A knotted1-like Homeobox Gene in Arabidopsis Is Expressed in the Vegetative Meristem and Dramatically Alters Leaf Morphology When Overexpressed in Transgenic Plants

Cynthia Lincoln, Jeff Long, Judy Yamaguchi, Kyle Serikawa, and Sarah Hake

Department of Plant Biology, University of California, Berkeley, California 94720
Plant Gene Expression Center, U.S. Department of Agriculture, Agricultural Research Service, 800 Buchanan Street, Albany, California 94710

The homeobox gene knotted1 (kn1) was first isolated by transposon tagging a dominant leaf mutant in maize. Related maize genes, isolated by virtue of sequence conservation within the homeobox, fall into two classes based on sequence similarity and expression patterns. Here, we report the characterization of two genes, KNAT1 and KNAT2 (for knotted-like from Arabidopsis thaliana) that were cloned from Arabidopsis using the kn1 homeobox as a heterologous probe. The homeodomains of KNAT1 and KNAT2 are very similar to the homeodomains of proteins encoded by class 1 maize genes, ranging from 78 to 95% amino acid identity. Overall, the deduced KNAT1 and KNAT2 proteins share amino acid identities of 53 and 40%, respectively, with the KN1 protein. Introns positions are also fairly well conserved among KNAT1, KNAT2, and kn1. Based on in situ hybridization analysis, the expression pattern of KNAT1 during vegetative development is similar to that of class 1 maize genes. In the shoot apex, KNAT1 transcript is localized primarily to the shoot apical meristem; down-regulation of expression occurs as leaf primordia are initiated. In contrast to the expression of class 1 maize genes in floral and inflorescence meristems, the expression of KNAT1 in the shoot meristem decreases during the floral transition and is restricted to the cortex of the inflorescence stem. Transgenic Arabidopsis plants carrying the KNAT1 cDNA and the kn1 cDNA fused to the cauliflower mosaic virus 35S promoter were generated. Misexpression of KNAT1 and kn1 resulted in highly abnormal leaf morphology that included severely lobed leaves. The expression pattern of KNAT1 in the shoot meristem combined with the results of transgenic overexpression experiments supports the hypothesis that class 1 kn1-like genes play a role in morphogenesis.

INTRODUCTION

Development of the shoot portion of plants originates from a distinct region of the shoot apex, termed the shoot apical meristem. The shoot meristem forms during embryogenesis and functions throughout the vegetative and reproductive phases of plant development to repetitively generate lateral organs, such as leaves or flowers, and stem tissues. In addition to initiating new tissues and organs, the shoot meristem must maintain or replenish itself (Steeves and Sussex, 1989). In the shoot apical meristem of most angiosperms, cytological variations have led to the description of three major regions or zones. The central zone consists of slowly dividing initials that serve as a source of cells for other regions of the meristem. The peripheral zone surrounds the central zone and consists of more rapidly dividing cells undergoing organogenesis; lateral organs such as leaf primordia arise in a precise, genetically determined pattern (phyllotaxy) within this zone. Finally, the rib zone forms a transition between the apical meristem and the rest of the shoot apex and contributes tissues to the pith or central portion of the stem (Wardlaw, 1957; Medford, 1992). Despite extensive knowledge of the complex structural organization of the shoot apical meristem, very little is known about the molecular mechanisms responsible for meristem initiation and function.

Fate mapping experiments have shown that cell position is more important than cell lineage in determining the final pattern of differentiated tissues within the shoot (reviewed in Poethig, 1989; Irish, 1991). How do cells in the shoot meristem acquire positional information and then differentiate accordingly? In animals, genetic analysis has shown that cells receive information from regulatory molecules whose expression patterns are established early in embryo development. The products of homeobox genes are one such class of regulatory molecules (Gehring, 1987; McGinnis and Krumlauf, 1992). The homeobox, first identified in Drosophila homeotic genes, and...
subsequently in other invertebrate, vertebrate, fungal, and plant genes, encodes the evolutionarily conserved DNA binding homeodomain (Gehring et al., 1990). High-resolution structural studies of homeodomain–DNA complexes have shown that the homeodomain is composed of three major α-helical regions; residues in the highly conserved third helix and in the N-terminal arm of the homeodomain play crucial roles in sequence-specific recognition of DNA (Qian et al., 1989; Kissinger et al., 1990; Otting et al., 1990; Wolberger et al., 1991). Homeodomain proteins are thought to act as transcriptional regulators that control the expression of specific target genes.

Amino acid sequence similarities within the homeodomain and flanking regions have been used to subdivide the large number of known homeodomain proteins into related classes or families, such as the Antennapedia (Antp), engrailed (en), and POU classes (Scott et al., 1989). Four novel classes of homeobox genes have been identified in several plant species, including maize (Vollbrecht et al., 1991; Bellman and Werr, 1992), rice (Matsuoka et al., 1993), soybean (Ma et al., 1994), parsley (Korfhage et al., 1994), and Arabidopsis (Ruberti et al., 1991; Mattson et al., 1992; Schena and Davis, 1992; Schena et al., 1993; Schindler et al., 1993; Korfhage et al., 1994; Rerie et al., 1994). Although there are dramatic differences in the developmental processes used by plants compared with animals, the discovery of plant homeobox genes suggests that some of the fundamental regulatory mechanisms that control development have been conserved between these two distinct groups of organisms.

Characterization of the maize homeobox gene, knotted1 (kn1), provided the first evidence that plant homeobox genes may function in specifying cell fate. The kn1 locus is defined by a series of dominant neomorphic mutations that disrupt leaf development, leading to the formation of finger-like outgrowths, or knots, on the leaf blade (Freeling and Hake, 1985; Vollbrecht et al., 1991; Hake, 1992). In Kn1 mutants, ectopic expression of the kn1 gene product in developing leaves has been correlated with the mutant phenotype. Although the role of the wild-type kn1 gene product is unknown, its expression pattern during vegetative and floral development in mutant and wild-type plants suggests that kn1 participates in the switch from indeterminate to determinate cell fates (Smith et al., 1992; Jackson et al., 1994). Overexpression of kn1 in transgenic tobacco plants causes leaf cells to take on alternate cell fates. The transgenic tobacco phenotypes range from abnormal leaf shapes to the formation of ectopic shoots on leaf surfaces (Sinha et al., 1993).

