The Dominant Developmental Mutants of Tomato, *Mouse-ear* and *Curl*, Are Associated with Distinct Modes of Abnormal Transcriptional Regulation of a *Knotted* Gene

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The *Curl* (*Cu*) and *Mouse-ear* (*Me*) mutations of tomato cause two seemingly unrelated developmental syndromes with a wide range of pleiotropic phenotypes. Yet, the distinct morphogenic alterations in shoots, leaves, and inflorescences conferred by the two mutations appear to be caused by unchecked meristematic activity that characterizes dominant mutations in *Knotted1* (*Kn1*)-like genes of monocot plants. We have been unable to separate the two closely linked *Cu* and *Me* mutations, and they may lie in the same gene. A homeobox-containing class I *Kn1*-like gene, *TKn2*, also maps to the same location. Significantly, the dominant mutations are associated with two aberrant modes of *TKn2* transcription. Overexpression of the two in-frame wild-type transcripts of *TKn2* is associated with the *Cu* mutation, whereas misexpression of an abundant and oversized fusion mRNA is associated with the *Me* mutation. Available molecular evidence strongly suggests that the defective *Me*-*TKn2* transcript is generated via a novel splicing event that merges transcripts of two closely linked genes. The translated fusion product is comprised of most of the 5' end of the adjacent PPi-dependent fructose 6-phosphate phosphotransferase (*PFP*) transcript spliced in-frame to coding position 64 of the *TKn2* transcript, leaving the *TKn2* homeobox intact. We suggest that class I *Kn1*-like genes were selected early during evolution to regulate basic programs of aerial meristems and that subtle alterations in their function may be the basis for the wide diversity in growth parameters of shoot systems, leaves, and inflorescences among plant species.

INTRODUCTION

The final morphology of all plant organs is shaped by early developmental events in their meristems (Sussex, 1988). In generating the immense variation and developmental flexibility observed in shoots, it appears that all plant species must use homologous regulatory systems in their meristems. It follows, therefore, that to dissect plant morphogenesis, it is essential to study the mechanisms by which a subtle variation in the operation of a given meristematic gene results in gross morphological alterations. Such an opportunity is provided by members of the meristem-specific homeobox-containing *Knotted1* (*Kn1*) gene family.

The major reason for considering class I *Kn1*-like genes (hereafter *Kn1* genes) as legitimate meristematic regulators is that they constitute the only group of genes that incite meristematic activity when ectopically expressed outside of the apical meristems (Hake et al., 1995). Another reason is that they are expressed in the relevant meristems throughout development, as opposed to floral homeotic genes of the MADS box family, for example, which operate only in floral meristems and only in the context of flower differentiation.

The *kn1* gene was cloned by transposon tagging and was the first plant gene shown to contain a conserved homeobox (Hake et al., 1989; Vollbrecht et al., 1991). Kerstetter et al. (1994) classified the 13 different members of the *Kn1* family of maize into two classes based on sequence homology. In addition, *Kn1* genes of class I are expressed mainly in vegetative shoot apical meristems, inflorescence meristems, and stems, but not in root meristems or differentiated leaves and flowers, whereas genes of the second class may be differentially expressed in all organs.

Dominant mutations in class I *Kn1* genes have been identified in the monocots maize and barley. They were caused either by gene duplication or by insertion elements that alter gene expression (Veit et al., 1990; Greene et al., 1994; Muller et al., 1995). Misexpression of the *kn1* gene in the lateral vasculature of the maize leaf results in typical outgrowths designated as “knots.” Ligulelike tissues appear in distal sites, the proportions of the blade are altered, and there is an overall retardation of growth (Freeling and Hake, 1985; Smith et al., 1992; Jackson et al., 1994; Sinha and Hake, 1994). Dominant mutations in the *rough sheath1* and *liguleless3* genes of maize, which affect the more proximal domain of the leaf, were identified with overexpression and misexpression of class I *Kn1* genes (Schneeberger et al.,...
1995; Sylvester et al., 1996). Likewise, Muller et al. (1995) discovered that the appearance of extra flowers on the lemma of the barley Hooded mutant florets is also associated with an overexpression of a knl homolog. Overexpression of the knl gene or its Arabidopsis ortholog in dicot species, such as tobacco, Arabidopsis, or tomato, results in leaf malformations, epiphyllic shoots, loss of apical dominance, and extreme growth retardation (Sinha et al., 1993; Chuck et al., 1996; Hareven et al., 1996). We have shown that although simple leaves of Arabidopsis, tobacco, or tomato become lobed and ruffled when knl is overexpressed, their architecture remains simple. Compound leaves of tomato, in contrast, respond to knl overexpression by forming ramified supercompound structures (Figures 1B and 1C; Hareven et al., 1996).

The observation that diverse pleiotropic effects—such as growth retardation and loss of apical dominance on the one hand and leaf ramification or ectopic apices on the other—are caused by unregulated expression of Knl-like genes suggests that finely tuned spatial and temporal expression of these meristem-specific genes may be a critical mechanism by which plants regulate their growth habit and organ morphogenesis.

Tomato is particularly useful for this type of study because its major meristematic programs are modified in comparison to the major model dicot system, Arabidopsis, and therefore permit a different range of mutant phenotypes. The tomato shoot is sympodial; its vegetative and reproductive cycles alternate regularly; the inflorescence meristems are determinate; and leaf architecture is compound. We took advantage of the immense developmental diversity in tomato to investigate the role of Knl-like genes in shaping organ and plant architecture in dicot species.

