Cloning and Characterization of CER2, an Arabidopsis Gene That Affects Cuticular Wax Accumulation

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Cuticular waxes are complex mixtures of very long chain fatty acids and their derivatives that cover plant surfaces. Mutants of the ECERIFERUM (cer2) gene of Arabidopsis condition bright green stems and siliques, indicative of the relatively low abundance of the cuticular wax crystals that comprise the wax bloom on wild-type plants. We cloned the CERP gene via chromosome walking. Three lines of evidence establish that the cloned sequence represents the CERP gene: (1) this sequence is capable of complementing the cer2 mutant phenotype in transgenic plants; (2) the corresponding DNA sequence isolated from plants homozygous for the cer2-2 mutant allele contains a sequence polymorphism that generates a premature stop codon; and (3) the deduced CER2 protein sequence exhibits sequence similarity to that of a maize gene (glossy2) that also is involved in cuticular wax accumulation. The CERP gene encodes a novel protein with a predicted mass of 47 kD. We studied the expression pattern of the CERP gene by in situ hybridization and analysis of transgenic Arabidopsis plants carrying a CER2-β-glucuronidase gene fusion that includes 1.0 kb immediately upstream of CER2 and 0.2 kb of CER2 coding sequences. These studies demonstrate that the CERP gene is expressed in an organ- and tissue-specific manner; CERP is expressed at high levels only in the epidermis of young siliques and stems. This finding is consistent with the visible phenotype associated with mutants of the CERP gene. Hence, the 1.2-kb fragment of the CERP gene used to construct the CERP-β-glucuronidase gene fusion includes all of the genetic information required for the epidermis-specific accumulation of CERP mRNA.

INTRODUCTION

The surfaces of the aerial portions of plants are covered by the cuticle, which serves as a barrier between a plant and its environment. The outer portion of the cuticle is composed of a complex mixture of acyl lipids, commonly termed cuticular waxes. Cuticular waxes are believed to play important roles in helping plants resist drought, frost, pathogens, and insects and in protecting them from UV irradiation as well as influencing the retention of applied chemicals (reviewed in Martin and Juniper, 1970).

Cuticular waxes are complex mixtures of very long chain fatty acids (VLCFAs) and their derivatives (reviewed in Tulloch, 1976). The chemical composition of these waxes varies from species to species. For example, the cuticular waxes found on the leaves of Arabidopsis are mainly composed of alkanes, alcohols, and fatty acids (Jenks et al., 1995). In contrast, the waxes found on maize seedling leaves are primarily composed of aldehydes, alcohols, and esters (Bianchi et al., 1985).

The amount of cuticular wax deposited on a surface is strongly influenced by developmental and environmental signals. For example, wild-type Arabidopsis stems and siliques are covered with a heavy layer of cuticular waxes, but Arabidopsis leaves accumulate considerably less wax (Koornneef et al., 1989; Hannoufa et al., 1993; Jenks et al., 1995). Similarly, as part of the coordinated juvenile-to-adult phase transition that occurs in maize, seedling leaves accumulate considerably more cuticular wax than do adult leaves (Bianchi et al., 1985; Evans et al., 1994; Moose and Sisco, 1994). In addition to altering the amount of wax deposited, developmental signals can affect the composition of cuticular waxes. For example, the composition of the waxes on Arabidopsis stems differs from the composition of those on Arabidopsis leaves (Hannoufa et al., 1993; Jenks et al., 1995). In contrast to the waxes on the leaves, the waxes on Arabidopsis stems are composed mainly of alkanes, ketones, and alcohols (Hannoufa et al., 1993).

Although advances have been made in our understanding of the biosynthesis of specific constituents of cuticular waxes (for reviews, see Kolattukudy et al., 1976; Post-Beittenmiller, 1996), many questions pertaining to the organization and regulation of this pathway remain unanswered (Kolattukudy et al., 1976; von Wettstein-Knowles, 1979; Cheesbrough and Kolattukudy, 1984). The precursor of VLCFAs is thought to be...
the saturated fatty acid stearate (18:0). This fatty acid is synthesized via de novo fatty acid biosynthesis, which occurs in plastids. In epidermal cells, a specific thioesterase releases the stearate molecule from the fatty acid synthase system of enzymes (Liu and Post-Beittenmiller, 1995). Subsequently, stearate is transported to the cytosol where it is elongated via an elongase system(s), which is probably localized on the membranes of the endoplasmic reticulum (Lessire and Stumpf, 1982; Lessire et al., 1982, 1989; Agrawal et al., 1984; Agrawal and Stumpf, 1985; Evenson and Post-Beittenmiller, 1995).

It has been possible to define some of the genes involved in cuticular wax accumulation because mutants of these genes condition a phenotype easily distinguished with the naked eye from the wax bloom that is present on wild-type plants. Such mutants have been identified in a number of species, including maize (reviewed by Schnable et al., 1994), barley (von Wettstein-Knowles, 1979, 1982), Sorghum bicolor (Jenks et al., 1992), and oilseeds rape (Macey and Barber, 1970). In Arabidopsis, at least 21 loci involved in this pathway (the ECRFERUM or CER loci) have been identified in this fashion (Koornneef et al., 1989; Hannoufa et al., 1993). The availability of mutants affecting cuticular wax accumulation and the isolation of the corresponding genes will assist in the elucidation of cuticular wax accumulation and the molecular mechanisms by which its production is regulated.