The kn1 homeobox sequence was used to isolate a family of maize homeobox genes that have been named knox, for knotted-like homeobox (Kerstetter et al., 1994). In addition to encoding homeodomains similar to those encoded by kn1, the knox gene products share a novel motif consisting of 24 amino acids adjacent to the N-terminal side of the homeodomain (Vollbrecht et al., 1991, 1993). The expression patterns of kn1 and three knox genes have been examined during vegetative development. In the shoot apex, the expression profiles of these maize homeobox genes appear to predict or define morphogenetic events such as leaf initiation (Jackson et al., 1994).

We are interested in elucidating the role of kn1 and related homeobox genes in plant development. Toward this goal, we have used the homeobox sequence of kn1 to isolate a family of related homeobox genes in Arabidopsis. The existence of knox homologs in Arabidopsis will permit further molecular and genetic analyses of this class of homeobox genes. In addition, sequence comparisons across species should help determine important functional domains within these genes. Finally, based on the expression pattern of kn1 and related genes in the shoot apex of maize, we anticipate that homologous genes will be useful markers for meristem organization in Arabidopsis. In this paper, we describe the isolation and characterization of two genes, KNAT1 and KNAT2 (for knotted-like from Arabidopsis thaliana) encoding KN1-like homeodomain proteins in Arabidopsis.

**Figure 1. Arabidopsis Genomic DNA Gel Blot Analysis.**

(A) Hybridization with the kn1 homeobox. Genomic DNA from the Columbia ecotype digested with either HindIII (H) or BglII (B) was hybridized with the kn1 sequence encoding the ELK and homeodomain under low-stringency conditions. DNA length markers are given at right in kilobases.

(B) Hybridization with KNAT1 cDNA. Genomic DNA from the Columbia ecotype digested with either EcoRI (E) or HindIII (H) was hybridized with the full-length KNAT1 cDNA at low stringency.

(C) Hybridization with the KNAT1 homeobox. The blot in (B) was stripped and reprobed with the KNAT1 homeobox sequence at low stringency.
RESULTS

Isolation of knl-like Genes from Arabidopsis

knl and related knox genes in maize encode a highly conserved block of 88 amino acids that begins with the ELK region (24 amino acids; named for invariant series of Glu, Leu, and Lys amino acids) and extends through the adjacent homeodomain (64 amino acids; Vollbrecht et al., 1993; Kerstetter et al., 1994). When an Arabidopsis genomic DNA gel blot was hybridized at reduced stringency with the knl sequence encoding this conserved extended homeodomain region, approximately six bands of different intensities were detected, as shown in Figure 1A, suggesting the presence of a family of knl-like genes. Using the same sequence as a probe, several different Arabidopsis cDNA libraries, made from either seedling, adult vegetative, or floral tissues, were screened. Independent cDNA clones were isolated and sequenced using degenerate oligonucleotide primers derived from the third helix of the knl homeobox. In this study, we have focused on the characterization of cDNAs and the corresponding genomic clones representing two different genes, KNAT1 and KNAT2.

The longest KNAT1 cDNA sequence, shown in Figure 2, contains a 1197-bp open reading frame encoding a polypeptide of 398 amino acids. The open reading frame present in the longest KNAT2 cDNA, shown in Figure 3, encodes a putative polypeptide of 310 amino acids. The predicted amino acid sequence of KNAT1 is compared with KN1 in Figure 4A. Overall, the two sequences share 53% amino acid identity. The highest identity is found within the 88 amino acids of the extended homeodomain region (the ELK region plus the homeodomain) located near the C terminus: the ELK regions are 87% identical, and the homeodomains are 89% identical. The homeodomain of KNAT2 is 80% identical to both KNAT1 and KN1 (Figure 4A). When the entire amino acid sequences are compared, the degree of identity between KNAT2 and either KN1 or KN1 drops to 74%-40%. The homeodomains of KNAT1 and KNAT2 contain the four invariant amino acids (WF-N-R), as well as identical residues or similar substitutions "recognition helix") of the homeodomain, 13 consecutive amino acids are completely conserved in all KN1-like proteins, including both KNAT1 and KNAT2.

The KNAT1, KNAT2, and KN1 amino acid sequences share several interesting features in addition to the conserved suggested acidic region is marked by asterisks. The homeodomain is indicated by a filled bar, and the putative nuclear localization sequence is marked by a dashed line. A putative polyadenylation signal is indicated by single underlining. Numerals at right indicate amino acid positions. Sequence data have been submitted to GenBank as accession numbers U14174 and U14175 for KNAT1 and KNAT2, respectively.

Figure 2. Nucleotide and Deduced Amino Acid Sequence of KNAT1.

The open triangle at the 5' end indicates the 5' end of the longest cDNA; the sequence upstream was derived from genomic clones. Hooked arrows indicate putative transcription start sites. Short open reading frames upstream of the translation start site are indicated by boldface type. The asparagine- and histidine-rich regions are double underlined. Sites for introns 1 to 4 are marked by filled triangles. The sequence is marked by a dashed line. A putative polyadenylation signal is indicated by single underlining. Numerals at right indicate amino acid positions. Sequence data have been submitted to GenBank as accession numbers U14174 and U14175 for KNAT1 and KNAT2, respectively.
homeodomain and ELK region. All three polypeptides contain a putative nuclear-targeting sequence located in the basic region preceding the first helix of the homeodomain (Figures 2 and 3; Raikhel, 1992; Varagona et al., 1992). Previous studies have shown that the KN1 protein is localized to maize nuclei (Smith et al., 1992). Immediately upstream of the ELK regions of KNAT1, KNAT2, and KN1, there is a cluster of negatively charged amino acids (Figures 2 and 3). Similar acidic domains are found in other classes of plant homeodomain proteins (Carabelli et al., 1993; Ma et al., 1994; Rerie et al., 1994). Acidic regions have been postulated to function as transcription activation domains (Ptashne and Gann, 1990; Frankel and Kim, 1991). Near the N terminus of KNAT1, there are four short regions rich in asparagine (Figure 2). A polyhistidine block is present near the N terminus of KN1 (Vollbrecht et al., 1991);
the KNAT1 amino acid sequence contains a much shorter stretch of histidines (Figure 2). Amino acid homopolymers are found in the protein-coding regions of many genes that have important developmental roles (Laughon et al., 1985; Wharton et al., 1988). Asparagine-rich sequences occur in several transcription factors of various types, including homeodomain proteins, although their function is not known (Smoller et al., 1990; Mevel-Ninio et al., 1991). Recent evidence suggests that polyglutamine and polyproline stretches may be involved in transcriptional activation (Gerber et al., 1994).