Two vastly different plant architectures, leaf morphologies, and inflorescence organizations are conditioned by the dominant Curl (Cu) and Mouse-ear (Me) mutations. However, the two syndromes share the basic features of extreme growth retardation, formation of supercompound leaves, ectopic meristem activity, and loss of apical dominance that are common to Knl overexpressing plants. We show here that the two phenotypic features of Cu and Me are correlated with overexpression and misexpression of the newly isolated tomato Kn2 (TKn2) gene. The differences in phenotype most likely reflect the type of gene product, an upregulated normal transcript in the case of Cu, and misexpression of an oversized fusion messenger that involves a neighboring gene transcript in the case of Me.

RESULTS

The Cu and Me Syndromes

The Me phenotype was detected in a single plant of the Rutgers cultivar that was heterozygous for the mutation (Harrison, 1955). The dominant Cu mutation originated in a branch of a chimeric plant of the Stockdale cultivar (Young, 1955). The two loci were independently mapped to positions 48 and 49 of chromosome 2, respectively, on the genetic map (Stevens and Rick, 1986). The two dominant mutations, named after their peculiar leaf phenotypes, condition two vastly different morphogenic syndromes, yet most of their pleiotropic effects can be attributed to exaggerated or ectopic meristem activity that is characteristic of dominant mutations in Knl-like genes. In this study, we first describe the morphological features of Me and Cu mutant phenotypes that are relevant to this working hypothesis and thus are important later for the interpretation of the molecular and developmental observations.

The Cu Syndrome

The phenotypes associated with the Cu mutation are presented in Table 1. Cu is characterized by compact foliage structures that are nevertheless formed in the correct phyllo-tactic pattern. They consist of compound ramified leaves with wrinkled, curled blades and an extremely corrugated leaf surface, presumably as a result of intercalary disproportionate growth (Figure 1D) and diminutive, unexpanded axillary branches. In addition, epiphyllic shoots of all types emerge from the adaxial surface of the supercompound leaves (Figures 1F and 1G). The growth of Cu/Cu plants is greatly retarded; internode length is approximately one-quarter that of the wild-type length, and leaves and immature fruits develop extreme dark green pigmentation.

The first inflorescence in Cu plants appears relatively late, after ~12 to 18 internodes. The sympodial nature of the shoot is maintained, but inflorescences appear at a variable spacing of three to eight nodes rather than at the regular three nodes (Figure 1A). Whereas flowers set fertile fruits, the relative size of their organs is altered. The most dramatic phenotype, indicative of a possible involvement of a Knl-like gene, is the appearance of ectopic shoots, up to 1 cm long, on distal adaxial sites of the short sepals (Figure 1E).

As summarized in Table 1, the phenotype of Cu/+ plants is similar to but milder than that of Cu/Cu. The lamina is slightly more expanded in Cu/+ plants than in Cu/Cu plants, but the leaves remain supercompound, curled, sessile, and dark green. Sepals of Cu/+ plants also form ectopic shoots, but less often than do Cu/Cu sepals.

The Me Syndrome

The primary shoot apex of the Me plant takes one of three different developmental fates. The shoot meristem may terminate after two to six leaves (i.e., internodes) with an unusual inflorescence shoot; it may be consumed after only two to four leaves, whereby subsequent growth continues in the form of lateral or ectopic "inflorescence" shoots (Figures
Figure 1. Wild-Type Tomato and the Cu Syndrome.

(A) Part of a wild-type, indeterminate tomato shoot. The shoot is sympodial, with each section composed of three nodes and terminal inflorescence. Growth continues from a bud in the axil of the leaf just below the terminal inflorescence.

(B) Typical wild-type compound leaf. One terminal leaflet, three to five pairs of lateral leaflets, and several intercalated folials are shown.

(C) Supercompound leaf of tomato plant expressing the 35S:kn1 gene of maize (reprinted with permission from Hareven et al. [1996]. Cell 84, 735-744; Figure 1B, page 736).

(D) Cu shoot; homozygous plant. The compact foliage structure contains axillary shoots and ectopic shoots of all kinds (see Figures 5A and 6), but the leaves are arranged in the normal phyllotaxis.

(E) Ectopic shoots on sepals of Cu fruit. Note the Cu phenotype of the miniature ectopic leaf.

(F) Cu leaf. Scanning electron microscopy of a ramified unexpanded leaf from the top of the shoot shown in Figure 1E.

(G) Ectopic primordia on the adaxial (upper) side of the Cu leaf. Primordia of unidentified, vegetative, and floral buds are marked with one, two, or three asterisks, respectively.

(H) Cu/Cu (left) and Cu/Me (right) shoots of 6-week-old plants (see text).
to three leaves, with no additional growth ensuing (data not shown).

The first two to six leaves are supercompound; however, their leaflets, which display distorted proportions, emerge in irregular pattern along the more distant part of the slightly rolled, convoluted midrib (Figure 2B).

The apex of the Me inflorescence shoot in its early "vegetative" stage (Figure 2E) is different from that of the wild type shown in Figure 2D. In addition to the much expanded apex, there is inward curving of leaf primordia, which also characterize tomato plants expressing the maize *knl* gene (Hareven et al., 1996). Apices of the inflorescence shoots are usually terminated by a complex and fasciated truss (Figure 2C).