In this study, we report the isolation and initial characterization of the CER2 gene, one of the Arabidopsis genes involved in cuticular wax accumulation. Our analyses demonstrate that the CER2 gene encodes a novel protein. By using in situ hybridization and transgenic Arabidopsis plants, we show that the CER2 gene is expressed in an organ- and tissue-specific manner consistent with the phenotypic expression of cer2 mutants.

**RESULTS**

**Chromosome Walking to the CER2 Locus**

As shown in Figure 1A, the CER2 locus is located on chromosome 4 between the visible markers IMMUTANS (IM) and APETALA2 (AP2) (Koornneef, 1987). As a first step in cloning the CER2 locus via chromosome walking (Bender et al., 1983), F2 families segregating for the genetic markers AGAMOUS (AG), IM, CER2, and AP2 were screened for genetic recombinants (see Methods). In total, 26 recombinants were isolated between IM and CER2 and 92 between CER2 and AP2.

To map the locations of these recombination breakpoints more precisely, plants carrying these recombinant chromosomes were analyzed with several restriction fragment length polymorphism (RFLP) markers. Of the 92 recombinants between CER2 and AP2, 11 occurred between CER2 and m600. Based on these results, the RFLP marker m600 is \( \sim 2.5 \) centimorgans (cM) from CER2. Assuming a value of 185 kb per cM for Arabidopsis chromosome 4 (Schmidt et al., 1995), this interval is estimated to be \( \sim 460 \) kb. Four yeast artificial chromosome (YAC) clones (EG24D9, EW14G12, EW9C10, and EW11E4; Figure 1B) that contain sequences homologous to m600 were identified by screening a number of Arabidopsis YAC libraries (Ward and Jen, 1990; Grill and Somerville, 1991). Both ends of each of these YACs were subcloned via either plasmid rescue (Burke et al., 1987) or \( \lambda \) subcloning (see Methods). These YACs were oriented relative to the genetic map and to each other by using the subcloned YAC ends as RFLP markers to analyze the collection of genetic recombinants and in cross-hybridization experiments involving the other YACs. The YAC end closest to the CER2 locus was then used to isolate another set of YACs closer to the CER2 locus. This cycle was repeated seven times (Figure 1B).

YAC CIC9C5 was subcloned into the \( \lambda \) insertion vector NM1149 as HindIII fragments of up to 8.5 kb in length (see Methods). The resulting DNA fragments were used as RFLP markers to analyze the genetic recombinants on both sides of CER2. These analyses established that two of the 26 recombinants between IM and CER2 have recombination breakpoints between marker C9L (the centromeric end of YAC CIC9C5) and CER2 (Figure 1B). Similarly, one of the 11 recombinants between CER2 and m600 has a breakpoint between CER2 and marker C9-15, which lies \( \sim 150 \) kb from the centromeric end of CIC9C5. Therefore, the CER2 locus is located within an \( \sim 150 \)-kb interval of YAC CIC9C5. The ends of this interval are defined by the positions of markers C9L and C9-15 on YAC CIC9C5.

**Complementation of the cer2-2 Mutant**

To define more precisely the chromosomal region that contains the CER2 gene, DNA fragments from the interval defined by the probes C9L and C9-15 were tested for their ability to complement the cer2 mutation. DNA fragments derived from the 150-kb interval containing CER2 were isolated from a \( \lambda \) genomic library prepared from DNA with wild-type Arabidopsis ecotype Landsberg erecta (Ler) (Voytas et al., 1990). Overlapping DNA fragments were subcloned into the binary vector pB1121 and used to transform Arabidopsis plants homozygous for the cer2-2 allele. Initially, this complementation test was performed by using an Agrobacterium-mediated Arabidopsis root explant transformation system (Huang and Ma, 1992). Although transgenic plants were obtained (data not shown), the resulting plants seldom initiated roots. In addition, because cuticular wax deposition is strongly influenced by tissue culture conditions (Figures 2A and 2D versus Figures 2C and 2F), it was difficult to score the CER2 phenotype on the resulting regenerated plants. Subsequently, a vacuum infiltration transformation procedure (Bechtold et al., 1993) was successfully used to obtain transgenic seed at a rate of approximately one per 150 seed.

Two small overlapping genomic fragments (pG1H and
Figure 1. A Chromosome Walk to the CERP Locus of Arabidopsis.

(A) A partial map of chromosome 4 that shows the estimated genetic and physical distances between RFLP and visible genetic markers and the numbers of genetic recombinants isolated within each interval. Genetic distances are estimated based on subsets of the recombinants.