In contrast to kn1, there are two short open reading frames in the 5' untranslated sequence of KNAT1 (Figure 2). Similar short open reading frames have been identified in the leader sequences of Athb-1 and Athb-2, both members of the homeodomain zipper family of genes in Arabidopsis (Ruberti et al., 1991; Carabelli et al., 1993) and sbh1, a kn1-like homeobox gene in soybean (Ma et al., 1994). The function of such leader peptides is not clear, but they may play a role in translational regulation, as demonstrated for Gcn4 expression in yeast (Hinnebusch, 1988) and opaque2 in maize (Lohmer et al., 1993).

Genomic clones corresponding to KNAT1 and KNAT2 were isolated from a λ DNA library, and exons were defined by comparing genomic and cDNA sequences. The genomic organization of both genes is shown in Figure 4B. All intron-exon junctions conform to consensus splice sites for plant introns (Brown, 1986). Although intron sizes differ greatly (Figure 4B), the positions of introns 1, 2, and 4 in both KNAT genes are almost identical to those in kn1 (Vollbrecht et al., 1991). These introns are in regions well conserved among KNAT1, KNAT2, and KN1 (Figure 4A). Intron 3 is in a less conserved region, and the intron position is more variable. The homeoboxes of KNAT1 and KNAT2 are interrupted by the fourth intron, which is located between helix 1 and helix 2 of the homeodomain. The position of this intron is conserved in kn1 and all of the isolated knox genes (Kerstetter et al., 1994).

High-stringency hybridization of a 5' noncoding portion of KNAT1 or KNAT2 to a gel blot containing Arabidopsis DNA digested with several enzymes detected one or two bands characteristic of single-copy genes (data not shown). Hybridization of the entire KNAT1 cDNA under low-stringency conditions detected a large number of bands (Figure 1B). This result is presumably due to the repetitive nature of the 5' coding region of KNAT1, because the homeobox sequence alone detected many fewer bands with low-stringency hybridization (Figure 1C). Based on the results of DNA gel blot hybridizations (Figure 1A) and characterization of clones identified in cDNA library screens (C. Lincoln and K. Serikawa, unpublished data), KNAT1 and KNAT2 appear to be members of a relatively small family of kn1-like genes in Arabidopsis.

The chromosomal locations of KNAT1 and KNAT2 were identified by determining the segregation of restriction fragment length polymorphisms, specific for each gene, among recombinant inbred lines. The KNAT1 gene maps to chromosome 5 at an approximately equal distance from markers m291 and r355.2 (Reiter et al., 1992). The KNAT2 gene maps to chromosome 1 between markers g4552 and m532 (Lister and Dean, 1993). At the time of publication, no mutant phenotypes had been mapped to the position of either KNAT1 or KNAT2.

Analysis of KNAT Gene Expression

Expression of KNAT1 and KNAT2 was examined using RNA blot analysis of poly(A)+-enriched RNA isolated from various Arabidopsis tissues. To avoid cross-hybridization of probes to related mRNAs, gene-specific probes were used and hybridizations were performed at high stringency. Figure 5A shows that two KNAT1 transcripts are detected in mRNAs isolated from flowers, inflorescence stems, and light- and dark-grown seedlings. In these tissues, the abundance of the two transcripts relative to one another did not vary significantly. Expression of both the large (~1.9 kb) and small (~1.6 kb) transcripts was highest in floral stem tissue. The level of KNAT1 expression was higher in dark-grown seedlings compared with light-grown seedlings. In situ hybridization experiments (see following discussion) have shown that the KNAT1 transcript is localized primarily to the shoot apex of young, light-grown seedlings. The tissue localization of expression in dark-grown seedlings was not determined. As shown in Figure 5A, KNAT1 expression was not detected in leaves, roots, or silique.

**Figure 5.** Analysis of KNAT1 and KNAT2 Expression in Different Organs of Arabidopsis.

(A) RNA gel blot analysis of KNAT1 expression. RNA was isolated from flowers (F) of all stages, inflorescence stems (ST), rosette leaves (L), roots (R), light-grown seedlings (LS), dark-grown seedlings (DS), and siliques (SI) of all stages. Two micrograms of poly(A)+ RNA was loaded per lane. The blot was hybridized with a 5'-specific probe of KNAT1.

(B) RNA gel blot analysis of KNAT2 expression. The blot in (A) was reprobed with a 5'-specific probe of KNAT2.

(C) Control hybridization. The same blot was reprobed with the constitutively expressed cytosolic cyclophilin gene ROC1 (Lippuner et al., 1994) to show the relative quantity of RNA in each lane. The approximate length of each transcript is shown at right in (A) and (B).
KnAT1 expression was concentrated in the peripheral and rib zones of the apical meristem; however, high levels of transcript were also seen immediately below the meristem in the subapical region of the shoot apex, where shoot widening takes place (Wardlaw, 1957). Expression extended to the base of developing leaf primordia and was detected in cells adjacent to the differentiating vascular tissue of the stem (Figures 6C and 6D). The expression pattern shown in Figure 6C is similar to that observed in younger plants grown under long-day conditions (Figures 6A and 6B). There was no detectable message in young leaf primordia, older leaves, or stipules. Occasionally, faint, patchy staining was observed in leaves (Figures 6C and 6D). We have interpreted this staining as nonspecific because similar staining was observed with the sense control probe, and our RNA gel blot results as well as the majority of antisense in situ hybridizations did not detect any KnAT1 RNA in leaves. Serial sections through the shoot apex of plants grown under short-day conditions revealed discrete areas or groups of cells on the flanks of the apical meristem where there was an absence of KnAT1 expression (Figures 6E and 6F, higher magnification). This absence of KnAT1 expression may correlate with leaf initiation sites. Control sections probed for 18S rRNA transcripts showed uniform signal throughout all tissues, indicating that the absence of KnAT1 expression in some cells was not due to altered RNA retention or accessibility (data not shown).