Genotype Leaf Morphology

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Leaf Compositiona</th>
<th>Ectopic Apical Shootsb</th>
<th>Apical Dominancet</th>
<th>Growth Habit</th>
<th>Inflorescence Architecture</th>
<th>Flower Modifications</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild type</td>
<td>Petiole, compound with nine leaflets</td>
<td>+</td>
<td>None</td>
<td>+++</td>
<td>Wild type</td>
<td>Wild type</td>
</tr>
<tr>
<td>Cu/Cu</td>
<td>Petioleless, curled, miniature</td>
<td>+++</td>
<td>+++</td>
<td>+</td>
<td>Extended sympodial sections</td>
<td>Reduced complexity, short</td>
</tr>
<tr>
<td>Cu/+</td>
<td>Same as Cu/Cu but less extreme</td>
<td>++</td>
<td>++</td>
<td>+</td>
<td>Like Cu/Cu</td>
<td>Cu/Cu-like, less</td>
</tr>
<tr>
<td>Me/Me</td>
<td>Petiolated expanded lamina, irregular architecture or filamentous</td>
<td>+++</td>
<td>None</td>
<td>Abolished</td>
<td>Modified</td>
<td>Fasciated, ramified</td>
</tr>
<tr>
<td>Me/+</td>
<td>Supercompound, irregular architecture</td>
<td>+++</td>
<td>None</td>
<td>+++</td>
<td>Wild type</td>
<td>Wild type</td>
</tr>
<tr>
<td>Me/Cu</td>
<td>Cu-like</td>
<td>++</td>
<td>++</td>
<td>+</td>
<td>Me/Me-like</td>
<td>Me/Me-like</td>
</tr>
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</table>

*+++, ++, and +: high, moderate, and low penetration, respectively, of the indicated phenotypes.

Molecular Organization of the *TKn2* Gene

The homeobox of *TKn1* (Hareven et al., 1996) was used to screen cDNA libraries constructed from mRNA of flowers, floral meristems, and shoot apices under relaxed conditions. Four new *Kn1*-like genes were identified (*TKn2, TKn3, TKn4, and TKn5; GenBank accession numbers U76407 to U76410, respectively*) and mapped using restriction fragment length polymorphism markers. *TKn2* was found to be tightly linked with marker TG454 (Tanksley et al., 1992) on chromosome 2. Previously, we had also mapped the Me gene to the same chromosomal location (see Methods for details).

To explore the possibility that *Cu* and *Me* may represent two different dominant mutations in the same gene and, in particular, *TKn2*, we investigated the molecular organization and transcription pattern of the *TKn2* gene. The complete amino acid sequence of the *TKn2* gene product is shown in Figure 3A. The homeodomain of *TKn2* retains all features of class I *Kn1* genes, as defined by Kerstetter et al. (1994). A detailed comparison of the homeodomains of six *Kn1* genes...
from various species (Figure 3C) indicates, however, that TKn2 along with the Arabidopsis SHOOTMERISTEMLESS (STM) gene and the soybean homeobox1 (SBH1) gene constitute a distinguishable subgroup of the class I Kn1 genes. Comparison of sequences of members of class I indicates that the two subgroups are distinguished by homology outside of the homeodomain as well (data not shown). In addition, the TKn2 genomic clone, schematically depicted in Figure 3B, contains only three introns, as does STM (Long et al., 1996); the genes that we grouped in the other kn1 subgroup have four introns.

Two types of wild-type TKn2 cDNA clones were identified. The type A cDNA is shown in Figure 3A. The type B cDNA clone contains two additional amino acids; the glycine and valine residues are inserted between positions 205 and 206 (arrow in Figure 3A), respectively, of the class A sequence.

To investigate the possible developmental significance of this putative cryptic splicing event, we looked for the presence

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**Figure 2. Essential Features of the Me Syndrome.**

(A) to (C) Vegetative and reproductive phases of Me plants. In (A), a young Me seedling that is 1 month old, with three leaves (L) and three inflorescence shoots (arrows), is shown. The upper shoot is part of the primary axis, and the second one is axillary. In (B), the advanced growth of an Me inflorescence shoot with a typical first Me/Me juvenile leaf (JV) displaying complete loss of apical dominance (arrows) and distal filamentous leaves (stars) is illustrated. In (C), the terminal portion of a fasciated inflorescence shoot of an Me/Me plant is shown.

(D) and (E) Scanning electron microscopy of a wild-type shoot apex (D) and early vegetative Me/Me inflorescence apex (E). Note the inward orientation of the Me leaf primordia and the absence of lateral leaflets (LL). The youngest three leaves (L) are shown in each apex.

(F) A heterozygous Me/+ ramified leaf with irregular branching pattern and altered shape of the single blades. MR, midrib.
of types A and B transcripts in mRNA populations from several plant organs: shoot apices, leaves, and flowers of wild-type plants and floral meristems of the anantha plant. As shown in Figures 4A and 4B, the two types of mRNA of TKn2 were detected in transcripts of all wild-type organs studied.

Cu and Me Are Characterized by Two Different Transcription Defects in TKn2

RNA gel blot analysis of TKn2 transcripts in wild-type plants revealed a low level of transcripts in shoot apices, upper

Figure 3. Molecular Characterization of the TKn2 Gene Product.

(A) Nucleotide and deduced amino acid sequence of the TKn2 cDNA clone. The homeodomain is underlined; the sites of the three introns are identified by arrowheads. The fusion site of the PFP-TKn2 transcripts in Me and the position of cryptic splicing are also indicated.

(B) Organization of the TKn2/1 genomic clone. Major indicative restriction sites and the four exons (a, b, c, and d) are displayed. Introns 1, 2, and 3 are 242, 2734, and 417 bp, respectively. Black regions of exons c and d identify the homeobox. Arrowheads mark the position of the PFP-TKn2 splice site (Me) and the insertion point of glycine and valine in the type B cDNA clone (GV). Probes 'A' and 'B' were used in DNA gel blot analysis of Cu genomic DNA.

(C) Subdivision of class I Kn1 genes. Amino acid comparison of homeodomains of seven class I Kn1 gene products is shown. Conserved positions for the STM/TKn2 subclass are shaded. Sequence (1) is from Long et al. (1996); sequence (2), Ma et al. (1994); sequence 3, Vollbrecht et al. (1991); sequence 4, Hareven et al. (1996); sequence 5, Schneeberger et al. (1995); and sequence 6, Lincoln et al. (1994).

Figure 4. Cryptic 5' Splicing Site of Intron 2 of the TKn2 Gene: Occurrence of Types A and B Transcripts in Wild-Type Organs and Mutants.