(B) A summary of the chromosome walk from the RFLP marker m600 to beyond CERP. Vertical dotted lines connecting YACs and chromosome 4 depict cross-hybridization. Probe C9-15 maps to the right of one of the 11 recombination breakpoints recovered between m600 and CERP. Similarly, probe C9L maps to the left of two of the 26 recombination breakpoints between CERP and IM. These results establish that the CERP locus is located within an ~150-kb interval of YAC CIC9C5. The position of the breakpoint associated with one of the 11 recombinants between CERP and m600 was not determined. Open circles and squares represent the centromeric and URA3-containing ends of the YACs, respectively. Cross-hatched circles and squares indicate YAC ends that contain repetitive sequences. Orientations were not determined for all YACs. The dashed horizontal lines represent chimeric YAC clones.

pG1RSc) isolated from the λ genomic clone G1 are illustrated in Figure 3A. They are capable of complementing the cer2-2 mutant phenotype (Figures 2G and 2J, and Figures 2H and 2K). Eight of 10 transgenic plants that were transformed with pG1H (representing at least three independent transformation events) and eight of nine plants that were transformed with pG1RSc (representing at least four independent transformation events; see Methods) exhibited a phenotype indistinguishable from that of the wild-type plants when examined with the naked eye.

One of the genomic DNA fragments, pG1H, capable of complementing the mutant phenotype was partially sequenced (GenBank accession number U40894). One end of pG1H contains the 3' portion of the ATR1 gene, which encodes an NADPH-cytochrome P450 reductase (GenBank accession number X66016). Adjacent to the ATR1 gene is a sequence with close identity to Arabidopsis expressed sequence tag (EST) 154C7T7 (GenBank accession number T76511). This 1.4-kb cDNA (EST 154C7T7) was obtained from the Arabidopsis Biological Resource Center (Columbus, OH) and subcloned into pBluescript such that its transcription is under the control of the cauliflower mosaic virus 35S promoter (Figure 3A).
resulting construct (pG1C1) was transformed into plants homozygous for the cer2-2 allele and was found to be sufficient to complement the cer2 mutant phenotype (Figures 2I and 2L). The EST 154C7T7 therefore represents the CER2 coding region.

Cuticular wax crystals on stems of wild-type, mutant, and transgenic plants were examined by scanning electron microscopy (Figure 2). Wild-type plants produce a large number of condensed tube-shaped wax crystals (Figures 2A and 2D). In contrast, cer2 plants produce relatively few crystals (Figures 2B and 2E). Four transgenic cer2-2 plants transformed with a CER2 genomic fragment (the pG1RSc or pG1H constructs; Figure 3A) or constitutively expressing the CER2 cDNA (construct pG1C1; Figure 3A) produce wax crystals in numbers similar to those on wild-type plants (Figures 2G to 2I versus Figure 2A). Although the crystals present on the plant carrying the pG1H construct differed somewhat in shape from those present on wild-type plants (Figure 2K versus Figure 2D), in the remaining three instances, the shape of the wax crystals was similar to that of the wild type (Figures 2J and 2L versus Figure 2D).

**Sequence Analysis of the CER2 Gene**

As shown in Figure 4A, the DNA sequence of the 1407-nucleotide EST 154C7T7 contains a 134-nucleotide 3' untranslated region that includes a putative polyadenylation signal (AATAAA) and a 24-nucleotide poly(A) tail. The size of this
cDNA is indistinguishable from the size of the 1.4-kb mRNA detected when it is used as a probe on RNA gel blots (see below). However, to provide additional evidence that this clone represents a near full-length cDNA, the region of pG1H that includes the CER2 coding region was sequenced (Figure 4A). Two putative TATA boxes (TATAAG and TATATA) that exhibit a high degree of similarity to the plant TATA consensus sequence (Joshi, 1987) were identified at positions -37 and -61 (relative to the 5' end of the cDNA), respectively. In addition, two putative CAAT boxes were identified at positions -68 and -85. Together, these data support the view that the EST 154C7T7 cDNA is almost full length. The only sequence polymorphism between the cDNA derived from the Columbia ecotype and the genomic clone derived from the Ler ecotype is a single conservative nucleotide substitution at position +1495.

The CER2 cDNA contains an open reading frame that could encode a protein of 421 amino acid residues with a predicted molecular mass of 47 kD. No alternative open reading frames of significant length were identified. Computer-based homology searches using various derivatives of the BLAST (Altschul et al., 1990) and FASTA (Pearson and Lipman, 1988) algorithms failed to reveal any significant sequence similarities between the deduced CER2 protein and entries in the nonredundant nucleotide and protein databases that have a known biochemical function. However, the deduced CER2 protein exhibits a high level of sequence similarity (35% amino acid identity and 63% similarity over the entire protein) to that encoded by glossy2 (g2), a gene that plays an undefined role in cuticular wax accumulation in maize (GenBank accession number X88779; Tacke et al., 1995). The deduced CER2 protein does not contain a recognizable protein-sorting signal sequence or a transmembrane domain when analyzed with the PSORT algorithm (Nakai and Kanehisa, 1992). However, the TMpred algorithm (Hofmann and Stoffel, 1993) predicts a putative transmembrane domain between residues 147 and 172 of the deduced CER2 protein (Figure 4B).

The cer2-2 Mutation Contains a Premature Stop Codon

CER2-specific polymerase chain reaction (PCR) primers (Figure 3B) were used to amplify the cer2-2 mutant allele from

![Figure 3](image-url). Structure of the CER2 Gene and Constructs.