The expression of KnAT1 mRNA was also examined during the floral transition and the following stages of inflorescence and floral development. After floral induction in Arabidopsis, the shoot apical meristem enters the reproductive growth phase. We will use the term "inflorescence meristem" to refer to a shoot apical meristem that has undergone the floral transition. The primary inflorescence meristem of an indeterminate plant, such as Arabidopsis, gives rise to determinate floral meristems. Lateral, secondary inflorescences (paracles), which are subtended by cauline (bract) leaves, arise as a result of a basipetal activation of buds (Hempel and Feldman, 1994). The growth pattern of the paracles is essentially identical to the pattern exhibited by the primary inflorescence. After the development of several flowers and paracles, rapid internode elongation (or bolting) occurs along the primary inflorescence axis (Bowman, 1994).

To investigate the pattern of KnAT1 expression in the shoot apex during the transition to flowering, 16-hr photoperiods were used to synchronously induce flowering in plants grown for ~30 days in noninductive 8-hr photoperiods (see Methods). Shoot apices were harvested and fixed after different lengths of time following the start of the inductive photoperiod. As shown in Figure 7, the distribution of KnAT1 transcripts in the shoot apex is altered following floral induction. At hour 16 postinduction, KnAT1 expression was still concentrated in the peripheral zone of the meristem; lower levels of mRNA were detected in the subapical region of the shoot apex, at the base of leaf primordia, and in cells adjacent to developing vascular tissue in the stem (Figure 7A). A late-transition-stage apex, characterized by expansion of the rib meristem and doming
Figure 6. KNAT7 Expression in the Vegetative Shoot Apex.

Longitudinal sections were hybridized to digoxigenin-labeled antisense probes.

(A) and (B) Serial sections (8 μm thick) through 6-day-old seedlings grown in 16 hr of light. Bar in (B) = 100 μm.

(C) and (D) Serial sections (8 μm thick) through the shoot apex of an ~23-day-old plant grown in 8 hr of light. Bar in (D) = 100 μm.

(E) and (F) Higher magnifications of sections shown in (C) and (D), respectively. Bar in (F) = 30 μm.

In (F), the arrow indicates a group of cells that are not expressing KNAT7. These cells may correlate with a site of leaf initiation. cz, central zone; h, hypocotyl; lp, leaf primordium; m, meristem; pz, peripheral zone; rz, rib zone; s, stipule; sr, subapical region; v, vascular tissue.
Figure 7. Distribution of KNAT1 mRNA in the Shoot Apex during Transition-to-Flowering Stages.

All sections are longitudinal and median or close to median and were hybridized to digoxigenin-labeled antisense probes. Plant growth conditions and stages are as described by Hempel and Feldman (1994); hours indicate time points after an inductive 16-hr photoperiod (hour 0 is the time point midway [8 hr] through the first inductive time period).

(A) Hour 16 after floral induction.
(B) Hour 40 after floral induction.
(C) Hour 64 after floral induction.
(D) Hour 88 after floral induction.
(E) Hour 136 after floral induction.
(F) Higher magnification of the inflorescence and floral meristem shown in (E).

In (A) to (E), bars = 100 μm. In (F), bar = 30 μm.

c, cortex; cl, cauline leaf; fm, floral meristem; fp, floral primordium; im, inflorescence meristem; lp, leaf primordium; p, paraclade; pi, pith; pv, provascular trace.
of the apex, is shown in Figure 7B. At this stage, \textit{KNAT1} expression became restricted to the lower portion of the apex; there was no detectable message in the inflorescence meristem. Expression continued at the base of developing leaves, but was excluded from provascular strands associated with the shoot apex. By hour 64, elongation of the inflorescence axis was beginning to occur (Figure 7C). By hour 88, floral primordia could be seen (Figure 7D). At these stages, \textit{KNAT1} expression was confined mainly to the outer cell layers or cortex of the primary inflorescence stem. A low level of expression could be seen at the base of the inflorescence meristem and, depending on the plane of the section, in cells encircling the base of the floral primordia (Figure 7D). The \textit{KNAT1} transcript was absent from the pith and from the base of leaf primordia associated with developing paraclades (Figures 7C to 7E). As elongation of the primary inflorescence axis proceeded, the \textit{KNAT1} message became restricted to the cortical cell layers adjacent to the developing vascular tissue of the stem (Figures 7E and 7F). As shown in Figure 7F, expression extends into the cortex of the developing pedicel and paraclade, but stops abruptly at the base of the flower and lateral inflorescence meristems.

The pattern of \textit{KNAT1} expression in the inflorescence remained constant throughout flowering (compare Figures 7E and 8A). The \textit{KNAT1} message was localized primarily to the inner layers of the cortex along the length of the primary inflorescence stem and in the elongating stems of paraclades (Figures 8A to 8C). The \textit{KNAT1} message was not detected in cauline (bract) leaves (Figure 8C). The \textit{KNAT1} transcript was absent from the outer three whorls (sepals, petals, and stamens) of floral organs at all stages of development (Figures 8A and 8D) (for a description of stages, see Smyth et al., 1990). However, \textit{KNAT1} mRNA was detected in the fourth floral whorl in the region that will become the style. Expression was first seen at stage 8 and continued until stage 12. In the style, a ring of expression occurred in cells surrounding the transmitting tissue (Figure 8D). For all in situ hybridization experiments performed on inflorescence and floral tissues, control sections hybridized with a sense probe showed no signal above background (data not shown).

To investigate the pattern of \textit{KNAT1} expression during embryogenesis, in situ hybridization experiments were performed using longitudinal sections of embryos at the early-heart, late-
heart, linear-cotyledon, and curled-cotyledon stages (West and Harada, 1993). A hybridization signal above background was not detected in embryos at any of these stages, indicating that KNAT1 mRNA is either not detectable owing to low abundance or not present during mid to late embryo development (data not shown).

**Altered KNAT1 Expression Affects Arabidopsis Development**

The KNAT1 coding sequence was transcriptionally fused to the constitutive 35S promoter from cauliflower mosaic virus (CaMV), and the 35S–KNAT1 expression construct was transformed into Arabidopsis. The CaMV 35S promoter is active in most cell types, although the level of activity is variable in different tissues (Benfey and Chua, 1990). Only five independent 35S–KNAT1 transgenic lines were recovered and characterized owing to a low regeneration frequency and a reduction in the fertility of T1 plants. The T2 generation for all five lines was characterized with respect to differences in phenotype.

