry**

Flow cytometry was done according to Boudolf et al. (2004b). The endoreduplication index (EI) was calculated from the number of nuclei of each represented ploidy level multiplied by the number of endoreduplication cycles necessary to reach the corresponding ploidy level.

**Light microscopy**
Cotyledons were harvested, cleared overnight in ethanol, and stored in lactic acid for further use. Cotyledons were mounted on slides, covered, and observed under a microscope fitted with differential interference contrast (DIC) optics (DMLB; Leica, Wetzlar, Germany). Digital images were handled with Adobe Photoshop 6.

**Propidium iodide staining**

The vital dye propidium iodine (PI) was used to stain cell walls. Plant material was incubated for 2 min in a working solution of 10 μM PI in water. Accumulation of PI was observed under epifluorescence light with the appropriate filter set (excitation filter, 535 to 550 nm; dichroic mirror, 565 nm; barrier filter, 590 nm).

**Kinase assay**

Agarose-conjugated anti-GFP monoclonal antibody (MBL) was washed three times with 500 μl cold lysis buffer containing 50 mM Tris-HCl (pH 7.2), 250 mM NaCl, 0.1% NP-40, 2 mM EDTA, 10% glycerol and 1 tablet 10 ml⁻¹ protease inhibitor cocktail (Roche). Protein extracts were prepared from 7-day-old seedlings, induced for 2 days on agar medium containing 10 μM β-estradiol, of Arabidopsis Col-0, and from F1 crosses between lines harboring a β-estradiol-inducible construct overexpressing CYCA2;3-GFP and Col-0 (Col-0×CYCA2;3), and plants overexpressing either CDKA;1 or CDKB1;1 (CDKA;1×CYCA2;3 and CDKB1;1×CYCA2;3). In a total volume of 200 μl of homogenization buffer (HB) containing 25 mM Tris-HCl (pH 7.6), 60 mM β-glycerolphosphate, 15 mM nitrophenyl phosphate, 15 mM EGTA (pH 8), 15 mM MgCl₂, 85 mM NaCl, 1 mM dithiothreitol, 0.1 mM vanadate, 1 mM NaF, 0.1 mM benzamidine, 1 mM phenylmethylsulfonylfluoride, 0.1% NP-40, and 1 tablet 10 ml⁻¹ protease inhibitor cocktail (Roche), 530 μg of protein extract was loaded on 30 μl of 50% gel slurry of agarose-conjugated anti-GFP MBL and incubated on a rotating wheel for 2 h at 4°C. After a brief centrifugation at 2500g and removal of the supernatant, the beads were carefully washed three times with cold lysis buffer and once with kinase buffer (50 mM Tris-HCl [pH 7.8], 15 MgCl₂, 5 mM EGTA, and 2 mM dithiothreitol). The supernatant was removed carefully. The histone H1 kinase reactions were initiated by resuspending the pellets anti-GFP agarose with 35 μl of the reaction mixture containing 5 μCi [γ-³²P]ATP (3000 Ci mmol⁻¹), 0.5 mg ml⁻¹ histone H1, 50 mM Tris-HCl (pH 7.8), 15 mM MgCl₂, 5 mM EGTA, 1 mM dithiothreitol, 60 μg/mL cAMP-dependent kinase inibitor, and 10 μM ATP. After 20 min incubation at 30°C, the kinase reactions were stopped by the addition of 10× SDS/PAGE loading buffer. Aliquots were boiled, loaded on a 12% (w/v) acrylamide gel, and stained by Coomassie Blue. The gel was dried overnight and
incorporation of [γ-33P] ATP into histone H1 was detected by autoradiography. The background signal measured in the Col-0 sample was subtracted from the signals obtained with the other samples.

Supplemental Data

The following materials are available in the online version of this article.

Supplemental Figure S1. Effect of co-expression of CYCA2;3-nGFP and CDKB1;1-cGFP.

ACKNOWLEDGMENTS

The authors thank their colleagues of the cell cycle group for fruitful discussions, Dr. Takashi Aoyama for providing the inducible CYCA2;3-GFP expressing lines, and Martine De Cock for help in preparing the manuscript.
Figure legends

**Figure 1.** In vivo interaction between CDKB1;1 and CYCA2;3. A, Subcellular localization of CDKB1;1, CYCA2;3 and the CYCA2;3-CDKB1;1 complex. Tobacco epidermal cells were transfected with constructs encoding the indicated fusion proteins. B, Confocal images of a root of an Arabidopsis plant co-expressing CDKB1;1-cGFP and CYCA2;3-nGFP.