(A) Sequence organization of the 3' cryptic splice site of intron 2. Alternative splice sites are indicated by arrows. 5' and 3' consensus base pairs are underlined and indicated in italics. Lowercase letters indicate the base pairs at the ends of intron 2. The addition of 6 bp of GTGTAG results in the insertion of G and V amino acids between the S and A residues.

(B) Scheme of the experiment. Primers 1 and 2 flanking the site of interest were used to generate 32P-labeled reverse transcriptase-polymerase chain reaction products from RNA of different organs or tomato lines. cDNA products subsequently were digested with HindIII, leaving 130- or 136-bp fragments that were fractionated on a sequencing gel along with appropriate size markers.

(C) Lane 1 contains fractionated wild-type cDNA fragments from young leaves; lane 2, growing leaves; lane 3, flowers; lane 4, shoot apexes; lane 5, Me/Me flowers; lane 6, Cu shoot apexes; lanes 7 and 8, size markers prepared from type A and B cDNA clones, respectively; and lanes 9 to 12, sequencing reaction products solely to show the 6-bp difference.
parts of stems, early floral buds, and carpels (Figure 5A). Much higher levels of steady state mRNA were found in the floral meristems of the anantha mutant inflorescences (Figure 5A, lane 9). anantha inflorescences (Helm, 1951) serve as an excellent internal standard for the calibration of RNA levels because they provide a relatively homogeneous material that is rich in meristematic tissue and characterized by high expression levels of meristematic markers (Pri-Hadash et al., 1992), including Kn1 genes (Hareven et al., 1996). The wild-type expression pattern was dramatically altered qualitatively and quantitatively in Me and Cu plants. In Cu plants, there was at least fivefold overexpression of the 1.6-kb TKn2 transcript in leaves, shoot apices, and young floral buds but not in mature petals, anthers, or carpels, suggesting differential upregulation of TKn2 in Cu plants (Figure 5B). We failed to obtain undegraded RNA from Cu sepals. Dot blot analysis indicates, however, that in comparison with the wild type, TKn2 is upregulated two- to threefold in Cu sepals.

In Me, the gene was upregulated in all tested organs, including young leaves and flowers. Most significant, however, is the fact that the majority of the TKn2 transcripts in Me plants are ~2.7 kb, as compared with ~1.6 kb in the wild type (Figure 6A). Separate experiments verified that the large transcript of Me is polyadenylated and is not recognized by any other Kn1 gene probes (data not shown). Thus, the Me and Cu syndromes are apparently identified by transcriptional defects at the very same gene, TKn2.

In situ localization of TKn2 mRNA in wild-type plant organs revealed a pattern very similar to that of TKn1 (Hareven et al., 1996). The gene was expressed in vegetative apices (Figure 7A), in provascular tissues and growing points of leaf primordia (Figures 7B and 7C), and in floral meristems and floral primordia (Figures 7E and 7F). It was also expressed along the vascular strands of all developing organs.

The unequal growth of the lamina attracted our attention to the localization of TKn2 transcripts in Cu leaves. As shown in Figure 7D, almost all of the signals were localized to the spongy mesophyll cells. No overexpression was detected in the adaxial palisade (columnar) tissue of the leaf or along the vascular strands, where the wild-type gene is normally expressed (compare with Figures 7B and 7C).

Analysis of Transcripts and Coding Regions of TKn2 in Cu and Me Plants

Sequence analysis of amplified Cu–TKn2 transcripts verified that they are identical in every respect to the wild-type gene. The size of the amplified but not yet sequenced segments of all three introns was identical with that of the wild type (see the legend to Figure 3B). Genomic DNA gel blots, containing digests with eight different restriction enzymes, were probed separately with the TKn2 cDNA clone and genomic flanking sequences A and B, as shown in Figure 3B, and did not reveal any genomic alterations. Moreover, the nucleotide sequence of 1450 bp 5’ to the translation initiation site of the Cu–TKn2 gene was also normal.

To characterize the long TKn2 transcripts found in Me/Me plants, we prepared a cDNA library from floral RNA by using the 5’ end of the wild-type TKn2 cDNA clone as a probe. The longest of these clones, Me–TKn2/7 (2644 bp), contains a 5’ sequence of 1615 bp that is not recognized by the TKn2 probe. Shorter versions of this sequence were found in most other isolated clones. In the complete Me–TKn2/7 clone, an untranslated region followed by a reading frame potentially coding for 358 amino acids was spliced to a truncated version of the TKn2 gene missing the first 64 N-terminal residues. The 5’ 1.6 kb of foreign sequence in Me–TKn2/7 was homologous to the β subunit of pyrophosphate fructose 6-phosphate 1-phosphotransferase (PF; EC 2.7.1.90) of potato (Carlisle et al., 1990), which catalyzes, in plants, the reversible transfer of a phosphate group from PPi to fructose 6-phosphate to yield fructose 1,6-bisphosphate. On the assumption that the tomato and potato genes are similar, the Me–TKn2/7 clone consists of all of the translated N-terminal...
region of the PFP gene but is missing the 45 C-terminal residues of the wild-type PFP protein.

The splice site of the TKn2 gene resides within an exon, but as illustrated in Figure 8, the flanking sequence agrees well with the plant consensus sequence for 3’ splice sites. The S’ (PFP) splice site is a part of legitimate exon–intron border, most probably intron 13 if the organization of the tomato gene is identical to that of the castor bean gene (Todd et al., 1995). We have also verified that base sequences of these presumptive transcripts, we searched among the iso-

lated Me–TKn2 cDNA clones for those that were not recognized by the PFP probe. One of 12 Me–TKn2 cDNA clones consisted of a complete, normal TKn2 wild-type sequence. Moreover, reverse transcriptase–polymerase chain reaction with appropriate primers successfully amplified both fusion and wild-type cDNA forms from Me flowers, but only wild-type cDNA was amplified from wild-type tissue. Evidently, the formation of aberrant fusion transcripts is not the only option available for TKn2 in the Me genomic domain. As shown in Figure 6B, transcripts of two sizes were found for the PFP gene as well—2 kb of the wild-type size and 2.7 kb of the fusion PFP–TKn2 size. Significantly, unlike TKn2 of Me plants, only up to 40% of the PFP transcripts are of the large size.