Two of the five transformed lines exhibited extreme alterations in morphology; one line had less severe morphological defects, whereas later adult leaves are larger, spatulate, and serrate whereas earlier adult leaves are smaller, more ovate, and serrate (Bowman, 1994). In the class of KNAT7 transformants with the most extreme phenotype, the first two leaves were normal in appearance but the two KNAT7 transcripts seen in flowers, inflorescences, and vegetative shoot apices of wild-type plants (Figure 5A), a single transcript of ~1.6 kb in leaves of transgenic plants was expected based on the length of the KNAT7 cDNA insert used in preparing the 35S–KNAT7 construct (see Methods). No hybridization was seen in RNA isolated from a transgenic line (line C38), which was normal with respect to leaf phenotype (Figure 10A, lane 3). The results of DNA gel blot analysis suggested that the 35S–KNAT7 insertion in line C38 has undergone some type of rearrangement (data not shown).

**Expression of the Maize kn1 Gene Product in Arabidopsis**

We were interested in determining whether expression of the kn1 gene product in Arabidopsis would result in phenotypes similar to those of 3SS–kn1 transgenic tobacco plants (Sinha et al., 1993) and how these phenotypes would compare with Arabidopsis plants transformed with the 3SS–KNAT7 construct. A 3SS–kn1 chimeric gene was introduced into Arabidopsis, and the resulting transgenic plants were examined for phenotypic alterations. A total of 11 independent T1 lines were obtained. The T2 progeny from all lines was examined for changes in plant morphology. Four T2 lines had highly abnormal morphological phenotypes, whereas the remaining seven lines were less severely affected or normal in phenotype. The phenotype of the most severely affected class of kn1 transformants resembled the phenotype of the 3SS–KNAT7 transformants in several ways: rosette and cauline leaves were curled, wrinkled, and/or mildly to deeply lobed (Figure 9D), and the size and shape of floral organs, particularly petals and stamens, were reduced or abnormal (data not shown).

To determine the relative levels of kn1 expression in the 3SS–kn1 transformants, RNA was isolated from mature rosette leaves of T2 plants with either severe or normal phenotypes. In leaves from three different T2 lines that displayed mild to severe leaf phenotypes, a 1.6-kb transcript was detected on RNA gel blots hybridized with a kn1 probe (Figure 10B, lanes 3, 4, and 5). No signal was detected in RNA extracted from a transformed line that had normal leaves (Figure 10B, lane 2) or from wild-type plants (Figure 10B, lane 1).
DISCUSSION

**KNAT1 and KNAT2 Are Members of a Large Family of kn1-like Homeobox Genes**

In this report, we describe the characterization of two genes, *KNAT1* and *KNAT2*, encoding KN1-like homeodomain proteins in Arabidopsis. *KNAT1* and *KNAT2* are members of a large family of kn1-like genes that have been identified in several plant species including maize (Vollbrecht et al., 1991), rice (Matsuoka et al., 1993), tomato (N. Sinha and S. Hake, unpublished data), sunflower (D. Jackson and S. Hake, unpublished data), and soybean (Ma et al., 1994). Within the homeodomain, the KNAT1 and KNAT2 proteins share several characteristic features with other members of the KN1-like family. Both predicted proteins have an invariant core sequence of 13 amino acids in the third or recognition helix, a conserved intron position in the second helix, and a three-amino acid insertion between the first and second helices of the homeodomain. Immediately adjacent to the homeodomain of KNAT1 and KNAT2, a series of 24 amino acids that contains repeating hydrophobic residues (the ELK domain) is also conserved. This novel motif is present in all KN1-like proteins that have been identified. The conserved features present in the extended homeodomain regions of KNAT1, KNAT2, and other KN1-like proteins distinguish their
respective genes from other types of homeobox genes reported in plants (Bellmann and Werr, 1992; Mattsson et al., 1992; Schindler et al., 1993; Schena et al., 1993; Schindler et al., 1993; Korfhage et al., 1994; Rerie et al., 1994).

The kn1-like gene family in maize (knox genes) consists of approximately 12 genes that have been subdivided into two classes based on sequence similarity within the homeodomain (Kerstetter et al., 1994). Class 1 knox genes are more similar to kn1 (73 to 89% identity in the homeodomain) compared with class 2 genes (55 to 58% identity with the KN1 homeodomain). Based on genetic evidence, two class 1 knox genes correspond to the dominant morphological mutations Rough sheath1 (Rsl1) and Liguleless3 (Lgs3) (P. Becraft, J. Fowler, and M. Freeling, personal communication). Both mutants are phenotypically similar to kn1 (Freeling, 1992). The extended homeodomain regions of KNAT1 and KNAT2 share a high degree of identity with class 1 knox genes. Within this class, the KNAT1 homeodomain is more similar to the homeodomain encoded by the knox gene rsl1 (95% identity) than it is to the KN1 homeodomain (89% identity). An alignment of the complete amino acid sequences of KNAT1 and RSL1 reveals that these two predicted proteins share an overall identity of \( \sim 61\% \), which is slightly higher than the sequence identity between KNAT1 and KN1 (\( \sim 53\% \)). The intron–exon structure of KNAT1 is almost identical to both that of kn1 and rsl1 (P. Becraft, R. Schneeberger, S. Hake, and M. Freeling, manuscript submitted). Based on shared amino acid substitutions within the homeodomain, KNAT2 appears to be more closely related to the class 1 genes knox5, knox11, and lg3. Outside the extended homeodomain–encoding region of each KNAT gene, sequence homology is less well conserved. The 5' coding regions of KNAT1 and KNAT2 differ significantly from those of kn1, rsl1, and several other class 1 knox genes. Three kn1-like Arabidopsis genes (KNAT3, KNAT4, and KNAT5), which are more similar to class 2 knox genes, have also been identified (K. Serikawa and P. Zambrayski, unpublished data).

Figure 10. Expression of KNAT1 and kn1 Transcripts in Arabidopsis Transformed with 35S–KNAT1 or 35S–kn1 Constructs.

(A) RNA gel blot analysis of KNAT1 transgenic lines. Total RNA was isolated from inflorescence tissue (lane 1) or rosette leaves (lanes 2 to 5) from the wild type (wt; lanes 1 and 2) and the independent 35S–KNAT1 transgenic line C38 (lane 3), line E17 (lane 4), and line B6 (lane 5). Eight micrograms of RNA was loaded per lane. The blot was probed with a 5' portion of the KNAT1 cDNA.

(B) RNA gel blot analysis of kn1 transgenic lines. Total RNA was isolated from rosette leaves of the wild type (wt; lane 1) and the independent 35S–kn1 transgenic line J15 (lane 2), line J3-2 (lane 3), line J1-29 (lane 4), and line J2-25 (lane 5). Ten micrograms of RNA was loaded per lane. The blot was probed with the kn1 homebox.