(A) Two genomic fragments were cloned into pBl121 to generate plasmids pG1RSc and pG1H, and a cDNA was cloned into pBl121 to generate plasmid pG1C1.

(B) The CER2 gene structure is shown. The exons are indicated as boxes. The primer pairs p1 and p3, p2 and p5, and p4 and p6 were used to PCR amplify the cer2-2 allele.

(C) The chimeric reporter gene construct pCER2-GUS contains the 1.2-kb HindIII-BamHI fragment of pG1H fused in-frame with the GUS reporter gene in the vector pBl101-3.

B, BamHI; E, EcoRI; H, HindIII; NOS-pro, promoter region of nopaline synthase; NOS-ter, terminator of nopaline synthase; NPTII, neomycin-phosphotransferase; S, SacI; SI, SacII; X, Xhol.
The CER2 Locus is a Single-Copy Gene in the Arabidopsis Genome

The CER2 cDNA was used to hybridize a DNA gel blot containing Ler genomic DNA digested by five different restriction enzymes. As shown in Figure 5, using even relatively low-stringency washes (1 x SSC [0.1 M NaCl, 0.015 M sodium citrate]) at 65°C, a single hybridization band was detected when the genomic DNA was digested with BglII, EcoRI, HindIII, and XbaI. As expected from the restriction map of the cloned CER2 gene (Figure 3B), two hybridization bands were detected when the DNA was digested with EcoRV. Therefore, these data indicate that CER2 is a single-copy gene. When this experiment was repeated at even lower stringency (whereby the hybridization was conducted at 45°C and the final wash was performed with 1 x SSC at 45°C), several additional weakly hybridizing bands were revealed (data not shown), suggesting that some CER2 cross-hybridizing sequences are present in the Arabidopsis genome.

Accumulation of CER2 mRNA in Mutants and Wild-Type Plants

The CER2 cDNA clone was used as a probe in RNA gel blotting experiments. Total RNA and poly(A)-enriched RNA were
isolated from aerial parts of adult wild-type plants and mutants homozygous for the cer2-2 allele. As shown in Figure 6, these hybridization experiments revealed a single 1.4-kb mRNA in RNA isolated from a pool of leaves, stems, young siliques, and inflorescences. The amount of steady state CER2 mRNA in the cer2-2 mutant plants is approximately five- to 10-fold lower than that in wild-type plants.

Expression Patterns of the CER2 Gene

Based on the phenotype associated with cer2 mutations, the CER2 mRNA would be expected to accumulate in the epidermis of siliques and stems. To test this hypothesis, in situ hybridizations were performed on cross-sections of stems and siliques. As shown in Figures 7E and 7G, strong hybridization was detected only in the epidermis of cross-sections of young stems. Similar results were obtained from cross-sections of siliques (data not shown).

These studies were extended using a β-glucuronidase (GUS) reporter construct in transgenic Arabidopsis plants. The 1.2-kb HindIII-BamHI fragment of pG1H that includes positions -1009 to position +234 of the CER2 gene was fused in-frame with the GUS reporter gene in the binary vector pBI101.3. The resulting construct (pCER2–GUS; Figure 3C) was transformed into Arabidopsis cer2-2 plants that were derived from a cross of Ler marker line and Columbia IM marker line (see Methods). Samples from six individual transgenic plants (T1) and their derivatives (T2) representing at least three independent transformation events (see Methods) were stained for GUS activity with 5-bromo-4-chloro-3-indolyl β-D-glucuronic acid. All six transgenic plants showed similar expression patterns; a typical pattern is shown in Figure 7A. The CER2–GUS chimeric gene is expressed in siliques and stems; the most prominent expression occurs in mature ovaries and young siliques. Only the upper portions of stems and older siliques (arrow in Figure 7A) stained for GUS activity. Hence, the localization of GUS activity roughly corresponds to those regions that are undergoing elongation. The expression of the CER2–GUS gene was examined in cross-sections of GUS-stained stems and siliques. When GUS activity was assayed in the presence of ferric ions (see below), GUS staining was detected only in the epidermal layers of these organs (Figures 7B and 7D; data not shown). Expression of the CER2–GUS gene was not detected in rosette leaves (before or after bolting), cauline leaves, sepals, petals, or roots (data not shown).

In initial reporter gene experiments, GUS staining was conducted without the addition of ferric ions. Under these conditions, GUS staining was observed not only in the epidermis of stems and siliques but also in the vascular system and anthers (Figure 7A; data not shown). In subsequent experiments, GUS staining was conducted in the presence of ferric ions, as suggested by De Block and Debrouwer (1992).
Figure 7. Tissue-Specific Expression of the CER2 Gene.

(A) to (D) show the histochemical localization of CER2 promoter activity in the aerial portions of transgenic plants harboring the CER2–GUS gene. (E) to (G) show the in situ localization of the CER2 mRNA in cross-sections of stems.

(A) GUS activity is detectable in stems (ST), siliques (OS and YS), ovaries (O), and anthers (A). The arrow indicates a silique (OS) on which only the upper but not the lower portion exhibits GUS staining. OS and YS designate siliques of ~6- and 1.5-mm lengths, respectively. This Arabidopsis stem was folded into a spiral and stained in the absence of ferric ions.