Because the majority of TKn2 mRNA is fused to that of PFP, its distribution in leaves and flowers of Me plants, as shown in Figures 7G and 7H, respectively, reflects that of the fusion transcript. The expression pattern of PFP, as detected by a specific antibody for the potato protein (gift of B. Plaxton, Queen’s University, Kingston, Ontario, Canada), indicates that PFP is most abundant in regions of the leaves (Figure 7I), floral buds (Figure 7J), and Me floral buds (Figure 7K) overlapping the TKn2 expression domains. Longer exposure as well as the RNA gel blots shown in Figure 6B suggest that PFP, as expected of a housekeeping gene, is constitutively expressed in all organs and tissues.

The Kn1-like aspects of Me imply that the chimeric PFP–TKn2 mRNA is translated and that the protein product is localized to the nucleus. Analysis of polysomal fractions of Me flowers shown in Figure 6C suggests that the 2.7-kb fusion transcripts are indeed associated with polysomes. In pilot experiments, we have also fractionated crude cytosolic and nuclear protein preparations from wild-type, Me/Me, and Me/+ plants and have probed these with the PFP antibody. A novel protein of the predicted size (~90 kD) was detected only in Me/Me and Me/+ but not in the wild-type or Cu nuclear protein preparations or in any of the cytosolic samples (data not shown). These preliminary results are consistent with the possibility that the translation product of the PFP–TKn2 transcripts is localized to the nucleus. The nuclear localization signals that exist within and near the homeodomain of Kn-like proteins (Meisel and Lam, 1996) are retained in the fusion transcript.

**Overexpression of TKn2 in Tomato and Tobacco Plants Induces Specific Morphogenetic Alterations**

Misexpression of the TKn2 gene in Cu and Me mutants (Figures 1D, 2B, 2C, and 2F) and of kn1 in transgenic tomato plants (Hareven et al., 1996; Figure 1C) results in different phenotypes. The kn1 gene was overexpressed under the control of the ubiquitous cauliflower mosaic virus 35S promoter, whereas expression of the TKn2 genes in Me and Cu plants is obviously driven by other regulatory regimes. For a more reliable comparison of TKn2 and kn1, we have gener-
ated tomato and tobacco transgenic plants expressing TKn2 under the control of the 35S promoter. Twenty-six tobacco 35S::TKn2 T₁ plants were studied. Like kn1-expressing plants, growth was generally retarded, internodes were shorter, and leaves were sessile (Sinha et al., 1993). Leaf shape of tobacco 35S::TKn2 plants was consistently different from that of 35S::kn1-expressing plants (Sinha et al., 1993). The first three to six leaves of T₁ plants were only slightly lobed and had curled margins. Leaves of mid-axis internodes, however, were petioleless and deeply incised to the extent of being nearly palmarated. Leaves of distal internodes had an elongated lanceolate-like shape and were very reduced in size (Figures 9A to 9D). Surprisingly, leaves of axillary branches, irrespective of their position along the primary stem, were only slightly lobed and mostly lanceolate. The flowers were normal and fertile.

Sixteen 35S::TKn2 transgenic tomato plants were obtained. All but two could not be transferred to soil and were constantly propagated in culture vessels from cuttings. Three types of leaves were recorded: leaves that are subdivided to the third order with leaflets emerging in irregular patterns reminiscent of Mel+ plants (Figure 9G); leaves with reduced lateral leaflets, some being as filamentous as late leaves of Me/Me plants; and regular compound leaves with excessive but quite regular comlike proliferation of appendages along the margins of their leaflets (Figures 9E and 9F).

The interaction between the Me-TKn2-defective gene and kn1 of maize was followed in MelMe plants expressing the 35S::kn1 gene. None of the parental genotypes ever gave rise to epiphytic shoots on midribs, as was reported for kn1-expressing plants in tobacco and Arabidopsis or that was observed in Cu mutant leaves. Nevertheless, multiple ectopic shoots of the type shown in Figure 1G appeared on midribs of the much retarded Me/Me;35S::Kn1 plants (data not shown). This observation is important because it means that the truncated TKn2-Me gene contributes to the accelerated appearance of a classical Kn1 effect (see Discussion) in homozygous plants.

Other interactions of Me or Cu with Lanceolate, trifoliata, and entire are also additive, suggesting that Me and Cu, as does kn1, exert their effect within the context of the other mutations. To illustrate this point further, comparison of the interactions of Me and kn1 with entire is shown in Figures 9H and 9I. Note how similar the phenotypic expression of kn1 (maize) in transgenic entire leaves is to that of TKn2 in some of the transgenic wild-type leaves.

**DISCUSSION**

**The Genetic Nature of the Me and Cu Mutations**

The Me and Cu genes are tightly linked to each other as well as to the homeobox-containing gene TKn2. Both mutations incite ectopic meristematic activity that results in ramification of the compound leaf, suppression of apical dominance, and retardation of growth. The formation of ectopic shoots on the adaxial surface of Cu leaves and sepals and the fasciated inflorescence shoots in Me plants also suggest ectopic meristematic activity that is characteristic of dominant Kn1 genes (Hake et al., 1995). These observations strongly imply that the two defective modes of transcription that are associated with the TKn2 gene of Cu and Me are responsible for the phenotypes of the two mutants.