(C) Control hybridization. The blot in (A) was reprobed with ROC1 (Lippuner et al., 1994) to show relative RNA loading.

(D) Control hybridization. The blot in (B) was reprobed with ROC1 to show relative loading.

KNAT1 and the Maize Class 1 knox Genes Have Similar Vegetative Expression Patterns

KNAT1 and KNAT2 are expressed in several different tissues during vegetative and reproductive phases of growth. During vegetative development, the expression pattern of KNAT1 in Arabidopsis closely resembles the expression patterns of several class 1 knox genes in maize. Based on RNA gel blot analysis, the class 1 genes kn1, rsl1, knox3, knox4, and knox8 are all strongly expressed in shoot meristem–enriched tissues, but are not detected in leaves (Kerstetter et al., 1994). In situ hybridization has shown that kn1, rsl1, knox3, and knox8 are expressed in the unexpanded stem and exhibit distinct, but overlapping domains of expression in the shoot apical meristem (Jackson et al., 1994). In the vegetative shoot apex of Arabidopsis, KNAT1 expression was seen in the meristem and in a region just proximal to the meristem that extends to the base of several newly initiated leaf primordia. In shoot meristems of plants grown under short-day conditions, the KNAT1 message was reduced or absent in discrete groups of cells located on the flanks of the meristem. No expression was detected in leaf primordia, even at very early stages of primordium formation. KNAT1 transcript was also present in the unexpanded stem of the rosette, where it appeared in cells flanking but not within provascular traces. Within the vegetative meristem, KNAT1 message was more abundant in the peripheral and rib zones than in the central zone. In this respect, KNAT1 is more similar to rsl1 and knox3, which both show more restricted patterns of expression in the maize shoot meristem (Jackson et al., 1994).

Although it is difficult to make direct comparisons between the expression patterns of KNAT1 in Arabidopsis and those of class 1 knox genes in maize, there are two significant features of the expression patterns that appear to be conserved. The Arabidopsis and class 1 maize genes are all expressed in the vegetative meristem, and each gene is selectively downregulated at the same time as or immediately prior to leaf primordium initiation. Predicting the location of incipient leaf primordia is easier in longitudinal sections of the maize shoot meristem than in Arabidopsis because the phyllotaxy is dichotous and the approximate number of leaf founder cells has
Loss of KNAT1 Meristem Expression Coincides with Floral Induction

In contrast to the similar vegetative expression patterns seen with KNAT1 and the class 1 knox genes, the distribution of KNAT1 transcript in the inflorescence differs significantly. In the inflorescence, KNAT1 expression is limited to specific cells within the cortex of the stem. This ring of KNAT1 expression is located immediately adjacent to the vascular cylinder. KNAT1 is absent from all floral organ primordia, but is present in the style. The function of KNAT1 in these apparently distinct cell types is not clear: kn1, rs1, knox3, and knox8 are expressed at high levels throughout the corpus of the inflorescence and floral meristem. These genes are not expressed in any lateral organs and disappear before the organs form (Jackson et al., 1994). Thus, KNAT1 is similar in its exclusion from cauline leaves, petals, sepals, and anthers but differs from the maize genes in its absence from both inflorescence and floral meristems. The similarity in the expression patterns of KNAT1 and several class 1 knox genes in the vegetative shoot meristem suggests that these genes play similar roles during vegetative development and that this function has been conserved. However, the function(s) of KNAT1 and the maize knox genes may be quite distinct during floral development.

Expression of KNAT1 in the meristem disappears at the same time the shoot apex undergoes the transition from vegetative to reproductive development. In angiosperms, this transition is a critical developmental event. Consequently, floral induction is regulated by a number of different developmental and environmental signals, including plant age, photoperiod, and temperature (reviewed in Bernier et al., 1994). The vegetative-to-inflorescence transition is characterized by changes in meristem structure, cellular metabolism, and gene expression (Bernier et al., 1981; Meeks-Wagner, 1994). Genes that display a modified pattern of expression during this transition may play an important role in specifying the developmental programs unique to either vegetative or inflorescence meristems. Arabidopsis mutants, such as embryonic flower (emf), that are disrupted in the transition from vegetative to reproductive development have been identified (Sung et al., 1992). emf mutant embryos flower precociously, producing inflorescence shoots directly upon germination. Based on the mutant phenotype conferred by emf, Sung et al. (1992) proposed that reproductive development is the basal or default state of the shoot apex in Arabidopsis and that negative regulation of the reproductive program is necessary for normal vegetative development to occur. Perhaps KNAT1 functions with EMF, or is regulated by EMF, to maintain the vegetative state of the shoot meristem.

In the early floral meristem (flower primordia at stages 1 and 2), the expression pattern of KNAT1 is the reciprocal of the pattern exhibited by the floral meristem identity gene LEAFY (LFY) and the floral organ identity genes APETALA1 (AP1) and AP2 (Mandel et al., 1992; Weigel and Meyerowitz, 1993; Jofuku et al., 1994). KNAT1 expression in flower primordia at stage 2 occurs in the developing pedicel; the region of expression extends...
up to and includes cells immediately below the rib meristem. In young flower primordia, LFY, AP1, and AP2 transcripts are present throughout the meristem, but expression stops at the base of the primordia where KNAT1 expression begins. It is possible that regulatory interactions between KNAT1 and LFY, AP1, and/or AP2 dictate these expression patterns.

**Ectopic KNAT1 Expression Alters Leaf Development in Arabidopsis**

To gain further insight into the possible function of KNAT1, we transformed Arabidopsis plants with a construct containing the KNAT1 cDNA under the control of the CaMV 35S promoter. Disruption of the concentration, timing, and/or tissue specificity of KNAT1 expression altered the morphology of both leaves and flowers. In the most severe cases, ectopic expression of KNAT1 in leaves dramatically altered leaf shape, resulting in highly lobed leaves instead of the characteristic entire leaf shape of wild-type plants. A similar leaf phenotype was observed in Arabidopsis plants overexpressing the maize kn7 gene. Similarities can be drawn between the transformants and the mutant phenotypes conferred by Kn1 and Rst in maize, which result from ectopic expression in leaves. Leaf blade cells of these maize mutants adopt cell fates normally restricted to the sheath or basal portion of the leaf (Freeling, 1992; Becraft and Freeling, 1994; Sinha and Hake, 1994). In at least one 35S–KNAT1 transformant, lobed leaves contained ectopic stipules, which are also normally positioned at the basal region of the leaf (G. Chuck and S. Hake, unpublished data).