(B) In a freehand-cut cross-section of a stem, GUS activity can be detected in the epidermis (E) after staining in the presence of ferric ions.

(C) GUS activity cannot be detected in a freehand-cut cross-section of a stem from a nontransgenic plant.

(D) Shown is a close-up view of GUS staining in the epidermis (E) of a 12-μm-thick section of a stem.

(E) Shown is in situ hybridization of a 35S-labeled CER2 antisense RNA probe with a cross-section of a stem. Hybridization signals are visible as dark silver grains in the epidermis (E); the blue color is the result of staining with toluidine blue for 1 min to reveal histological features (see Methods).

(F) In situ hybridization of a stem cross-section with a 35S-labeled CER2 sense RNA probe is shown. Hybridization signals are not detectable. For histological visualization, the specimen was stained with toluidine blue for 1 min.

(G) Shown is a close-up view of in situ hybridization of a 35S-labeled CER2 antisense RNA probe with a cross-section of a stem. Hybridization signals are detected in the epidermis (E). For histological visualization, the specimen was stained with toluidine blue for 2 min. The magnification for (A) is ×4.7, for (B) and (C) ~ ×45, for (E) and (F) ~ ×80, and for (G) ~ ×200.
Under these conditions, GUS staining was not detectable in the vascular system and was barely detectable in anthers (data not shown); however, GUS staining confirmed that the CER2-GUS gene is expressed in the epidermis of developing siliques and those portions of stems that are undergoing elongation.

DISCUSSION

CER2 Encodes a Novel Protein

We conducted a chromosome walk on chromosome 4 from the RFLP marker m600 to beyond the CER2 locus. The resulting 2.5-cM YAC contig spans ~800 kb. Three lines of evidence support the identification of the CER2 gene from this contig. First, two overlapping genomic fragments and a cDNA encoded by these fragments complement the cer2 phenotype upon transformation into cer2-2 Arabidopsis plants. Second, the RNA sequence of the cer2-2 mutant allele contains a nucleotide substitution relative to the wild-type allele that results in a premature stop codon in the encoded mRNA. Third, the CER2 sequence contains several charged and polar residues, making it unlikely to be part of an integral membrane protein. Hence, it is most likely that the CER2 protein is localized in the cytoplasm.

We are currently testing this hypothesis via immunolocalization experiments.

The nucleotide sequence of the CER2 gene is predicted to encode a 421-amino acid protein. Apart from GL2, this protein does not exhibit sequence similarity to any known sequence with a defined biochemical function. The CER2 protein does not appear to contain a protein-sorting signal sequence. Although one algorithm predicts that the CER2 protein contains a putative transmembrane region, this region contains several charged and polar residues, making it unlikely to be part of an integral membrane protein. Hence, it is most likely that the CER2 protein is localized in the cytoplasm.

We are currently testing this hypothesis via immunolocalization experiments.

The cer2-2 allele carries a mutation that results in a truncated protein that is most likely nonfunctional. Hence, cer2-2 probably is a null allele. The steady state level of CER2 transcripts is considerably reduced in cer2-2 plants relative to that of wild-type plants. Because the only difference between the sequenced cer2-2 allele and the wild-type allele is the nucleotide substitution at position +1150, it is likely that the premature stop codon in the cer2-2 mutant allele results in a transcript with reduced stability relative to the wild-type transcript.

Function of the CER2 Gene in Cuticular Wax Accumulation

In plants, de novo fatty acid biosynthesis occurs in plastids, using acetyl-coenzyme A and malonyl-acyl carrier protein (ACP) as precursors. The acetate moiety is elongated, two carbons at a time, to stearate via a series of condensation reactions catalyzed by the fatty acid synthase system of enzymes (reviewed in Ohlrogge et al., 1993). Each elongation cycle includes the condensation of acyl-ACP with malonyl-ACP, the reduction and subsequent dehydration of the derived [beta]-ketoacyl-ACP, and finally the reduction of the enoyl-ACP. The condensation reactions involved in the elongation of fatty acids from two to 18 carbons are catalyzed by the sequential action of three isozymes of keto-acyl synthase (KAS, i.e., KASIII, KASI, and KASII). The acyl group is then released from ACP by a thioesterase, thereby terminating the elongation reactions. The preferred substrate of the thioesterase present in most tissues is oleoyl-ACP. However, epidermal cells contain an additional thioesterase with a preference for stearoyl-ACP (Liu and Post-Bettenmiller, 1995).

These elongation reactions are thought to be catalyzed by an elongase system in a manner similar to de novo fatty acid biosynthesis (Lessire et al., 1989; Evenson and Post-Bettenmiller, 1995). This view is supported by the findings that the Arabidopsis gene FAE1 (which is involved in the elongation of oleate [18:1] to 11-eicosenate [20:1] and erucate [22:1] in seed) has sequence similarity to the gene coding for KASI (James et al., 1995), and the maize gene g18 (which is involved in cuticular wax biosynthesis) has sequence similarity to the genes coding for [beta]-ketoacyl reductases (X. Xu, C. Dietrich, M. Delledonne, T-J. Wen, Y. Xia, D.S. Robertson, B.J. Nikolau, and P.S. Schnable, manuscript in preparation). Thus, these findings indicate that the elongase system required for the biosynthesis of VLCFAs is composed of heteromeric subunits. However, because this system has not been purified, its structural organization remains unknown.