Interpretation of the Cu phenotype, with respect to the upregulation of TKn2, is formally simple because all features are dose dependent. The leaf defects are correlated with the organ-specific overexpression of TKn2 (Figure 7D). However, the ectopic shoots, emerging from only one specific adaxial site of the sepals, may represent yet another allele by which Kn1 genes can regulate development. It is possible that this intriguing phenomenon reflects differential sensitivity of the sepals to an overall change in the balance of hormones. It has been noted already that misexpression of Kn1 genes mimics in many ways responses to hormonal applications (Hake et al., 1995). These include uncoupling of flowering and apical dominance as in Cu-, Me-, and kn1-expressing plants, growth retardation and alteration of growth habit in Cu and Me, and extreme green pigmentation of leaves and fruits in Cu- and kn1-expressing plants. All of these features, just like site-specific shoots on sepals, do not necessarily correlate with local autonomous or even with local and restricted nonautonomous (Lucas et al., 1995) overexpression of Kn1 genes. They may indicate that plant hormones thus might play a critical role in mediating the developmental functions of Kn1 genes.

The interpretation of the Me phenotype is more complicated. The major product of the TKn2 gene is a chimeric PFP-TKn2 transcript, and the normal mRNA represents only a minority of the steady state TKn2 transcripts. The formation and distribution of this transcript are regulated by a different regime and not by the legitimate TKn2 promoter. Finally, some of the Me defects are not dose dependent and can be rescued by one copy of the wild-type TKn2 gene (i.e., Me/+) but not by the overexpressed Cu-TKn2 allele (i.e., in Cu/Me).

The following observations suggest that the truncated form of the Me-TKn2 product is upregulated, translated, and functioning, Kn style, in Me plants. Me/+ leaves undergo additional rounds of subdivision as do Cu- and kn1-expressing plants (Figures 1 and 2). The inward orientation of leaf primordia in the Me apex (Figures 2D and 2E), the suppression of apical dominance, the fasciated inflorescence shoots (Figure 2C), and the additive interaction with kn1 also imply, in the context of the Kn1 genes, overexpression and misexpression rather than a loss of function.

It is possible, of course, that the suppression of vegetative apices and the appearance of determinate inflorescence shoots in Me/Me (but not in Me/+ ) plants are due to a partial loss of TKn2 function by the truncated PFP-TKn2 factor. This possibility is made more likely because TKn2 is closely
Figure 7. In Situ Localization of TKn2 Transcripts and PFP Antigen in Wild-Type and Mutant Organs.

(A) to (D) Localization of TKn2 transcript in apical meristems and in leaf primordia. In (A), shoot apical meristems (AP) of a wild-type plant are shown. Signals are in L2 and L3 cell layers of the apex but are only marginally detected in L1 (future epidermal) cells. In (B) and (C), cross-sections in young (B) and mature (C) wild-type leaves are shown. TKn2 is expressed in the growing tips and in a relatively wide region around the vascular tissues. (D) is part of a cross-section in a convoluted Cu leaf. Note the concentration of signals in the spongy (bottom) mesophyll. Compare with (C).
related to the STM gene of Arabidopsis in which recessive mutations result in lethal apical meristems (Long et al., 1996). If the recessive Me phenotypes result from a partial loss of TKn2 function, then these lost functions are rescued by the wild-type allele in Me/+ genotypes but not by Cu in Me/Cu plants. Presumably, the Cu–TKn2 gene fails to provide the right cells at the right time with the Me–TKn2 gene product. Alternatively, although misexpression of Me–TKn2 incites meristematic activity ectopically, it also suppresses it in the early vegetative apex in the same way that it supports ramification in early leaves of Me/Me but suppresses lamina development in late leaves.

The Molecular Nature of the Me and Cu Mutations

All dominant mutations in Knl-like genes recorded to date were found in monocot species and are associated with subgroup 1 (Figure 3C) of the class I Knl genes (kn1, rough sheath1, and hooded). Cu and Me are the first dominant mutations reported in dicot species that are associated with the STM/SBH1/TKn2 subgroup 2 of class I Knl genes (Figure 3C). The regulation of the Cu–TKn2 gene was compromised in the abaxial spongy mesophyll of the leaf but not in the palisade tissue or in the three inner whorls of the flowers. The abnormal expression patterns were not due to the gross genomic alterations within the coding region, introns, or immediate flanking sequences of the Cu–TKn2 gene. The most likely possibility is that a minor sequence alteration was introduced in a putative vegetative silencer in the long intron 2. Mutations in remote flanking sequences that also have the potential of disrupting regulatory genetic modus operandi or even epigenetic changes cannot be excluded. Linkage studies suggest, however, that such a putative mutation should reside within 0.1 cM of the Cu mutation (50 to 100 kb on average).

In their recent analysis of the TKn2 gene in the Me plants, Chen et al. (1997) convincingly showed that the TKn2 gene (referred to as LeT6 in their study) of Me is fused at a position 1630 bp 5' to a 15-kb genomic duplication of the PFP gene. This result is consistent with a readthrough transcript originating in the duplicated Me promoter and misspliced at the indicated positions (Figure 8; Chen et al., 1997). It is also in agreement with the presence of regular-sized PFP transcripts and the scarcity of intact TKn2 transcripts. The latter observation also suggests that in agreement with the in situ hybridization results (Figure 7), the expression domains of the two genes do indeed overlap. It is not easy to determine why a 3' splice site was chosen in the middle of the first Me–TKn2 exon. Presumably, other more legitimate downstream 3' sites of any of the TKn2 introns result in a complete loss of function.