Tobacco plants transformed with a 35S–KN1 construct display ectopic formation of shoots on leaf surfaces in addition to leaf lobing (Sinha et al., 1993). Ectopic shoot formation has not been observed in Arabidopsis plants constitutively expressing KNAT1 or kn7. However, tobacco plants transformed with the 35S–KNAT1 construct have severe alterations in leaf morphology, including leaf lobing and ectopic shoot formation (J. Long, unpublished data). The parallel phenotypes produced by overexpressing KNAT1 and kn7 in Arabidopsis and tobacco suggest that these two genes are capable of regulating similar sets of downstream genes. It will be interesting to see whether other class 1 maize genes induce morphological transformations similar to those induced by kn7 in Arabidopsis or tobacco. Formation of ectopic shoots on leaf blades in tobacco KNAT1 and kn7 transformants supports the hypothesis that class 1 genes are involved in maintaining cells in an undifferentiated, meristematic state. In the transformants, continuous expression of KNAT1 or kn7 may disrupt the normal differentiation processes occurring in developing leaves such that groups of leaf cells acquire characteristics of apical meristems.

To understand how misexpression of KNAT1 in the 35S–KNAT1 transformants results in abnormal leaf morphology, it will be important to determine when during leaf development differences in leaf shape become apparent. The Arabidopsis transformant phenotypes suggest that changes in leaf shape occur later, after leaf primordia have formed. Ectopic expression of KNAT1 in developing leaves may alter growth patterns or the timing of cell differentiation within the leaf blade. In wild-type plants, young developing leaves are composed largely of rapidly dividing, undifferentiated cells. Differentiation of mesophyll cells and cessation of mitotic activity begin at the leaf tip and proceed toward the base. Older leaves retain a zone of mitotic cells in the lower portion of the leaf (Pyke et al., 1991). The presence of the KNAT1 gene product in developing leaves where the gene is not normally expressed may directly or indirectly alter the pattern of differentiation or interfere with cell division control. Localized areas of restricted or unchecked growth could produce lobing and puckering of leaf blades.

Based on sequence comparison and expression patterns, KNAT1 and KNAT2 belong to a subfamily of knl-like homeobox genes (designated class 1) that appear to play a role in shoot meristem organization. It is difficult to identify specific maize homologs for KNAT1 and KNAT2 on the basis of sequence similarities because they are similar to a number of maize class 1 genes. In addition, the vegetative expression pattern of KNAT1 resembles that of more than one class 1 knox gene. Ectopic expression of KNAT1 disrupts normal leaf development and may cause alterations in the patterns of leaf cell differentiation consistent with models for class 1 knox gene action in maize. Although KNAT1 and kn7 produce similar phenotypes when overexpressed in transgenic plants, this result does not necessarily imply that these two genes are functionally homologous. Identification of loss-of-function phenotypes corresponding to each of the maize class 1 genes should help elucidate the role of individual genes during development. In Arabidopsis, an antisense approach is being used to generate loss-of-function phenotypes for KNAT1 and KNAT2 and, when compared with similar phenotypes in maize, may help resolve the question of class 1 gene homology in these two plant species. Many important questions regarding the function of KNAT1 and related genes in Arabidopsis remain to be answered. For example, how is KNAT1 expression regulated in the shoot meristem and what downstream genes are targets for KNAT1? The striking leaf phenotypes observed in 35S–KNAT1 transformants can now be used to isolate suppressor mutations that may identify interacting genes.

**METHODS**

**Plant Growth Conditions**

Arabidopsis thaliana (Columbia ecotype unless stated otherwise) seedlings were grown in vitro on germination medium (Murashige and Skoog salts and vitamins supplemented with 10 g/L sucrose and 0.8% agar; Murashige and Skoog, 1962; Valvekens et al., 1988) under a 16-hr photoperiod (16-hr light/8-hr dark) or in total darkness at 22°C. Using green safelights, dark-grown seedlings were harvested and frozen in liquid nitrogen. Roots were harvested from 3- to 4-week-old plants grown in liquid germination medium that was constantly agitated. For collection
of leaves, stems, flowers, and siliques, plants were grown in the greenhouse under continuous illumination at 21°C day/18°C night. To delay initiation of floral primordia, plants were grown in 8-hr photoperiods (8-hr light/16-hr dark) at 22°C. After 23 to 27 days of growth in 8-hr photoperiods, flowering was induced by successive 16-hr photoperiods. These conditions result in the rapid and synchronous initiation of flower formation in Arabidopsis populations (Hempel and Feldman, 1994).

Screening of cDNA and Genomic Libraries

KNAT7 and KNAT2 (knotted-like from Arabidopsis thaliana) cDNA clones were initially obtained by screening a λZAPII (Stratagene) cDNA library constructed with poly(A)+ RNA from 2-week-old plants of the Wassilewskija ecotype. The probe used to screen the cDNA library was a fragment of the maize knotted1 (knl) gene extending from the sequence encoding the ELK region to the end of the homeodomain (Vollbrecht et al., 1991, 1993). Low-stringency conditions for plaque hybridization (9 x SSC [1 x SSC is 0.15 M NaCl, 0.015 M sodium citrate], 57°C) and washes (1 x SSC, 57°C) were used. Longer cDNA clones were isolated by screening a λZAPII library prepared from seedling (ecotype Columbus) poly(A)+ RNA and a hgtlO library prepared from RNA isolated from floral tissues (ecotype Landsberg). The seedling cDNA library was a gift from J. Ecker (University of Pennsylvania, Philadelphia, PA); the floral library was a gift from M. Meyerowitz (California Institute of Technology, Pasadena, CA). The probes used to screen the cDNA library were 5' fragments of the previously identified KNAT7 and KNAT2 cDNA clones. Probes were labeled with α-32P-dCTP using a Multiprime Labeling kit (Amersham). High-stringency hybridizations were performed at 55°C in a hybridization buffer containing 1% BSA, 2 mM EDTA, 0.5 M NaHPO4, pH 7.2, and 7% SDS (Church and Gilbert, 1984). Filters were washed in 0.2 x SSC, 0.2% SDS at 68°C. Low-stringency hybridizations were performed at 55°C in a hybridization buffer containing 1% BSA, 2 mM EDTA, 0.5 M NaHPO4, pH 7.2, and 7% SDS (Church and Gilbert, 1984). Filters were washed in 1 mM EDTA, 0.1 M NaHPO4, 5% SDS at room temperature and exposed to film. Additional washes at higher temperatures were performed if necessary.