The predominant constituents of cuticular wax isolated from Arabidopsis stems are derived from a fatty acid with a chain length of 30 carbons (Hannoufa et al., 1993; Jenks et al., 1995). These constituents include (listed in descending order of their contribution to total wax) alkanes, primary alcohols, symmetric ketones, aldehydes, fatty acids, and secondary alcohols (Hannoufa et al., 1993). According to the current view, these fatty acid derivatives are biosynthesized via a bifurcated pathway in which fatty acids are reduced to the corresponding aldehyde, which can then be reduced further to a primary alcohol or decarbonylated to an alkane. Subsequent modifications of the alkanes give rise to the symmetric ketones and secondary alcohols.

The total amount of cuticular wax present on stems of cer2 plants is ~40% of that found on wild-type stems (Hannoufa et al., 1993). This reduction occurs primarily in aldehyde, alkane, secondary alcohol, and ketone constituents. In contrast, additional fatty acids accumulate, and the amount of primary alcohols remains approximately unchanged. The predominant chain length of all of these constituents is two to four carbons shorter than that of the wild type (Hannoufa et al., 1993).

Hence, it appears that the cer2 mutation blocks the terminal or the terminal two steps of VLCFA elongation. The effect of this block is to reduce the chain lengths of all the fatty
acid-derived constituents. Because the absolute amounts of the alkanes, ketones, and secondary alcohols are reduced by the cer2 mutation, it appears that the decarbonylase is specific for C30 aldehyde. This prediction is further supported by the near-absence of C28-derived alkanes, ketones, and secondary alcohols in wild-type wax, even though C28 aldehydes constitute a significant portion (20%) of the aldehyde pool in this wax (Hannoufa et al., 1993).

In contrast, it appears that the aldehyde reductase is not as sensitive to reductions in the chain length of its substrate. The evidence for this hypothesis is the finding that the total amount of primary alcohol is relatively unchanged by the cer2 mutation, even though the average chain length of the aldehyde pool is reduced. Additional evidence for this hypothesis is provided by the finding that a significant proportion of the primary alcohols present in wild-type wax have chain lengths of C28 and C26 (Hannoufa et al., 1993).

Based on the observation that chain length is reduced in all of the constituents of cer2 wax, it has been proposed that the CER2 gene encodes a desaturase (McNevin et al., 1993). In contrast, Jenkins et al. (1995) have proposed that the CER2 gene product may be a stem-specific regulator of the elongase system. Because the predicted CER2 protein does not have sequence similarity to any of the enzymes required for de novo fatty acid biosynthesis (genes for all of which have been cloned), either the CER2 protein catalyzes one of the component reactions of the elongase, but has a novel structure, or it encodes a novel molecular function, perhaps of a regulatory nature. Because the FAE1 and GL8 proteins exhibit high degrees of sequence similarity to the corresponding enzymes involved in de novo fatty acid biosynthesis, the first of these possibilities is unlikely. In either instance, the function of the CER2 protein must be relatively specific for the terminal elongation steps.

The predominant constituents of the cuticular wax that accumulate on maize seedling leaves are derived from 32-carbon fatty acids. Seedlings homozygous for the gl2 mutation accumulate waxes that are two to four carbons shorter (Bianchi, 1978). Hence, even though the chemical compositions of the cuticular waxes of maize seedling leaves and Arabidopsis stems and siliques are quite different, the mutations at the gl2 and CER2 loci of both maize and Arabidopsis affect the terminal elongation reactions in VLCFA biosynthesis. Thus, the structurally similar CER2 and GL2 proteins share a similar (but not identical) function. This is particularly interesting because even though the cuticular waxes on Arabidopsis leaves are derived from 32- (like those of maize) and 34-carbon fatty acids (Hannoufa et al., 1993; Jenkins et al., 1995), the cer2 mutation does not affect the constituents of leaf waxes. This specificity is further supported by the inability of the CER2 gene promoter to express the GUS reporter gene to detectable levels in leaves.

**Expression of the CER2 Gene Is Tissue and Organ Specific and Developmentally Regulated**

Expression of the CER2 gene was analyzed via in situ hybridization and in transgenic Arabidopsis plants harboring a chimeric construct consisting of the CER2 promoter and part of the CER2 coding region fused to the GUS reporter gene. In situ RNA localization experiments demonstrated that the CER2 mRNA accumulates specifically in the epidermis. Analyses of the reporter gene construct revealed that the CER2-GUS gene is expressed in the epidermis of developing siliques and in those portions of stems that are undergoing elongation. This demonstrates that the tissue-specific accumulation of CER2 mRNA is correlated generally with the phenotype conditioned by cer2 mutations. Because in situ hybridization reveals the same tissue specificity as does GUS staining of transgenic plants, the 1.2-kb HindIII-BamHI fragment of the CER2 gene used to construct pCER2-GUS must include all of the genetic information required for the epidermis-specific accumulation of CER2 mRNA.