Different Knl Class I Genes Have Different Meristematic Functions

Functional differences between Knl-like genes may help to dissect elusive intrinsic meristematic programs. The sequence of TKn2 is more similar to STM of Arabidopsis than it is to TKn1 or TKn3 of tomato, and KNAT1 (Kn1-like from

**Figure 7.** (continued).

(E) Floral meristems of anantha plants.
(F) Floral primordia of wild-type plants. Three floral primordia (arrows) are shown.
(G) and (H) Distribution of TKn2 transcripts in Me floral primordia (G) and young leaf (H). The fasciated inflorescence primordia is fated to form the structure shown in Figure 2C. Note the wider distribution of signals in the primordial apices in comparison with the wild type. Tissues below the apex were also decorated after longer exposure.
(I) and (J) Immunolocalization of the PFP antigen in leaves (I) and floral primordia (J) of wild-type plants.
(K) Immunolocalization of the PFP antigen in fasciated inflorescence primordia of Me/Me plants. A 500-bp TKn2-specific fragment was used to prepare digoxigenin-labeled antisense and sense RNA probes. Sense probes gave no hybridization signals. The specific anti-PFP antibody for the potato protein was kindly supplied by B. Plaxton (see Carlisle et al., 1990). AC, apical cells; AP, apex; FP, floral primordia; GP, growing tips; PV, provascular strand; SM, spongy mesophyll; VB, vascular bundles.
Figure 9. Leaf Shapes and Architecture in Transgenic Plants and Double Mutant Combinations.

(A) to (D) Transgenic tobacco plants expressing the 35S::TKn2 gene. (A) shows a wild-type tobacco leaf. (B) to (D) show lower, middle, and upper leaves, respectively, of tobacco plants expressing the 35S::TKn2 gene. Note the palmate architecture of the leaf in (C) and the lanceolated shape of upper leaves in (D).

(E) to (G) Phenotypic expression of TKn2 in tomato transgenic plants. Two different leaf phenotypes of two independent transgenic plants are shown. Comb-like leaflets in a compound leaf of 35S::TKn2 transgenic plant are shown in (E) and (F). Note the similarity with respect to marginal outgrowth between this type of transgenic plant and e/e;35S::kn1 plants shown in (H). In (G), Me-like arrangement of leaflets in another tomato plant expressing the 35S::TKn2 gene is shown. Compare with Figure 2F.

(H) Interaction between entire and the maize kn1 gene in homozygous entire plants carrying one dose of the 35S::kn1 gene.

(I) Leaf architecture in Me/+;e/e plants. Note that the ramification site of the entire leaf is restricted to its distal region in both e/e;kn1 (H) and Me/+;e/e plants.
Arabidopsis thaliana) is more closely related to kn1 and TKnl than it is to STM, suggesting that functional differences among Kn1-like genes were established before these species diverged. Functional classification has been hindered, presumably for lack of appropriate criteria. Misexpression of all Kn1-like genes elicits ectopic meristematic activity, growth retardation, and loss of apical dominance, and it is also likely that null alleles in many class I Kn1 genes will have detrimental effects on meristems, similar to STM and rough sheath1. The morphogenic differences induced by the two Kn1 genes in the same organs, for example, kn1 and Cu in leaves, are not indicative of different functions, because the two genes are expressed under different spatial and temporal controls. One approach therefore is to compare the effects of different Kn1 genes in the same species and under the control of the same regulatory sequences.

In tomato, 35S::kn1 induces extreme but regular subdivision of the leaf, but no ectopic shoots are formed. 35S::TKnl2 confers much milder, irregular subdivision, similar to that of Me/+ leaves. The 35S::TKnl transgene conditions growth retardation so extreme that it permits shoots of only 10 to 15 cm, unexpanded leaves of only 1 cm in length, and unusual early flowering that results in abortive diminutive buds. In tobacco, 35S::kn1 induces lobed and rumpled leaves with occasional epiphyllous shoots (Sinha et al., 1993), and 35S::TKnl2 induces lobed, dissected, and lanceolate leaves (Figure 7), whereas most extreme growth retardation and rounded leaves with miniature epiphyllous shoots, corrugated surface, and dark pigmentation—all reminiscent of tomato Cu leaflets—are induced by TKnl1 (E. Lifschitz, unpublished data). The unique phenotypes caused by three different Kn1-like genes in the same species and under the same promoter are consistent with the idea that each Kn1 gene controls at least some distinct developmental program.

The Relationship between Expression Domains of Kn1 Genes and the Initiation and Architecture of Leaves

Initiation of Leaves

Suppression of Kn1 expression in the future initiation sites of leaves on the flanks of maize and Arabidopsis apices invoked the inference that such a downregulation is a prerequisite for leaf initiation (reviewed in Hake et al., 1995). It follows that ubiquitous expression of Kn1 genes alters phyllotaxis. This prediction has not yet been confirmed. In plants bearing dominant overexpressing mutations such as Kn1, rough sheath1, Cu, or Me, or in transgenic tobacco, Arabidopsis, and tomato plants expressing Kn1-like genes, phyllotaxis was never altered. In addition, we have shown here (Figure 7) and elsewhere (Hareven et al., 1996) that in contrast to maize and Arabidopsis, the tomato TKnl1 and TKnl2 genes are expressed across the meristematic domains of the apex.