**Figure 2.** Effect of co-expression of CYCA2;3-nGFP and CDKB1;1-cGFP. Col-0 seedlings (A and C) and plants co-expressing CYCA2;3-nGFP and CDKB1;1-cGFP (B and D) were grown for 12 DAG on agar medium and cotyledons were harvested. The cotyledons were stained with PI and observed under a confocal laser-scanning microscope (A and B) or subjected to flow cytometry (C and D).

**Figure 3.** Effect of CYCA2;3-GFP induction on the endoreduplication index (EI) in transgenic plants ectopically expressing CDKA;1, CDKB1;1, or CDKB1;1.N161. Cotyledons were harvested at 7 DAG. Seedlings were grown on agar medium without (-inducer) or with (+ inducer) 10 μM β-estradiol and subjected to flow cytometry. Col-0 was used as control. Values are means ± s.d. (n=3). Each biological repeat was carried out with seedlings obtained from independent F1 crosses.

**Figure 4.** Phenotype of cotyledon epidermal cells in Col-0×CYCA2;3-GFP plants (control) and plants co-expressing CYCA2;3-GFP and CDKA;1 (CDKA;1×CYCA2;3-GFP), CDKB1;1 (CDKB1;1×CYCA2;3-GFP) or CDKB1;1.N161 (CDKB1;1.N161×CYCA2;3-GFP). Seedlings were grown for 14 DAG on agar medium containing 10 μM β-estradiol. At 7 DAG, seedlings were transferred to fresh 10 μM β-estradiol-containing medium in order to sustain the induction of CYCA2;3-GFP. Left, images obtained with DIC microscopy; right, drawings of the outlines of the epidermal cells obtained by tracing the microscopy images with Adobe Photoshop 6. Arrow highlights aberrant stomatal morphology.

**Figure 5.** High kinase activity in CDKB1;1×CYCA2;3-GFP plants. Kinase activity assays of purified CYCA2;3-GFP complexes in Col-0×CYCA2;3-GFP, CDKA;1×CYCA2;3-GFP and CDKB1;1×CYCA2;3-GFP plants (F1 generation of approximately five independent crosses). Relative CYCA2;3-GFP-associated CDK activity was measured with histone H1 as substrate. For quantification, the control was arbitrary set at 100%.

**Figure 6.** Stabilization of CYCA2;3 in the absence of CCS52A1. Fluorescence in inducer-treated roots expressing CYCA2;3-GFP or mDB-CYCA2;3-GFP in Col-0 or ccs52a1-1
(CYCA2;3-GFP × ccs52a1-1 and mDB-CYCA2;3-GFP × ccs52a1-1) background and CYCA2;3-GFP in ccs52a2-1 (CYCA2;3-GFP × ccs52a2-1) background. Seedlings were grown for 5 days on agar without β-estradiol and for 2 days on agar medium with 10 μM β-estradiol. Cell walls were stained with PI. The fluorescence from the GFP fusion proteins was observed using confocal laser-scanning microscopy.

**Figure 7.** CYCA2;3 stabilization in ccs52a1-1 roots. Fluorescence in inducer-treated roots expressing CYCA2;3-GFP or in Col-0 or ccs52a1-1 (CYCA2;3-GFP × ccs52a1-1) background. Seedlings were grown for 5 days on agar medium without β-estradiol and for 2 days on agar medium containing 10 μM β-estradiol. Cell walls were stained with PI. The fluorescence from the GFP fusion proteins was observed with confocal laser-scanning microscopy.

**Figure 8.** Effect on endoreduplication of CYCA2;3-GFP stabilization in ccs52a1-1. Cotyledons (A) and roots (B) from seedlings harvested at 7 DAG. Seedlings were grown on agar medium without (- inducer) or with (+ inducer) 10 μM β-estradiol; the respective tissues were subjected to flow cytometry. Values are means ± s.d. (n=3).