The cer2 mutation does not affect leaf waxes (Jenkins et al., 1995). Consistent with this observation, GUS activity was undetectable in the leaves of transgenic plants harboring the CER2-GUS gene. Together, these results suggest that the CER2 gene is not involved in the accumulation of the cuticular waxes of leaves. However, because the cuticular wax of wild-type Arabidopsis leaves consists of VLCFAs and their derivatives having chain lengths of up to 34 carbons, we expect a CER2-like function to be required. However, based on the inability to readily detect CER2-cross-hybridizing sequences in DNA gel blots, this analogous function is not encoded by a gene with a high degree of sequence similarity to CER2.

**METHODS**

**Plant Materials and Isolation of Genetic Recombinants**

An Arabidopsis thaliana Landsberg erecta (Ler) genetic marker line carrying the recessive markers BREVIPEDICELLUS (BP), ECRERIFERUM2 (CER2), and APETAL2 (AP2) (Koornneef, 1987) was crossed to a Columbia stock carrying the mutant IMMUTANS (IM) (Wetzel et al., 1994). The resulting F1 plants were allowed to self-pollinate. Random F2 plants were also allowed to self-pollinate. The resulting F2 families were scored for recombinant phenotypes. Codominant cleaved amplified polymorphic sequences (CAPS) mapping using primers based on the AGAMOUS (AG) sequence (see Konieczny and Ausubel, 1993 for primer sequences and conditions) was used in some instances to score F2 plants and thereby identify recombinants with breakpoints between AG and CER2. The selected F2 plants were allowed to self-pollinate. Analysis of the resulting F3 families provided genotypic data for the IM locus. The cer2-2 mutant allele was generated via ethyl methanesulfonate mutagenesis of the Ler ecotype (Koornneef et al., 1989) and was obtained from the Arabidopsis Biological Resource Center (Columbus, OH) (stock No. CS8). The Arabidopsis ecotypes Ler and Columbia, the Ler marker line, and the Columbia M marker line were obtained from S. Roder and D. Voytas (Iowa State University). Arabidopsis plants were grown at 23°C, under 16 hr of daylight and 8 hr of dark.

**Isolation and Analysis of Arabidopsis Nucleic Acids**

Arabidopsis DNA was isolated from 20- to 30-day-old plants by using a modified cetyltrimethylammonium bromide procedure (Saghai-Maroof
et al., 1984). Digestions with restriction enzymes were conducted according to the manufacturer's specifications (Promega). Genomic DNA (0.5 μg) was loaded per lane and subjected to electrophoresis. RNA was isolated from the aerial parts of soil-grown adult plants, including leaves, stems, young siliques, and inflorescences via the method of Dean et al. (1985). Poly(A)-enriched RNA was isolated using the PolyA-Tract mRNA Isolation System I (Promega, Madison, WI). Fifteen micrograms of RNA and 150 ng of poly(A)-enriched RNA were loaded per lane and subjected to electrophoresis. Labeling of DNA fragments with phosphorus-32, electrophoresis, blotting of nucleic acids, and hybridizations were conducted according to standard procedures (Sambrook et al., 1989).

Isolation of λ Clones

An Arabidopsis λ library prepared from genomic DNA isolated from the Ler ecotype (Voytas et al., 1990) was screened according to standard procedures (Sambrook et al., 1989).

Yeast Artificial Chromosome (YAC) Manipulations and Subcloning of YAC Ends

The EGI, EW, ABI-1, and CIC YAC libraries (Ward and Jen, 1990; Grill and Somerville, 1991; Creusot et al., 1995) were screened as described by Gibson and Somerville (1992). Yeast chromosomal DNA were separated as described previously (Ausubel et al., 1994). The YAC DNA from agarose slices was purified by electrophoresis (Sambrook et al., 1989) or by using the GeneClean Kit (Bio-101, Vista, CA). YAC ends were subcloned via plasmid rescue (Burke et al., 1987) or λ subcloning. For λ subcloning, the recovered YAC DNA was digested by using the restriction enzyme HindIII, ligated to the λ insertion vector NM1149 (Murray, 1983), and in vitro packaged by using Gigapack II (Stratagene, La Jolla, CA). To isolate the subclones containing the YAC ends, the resulting λ subclone libraries were screened by using DNA fragments of pYAC4 flanking the cloning site as the centromeric end (the 0.5-kb HindIII-EcoRI fragment of pYAC4) and URA3 containing end (the 3-kb HindIII-EcoRI fragment of pYAC4) probes following standard procedures (Sambrook et al., 1989).

Polymerase Chain Reaction Primers and Conditions

The primers and conditions for CAPS mapping at the AG locus were described by Konieczny and Ausubel (1993). The paired primers p1 and p3, p2 and p5, and p4 and p6 were used to polymerase chain reaction (PCR) amplify the cer2-2 mutant allele. The primers were synthesized at the Iowa State University Nucleic Acid Facility by using a 394 DNA/RNA synthesizer from Applied Biosystems (Foster City, CA). The sequences of the CER2 primers (and their laboratory designations) are as follows: p1 (cer2-up), 5'-AGGTGGACGTAATAAAGTCTGAATG-3'; p2 (xy757), 5'-GCTTTGACCGTCGCTTCTTTGTGTA-3'; p3 (xy758), 5'-AAATCGAACCACTTCCCCACTG-3'; p4 (xy1283), 5'-AGGATGATAGAAGACAGATAAAGGAGG-3'; p5 (xy1436), 5'-GGCATCATCAGCATATACATCATATCCT-3'; and p6 (cer2-down), 5'-CATGGCAGACAAAAGAAGAACA-3'.