Leaf Architecture

The tomato TKnl1 and TKnl2 genes are expressed in leaf and floral primordia of tomato (Figure 7; Hareven et al., 1996) but not in the corresponding organs of maize and Arabidopsis (Jackson et al., 1994; Lincoln et al., 1994; Hake et al., 1995). We previously considered the possibility that Kn1 genes are required to promote compoundness, with the provision that the observed differential response of simple and compound leaves to kn1 misexpression may also be due to different developmental potentials at a critical developmental window (Hareven et al., 1996). Me is informative in this regard because ramified, simple, and even filamentous leaves are formed on the same plant (Figures 2A to 2C) and because Me/+ leaves are more compound than are Me/Me leaves and their leaflets are never laminar. Restriction of lamina expansion is thought to be a precondition for increased compoundness and has also been observed in ramified leaves of extreme kn1 phenotypes (Hareven et al., 1996) and along the palmed veins in 35S::TKnl2–expressing tobacco plants as well (Figures 9B to 9D). Thus, in addition to the route leading to simple leaves that is exemplified by the double mutant combination of the recessive trifolate and potato leaf genes (Stettler and Imber, 1965), modified expression of Kn1 genes (i.e., Me) may represent another route. The dominant Lanceolate gene (Dengler, 1984) may well be involved in this second allele.

Kn1 Genes and Growth Habit

The shape and architecture of a plant and consequently its economical success depend primarily on growth habit—the pattern in which vegetative and reproductive organs alternate and in which side branches emerge. Growth habit is determined in apical meristems in which Kn1-like genes are expressed. In most cases, the upregulation of Kn1 genes in their legitimate expression domains does not lead to morphogenetic alterations (Hake et al., 1995). Consequently, their role in regulating growth habit was neglected. Yet, common to all plants overexpressing Kn1 genes is the enhancement of branching, for example, uncoupling of apical dominance and flowering. Me and Cu alter the pattern of reproductive development by terminating vegetative growth prematurely.
and provoking reproductive development in Me or extending it in the Cu sympodial shoot and by permitting extensive proliferation of the inflorescence in Me but suppressing floral meristems in Cu. The formation of ectopic flowers in barley Hooded mutants (Muller et al., 1995) occurs in already determined reproductive organs. Although it is not clear to what extent the Hooded phenotype is different from the appearance of epiphyllous inflorescence meristems on transgenic tobacco leaves, it is nevertheless in agreement with a role of Kn1-like genes in regulating vegetative to reproductive transitions.

The study of the TKn2 gene in tomato and tobacco plants suggests that the very same meristematic regulatory gene operating under the same promoter can generate a range of variations in leaves—from supercompound to filamentous in Me or from lanceolate to palmated in 35S::TKn2 tobacco. Under different expression regimes, as in Me and Cu, TKn2 confers extreme variations in morphogenesis and growth habit in the same plant species.

It follows that subtle alterations in the activity of TKn2 and of a relatively small group of Kn1 genes may support a wide range of variations in inflorescence complexity, leaf morphology, and growth habit in tomato plants. Transcription factors of the MADS box family were selected early during evolution of plants (Ma et al., 1991; Pnueli et al., 1991) to regulate the fate and development of flowers and floral organs. Likewise, it is possible that Kn1 class I homeodomains were adopted as the most suitable regulators of growth mechanisms that are common to all aerial meristems.

METHODS

Plant Material

Seeds of anantha (LA539), Curl (Cu; LA325), entire (e; LA322), Mouse ear (Me; LA324), trilobate (t; LA579), and Lycopersicon pennellii (A716) were obtained from C.M. Rick (University of California, Davis). For tomato transformation, we used TK9/8. Generation of transgenic tomato plants and the line used for transformation were as described by Pruehl et al. (1994). Transformation of tobacco plants (Samsun 5) was done according to the method of Horsch et al. (1985). For the Me¹+e/e, and e/e,Kn1 double mutant lines shown in Figures 9H and 9I, transgenic line Mv, expressing the 35S::kn1 gene construct, was used as the male parent to pollinate Me or e homozygous plants. Appropriate segregants were selected from the F2 generation.

Mapping Procedure

L. pennellii was crossed to Me/Me plants, and F2 Me segregants were analyzed for linkage with chromosome 2 restriction length polymorphism markers. No recombinants were found between Me and TG454 among 83 F2 Me plants. The tomato Knotted2 (TKn2) and PPI-dependent fructose 6-phosphate phosphotransferase (PFP) clones were mapped using the population of an L. pennellii introgression line (Eshed and Zamir, 1995). Both clones revealed the L. pennellii polymorphism when probing DNA of IL2-2 and IL2-4, which share an overlapping introgressed region marked by TG454 and TG355 and were assigned to the same site on the restriction fragment length polymorphism map (Tanksley et al., 1992).

Nucleic Acid Procedures

cDNA libraries were prepared in the λZAP II vector (Stratagene, La Jolla, CA) from poly(A)+ RNA of shoot apices, floral buds, and anantha floral meristems. A genomic library of wild-type tomato line (93-137) was prepared in the λFIX vector (Stratagene), according to the manufacturer’s protocol. The polysome fractions were analyzed according to the method of Barkan (1993). Other nucleic acid procedures were performed as described by Maniatis et al. (1982) or Ausubel et al. (1986).

Primers

The following primers were used for the polymerase chain reaction procedures reported in the text: primer 1, 5′-CTTCTAGAAGGGGTTGATGTC-3′; primer 2, 5′-CCATCGATGGGCACACAAGTAATATGC-3′; primer 3, 5′-ATGGAGGGTGGTTCTAGTGGAAATACTAGT-3′; and primer 4, 5′-CTTACTCCCCAGTCCTTGGAGCTC-3′. Primers 1 and 2 were used for the experiment reported in Figure 4B and for amplification of intron 2 from Cu DNA. Primers for the reverse transcriptase-polymerase chain reaction isolation of TKn2 cDNA from Cu were 2 and 3. Primers 2 and 4 were used in the attempt to isolate a fusion transcript from Me and wild-type RNA.

Cytological Procedures

In situ hybridization using digoxigenin-labeled RNA probes (Jackson, 1991) was performed as described by Hareven et al. (1996). Preparation of tissues for scanning electron microscopy was according to the method of Smyth et al. (1990). Immunogold labeling was as described by Shahar et al. (1992) and Samach et al. (1995).

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