**Figure 9.** Phenotype of cotyledon adaxial epidermal cells in Col-0 (control), CYCA2;3-GFP, ccs52a1-1, and CYCA2;3-GFP × ccs52a1-1 plants. Seedlings were grown for 14 days on agar medium containing 10 μM β-estradiol. At 7 DAG, seedlings were transferred to fresh 10 μM β-estradiol-containing medium to sustain the induction of CYCA2;3-GFP. Left, images obtained with DIC microscopy; right, drawings of the outlines of the epidermal cells obtained by tracing the microscopy images using Adobe Photoshop 6.
Table I. List of CYCA2;3 co-purified proteins identified by MS

<table>
<thead>
<tr>
<th>Locus</th>
<th>Gene description</th>
<th>Sequence coverage (%)</th>
<th>Protein score/threshold</th>
<th>Total ion score/threshold</th>
<th>Best ion score/threshold</th>
</tr>
</thead>
<tbody>
<tr>
<td>At2G27960</td>
<td>CKS1</td>
<td>62</td>
<td>168/58</td>
<td>121/24</td>
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<td>At4G16143</td>
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<td>At1G01880</td>
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<td>79/58</td>
<td>58/25</td>
<td>20/25</td>
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<td>At5G63960</td>
<td>DNA-directed DNA polymerase delta catalytic subunit, putative (POLD1)</td>
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<td>At2G46280</td>
<td>Eukaryotic translation initiation factor 3 subunit 2</td>
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<td>63/58</td>
<td>30/26</td>
<td>30/26</td>
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<td>At1G07890</td>
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<td>33/26</td>
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<td>At1G57720</td>
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<td>28/24</td>
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Combined peptide mass fingerprint and peptide sequence spectra were searched against the TAIR 8.0 database. Threshold values were set for P=0.05.
Table II. Effect of CYCA2;3-GFP induction on DNA ploidy level distribution in transgenic plants expressing CDKA;1, CDKB1;1, or CDKB1;1.N161

Cotyledons were harvested at 7 DAG. After flow cytometry, the EI was calculated. Col-0 was used as control. Values are means ± s.d. (n=3).

<table>
<thead>
<tr>
<th>Ploidy</th>
<th>Col-0</th>
<th>Col-0 × CYCA2;3-GFP</th>
<th>CDKA1;1 × CYCA2;3-GFP</th>
<th>CDKB1;1 × CYCA2;3-GFP</th>
<th>CDKB1;1.N161 × CYCA2;3-GFP</th>
</tr>
</thead>
<tbody>
<tr>
<td>2C</td>
<td>28.1±0.6</td>
<td>26.4±0.3</td>
<td>26.6±0.8</td>
<td>27.4±0.9</td>
<td>11.8±1.0</td>
</tr>
<tr>
<td>4C</td>
<td>36.8±0.4</td>
<td>30.6±0.8</td>
<td>35.1±0.7</td>
<td>30.2±1.4</td>
<td>28.7±1.2</td>
</tr>
<tr>
<td>8C</td>
<td>29.8±0.4</td>
<td>33.8±0.7</td>
<td>33.3±1.0</td>
<td>35.5±0.4</td>
<td>42.2±4.0</td>
</tr>
<tr>
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<td>9.1±1.2</td>
<td>5.1±0.3</td>
<td>6.9±1.0</td>
<td>17.0±4.4</td>
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</tbody>
</table>

+ 10 μM β-estradiol

| 2C     | 26.9±0.3 | 28.9±1.9 | 28.0±1.2 | 47.1±1.4 | 12.1±0.8 |
| 4C     | 37.1±0.2 | 37.1±0.0 | 40.7±1.2 | 35.2±1.0 | 32.0±2.0 |
| 8C     | 30.2±0.4 | 31.1±1.0 | 27.8±1.0 | 16.5±2.0 | 48.4±1.3 |
| 16C    | 5.2±0.1  | 2.8±0.9 | 2.9±1.0 | 1.0±0.4 | 7.4±1.8 |
### Table III. Effect of CYCA2;3-GFP stabilization in ccs52a1-1 on DNA ploidy level distribution.

Cotyledons and roots were harvested at 7 DAG and subjected to flow cytometry. Values are means ± s.d. (n=3).

<table>
<thead>
<tr>
<th>Ploidy</th>
<th>Col-0</th>
<th>CYCA2;3-GFP</th>
<th>ccs52a1-1</th>
<th>CYCA2;3-GFP × ccs52a1-1</th>
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<td><strong>Cotyledons</strong></td>
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<td></td>
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<tr>
<td><strong>Without β-estradiol</strong></td>
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<tr>
<td>2C</td>
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<tr>
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<tr>
<td><strong>+ 10 μM β-estradiol</strong></td>
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</tr>
<tr>
<td>2C</td>
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<tr>
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<td>8C</td>
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