Construction of pGIH, pGIrSc, pGIcI, and pCER2-GUS and Plant Transformation

DNA fragments from the genomic clone G1 and the entire insert from the cDNA clone (expressed sequence tag [EST] 154C7T7) were subcloned in pBI121 (Clontech, Palo Alto, CA) to generate pGIH, pGIrSc, and pGIcI. To construct pCER2-β-glucuronidase (GUS), the 1.2-kb HindIII-BamHI fragment of pGIH was subcloned into the HindIII-BamHI cloning sites of pBluescript (Clontech). The resulting plasmids were introduced into Agrobacterium tumefaciens C58C1 (Koncz and Schell, 1986) via a freeze–thaw transformation procedure (An et al., 1988). Agrobacterium-mediated root explant transformation was conducted according to the procedure of Huang and Ma (1992). For the vacuum infiltration transformation, a laboratory protocol from the P. Green Laboratory (Michigan State University, East Lansing) (A. van Hoof and P. Green, manuscript submitted for publication), an adaptation of the method of Betchold et al. (1993), was used. Seed harvested from the vacuum infiltration–treated plants (T0) in same pot were bulked. Transgenic plants (T1) from different bulks were considered to represent independent transformation events.

Analysis of GUS Activity

Histochemical analyses of GUS activity with 5-bromo-4-chloro-3-indolyl-β-D-glucuronidase (β-g-glucuronidase) was performed as described previously (Jefferson, 1987) with modifications proposed by De Block and Debrouwer (1992). To monitor CER2–GUS expression in cross-sections, stems were harvested, cut into 5- to 1-cm lengths, and incubated for 10 hr in the presence of 2 mM potassium ferricyanide to reduce background staining in vascular tissues caused by peroxidase activity. Chlorophyll was removed with ethanol from freehand-cut sections. For thinner sections, stained stems were washed in 50 mM phosphate buffer, pH 7.0, fixed in 20% ethanol, 5% formaldehyde, and 5% acetic acid for 2 hr, dehydrated with an ethanol and 1-butanol series, embedded in Paraplast, and cut into 12-μm sections with a microtome.

In Situ Hybridization

Stems were harvested and cut into 0.5- to 1-cm sections, fixed with FAA (50% ethanol, 5% acetic acid, 10% formalin), dehydrated with an ethanol and 1-butanol series, and embedded in Paraplast+. Sections (8 μm) were cut with a microtome and placed on poly-L-lysine–coated slides. To prepare the riboprobes, the 0.47-kb Xhol-Sacl fragment of pGIc1 was subcloned into pBluescript SK+ (Stratagene, La Jolla, CA) to generate pGIc1XSc. T3 (antisense transcript) and T7 (sense transcript) polymerases were used to generate 35S-labeled riboprobes from linearized pGIc1XSc following the manufacturer's protocol (Promega). Prehybridization treatments, hybridization conditions, and post-hybridization treatments were performed as described previously (Raikhel et al., 1989). Slides were coated with Nodak NBT-2 emulsion and exposed at 4°C. Specimens were developed after a 5-day exposure and counterstained with 0.015% toluidine blue for 1 or 2 min.
DNA Subcloning, Sequencing, and Analysis

For sequencing, various fragments of the CER2 genomic clone G1 were subcloned into pBlueScript KS+ and pBlueScript SK+ (Stratagene). The cDNA clone (EST 154C7T7) was subcloned into the Sall–HindIII sites of pGem3z(-) (Promega). PCR-amplified fragments for sequencing were purified by electroelution (Sambrook et al., 1989). DNA sequencing of plasmids and PCR products was performed at the Iowa State University Nucleic Facility by using the double-stranded dye terminator technique on an automated DNA sequencer (model 373; Applied Biosystems). In all instances, both DNA strands were sequenced. Sequence comparisons and analyses were performed using the Genetics Computer Group (Madison, WI) sequence analysis software package (version 8) and the PSORT, TMpred, BLAST, and FASTA algorithms, as described previously (Pearson and Lipman, 1988; Altschul et al., 1990; Nakai and Kanehisa, 1992; Hofmann and Stoffel, 1993).

Scanning Electron Microscopy

Scanning electron microscopy examinations of stem cuticular wax crystals were conducted at the Iowa State University Bessey Microscopy Facility. Samples were frozen in liquid nitrogen by using a cryo-system (model SP2000A; EMSCOPEx Laboratories, Kent, UK), coated with gold, and observed with a scanning electron microscope (model JSM-35; JOEL, Tokyo, Japan) at 15 kV. Samples were analyzed from two Ler wild-type plants, one cer2-2 mutant plant, one transgenic plant harboring pG1H and another harboring pG1RSc, and two transgenic plants harboring pG1C1.

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