DNA Sequence Analysis

Dideoxy sequencing of cDNA and genomic clones was performed using a Sequenase kit, Version 2.0 (United States Biochemical), and specific oligonucleotide primers. Degenerate primers derived from the knl homeobox sequence have been described by Kerstetter et al. (1994). Double-stranded DNA was used as a template and sequenced in both directions with the exception of intron sequences, which were sequenced only in one direction. Analysis of DNA and amino acid sequences was performed using the IG Molecular Biology Software System Release 5.4 (IntelliGenetics, Inc., Mountain View, CA) and National Center for Biotechnology Information BLAST E-MAIL server.

RNase Protection Analysis

The 5' ends of the KNAT1 and KNAT2 transcripts were determined using the Ambion (Austin, TX) RPAI1 RNase protection kit according to the manufacturer’s instructions. For KNAT1, 450-bp and 578-bp genomic fragments were subcloned into plasmids in vitro. The resulting probe was hybridized to total RNA and digested with RNase, and the size of the protected product was determined on a 6% sequencing gel. For KNAT2, the same procedure was followed except a 244-bp genomic fragment was used.

DNA Gel Blot Analysis

DNA was isolated from leaf or seedling tissue using the procedure of Dellaporta et al. (1983). Restriction digests of ~3 μg of DNA were performed, and the resulting fragments were separated in a 1% agarose gel and blotted onto a Magna nylon transfer membrane (Micron Separations, Inc., Westboro, MA). High-stringency hybridizations were performed at 68°C in a solution containing 7% SDS and 0.25 M NaH2PO4 (Robbins Scientific Co., Sunnyvale, CA). Filters were washed in 0.2 x SSC, 0.2% SDS at 68°C. Low-stringency hybridizations were performed at 55°C in a hybridization buffer containing 1% BSA, 2 mM EDTA, 0.5 M NaHPO4, pH 7.2, and 7% SDS (Church and Gilbert, 1984). Filters were washed in 1 mM EDTA, 0.1 M NaHPO4, 5% SDS at room temperature and exposed to film. Additional washes at higher temperatures were performed if necessary.

RNA Gel Blot Analysis

Total RNA from different tissues was isolated using a modified phenol–SDS method (Timpte et al., 1994). Poly(A)+ RNA was isolated using a Poly-A-Tract mRNA isolation kit (Promega). RNA was glyoxalated, size fractionated in a 1% agarose gel, and transferred to a Magna nylon transfer membrane as previously described (Sambrook et al., 1989). Hybridization was performed at 42°C in a solution containing 50% formamide, 5 x SSPE (1 x SSPE is 0.15 M NaCl, 10 mM sodium phosphate, 1 mM EDTA, pH 7.4), 5 x Denhardt’s solution (1 x Denhardt’s solution is 0.02% Ficoll, 0.02% polyvinylpyrroloidine, 0.02% BSA), 2% SDS, and 1 mg/mL denatured salmon sperm DNA. Filters were first washed in 1 x SSPE, 0.5% SDS at 68°C. The random primer–labeled KNAT7 probe contained the 5' noncoding sequence and ~150 bp of the first exon. The 5' KNAT2 probe contained sequence from exons 1, 2, and 3. The cytosolic cyclophilin gene ROC7 was used as a loading control (Lippuner et al., 1994).

In Situ Hybridization

Antisense and sense transcripts for KNAT1 clones were synthesized and labeled in vitro with digoxigenin-11-UTP (Boehringer Mannheim) using T7 or T3 polymerase. In vitro transcription reactions were performed following the manufacturer's protocol, except the ratio of labeled to unlabeled UTP was 1:1. The cDNA clones used were a 1.4-kb cDNA containing the homeobox but lacking the 3' portion of KNAT7 and a subclone containing a 700-bp XbaI fragment from the 5' portion of KNAT1 lacking the homeobox. Both probes gave identical results. Riboprobe purification, hydrolysis, and quantification were performed as described in the Boehringer Mannheim Genius System user's guide.

Tissue sections were fixed in 4% formaldehyde overnight at 4°C (Jackson, 1991). The fixed tissue was passed through an ethanol series and Histoclear (National Diagnostics, Atlanta, GA) before being embedded in ParaplastPlus (Fisher Scientific, Pittsburgh, PA). Tissue sections (8 μm thick) were mounted on ProbeOnPlus slides (Fisher Scientific). Section pretreatment and hybridization were performed according to Jackson (1991) with the following modifications: (1) immediately prior to protease treatment, slides were placed in 0.2 M HCl for 20 min, rinsed in H2O, and then incubated in 2 x SSC for 20 min followed by another H2O rinse; (2) for the protease treatment, 1 mg/mL proteinase K (Sigma) was used and slides were incubated for 30 min at 37°C; (3) riboprobes were used at a concentration of ~0.5 ng/μL per kb probe complexity. After hybridization, slides were washed
twice at high stringency (0.2 x SSC, 55°C) followed by two rinses in NTE (0.5 M NaCl, 10 mM Tris-HCl, pH 7.5, 1 mM EDTA) at 37°C. The slides were incubated at 37°C in NTE containing 20 mg/mL RNase A for 30 min followed by several rinses in NTE and a final wash in 0.2 x SSC at 55°C. Blocking steps and detection of hybridized transcripts using anti-digoxigenin antisera conjugated to alkaline phosphatase (Boehringer Mannheim) were performed as described by Coen et al. (1990). Sections were passed through an ethanol series and Histoclear before mounting in Merckcglas (EM Science, Cherry Hill, NJ).

Arabidopsis Transformation

Construction of 35S-kn7, which contains the maize kn7 cDNA inserted between the cauliflower mosaic virus (CaMV) 35S promoter and the terminator region of the nopaline synthase gene (NOS), has been previously described (Sinha et al., 1993). A 35S-KNAT7 expression construct was prepared by replacing the kn7 sequence in the 35S-kn7 plasmid with the coding region of KNAT7. Because a full-length cDNA clone was not available when the 35S-KNAT7 construct was made, 5' and 3' fragments from two different cDNA clones were ligated to create the 1.6-kb KNAT7 insert used in the 35S-KNAT7 plasmid. A construct consisting of the 35S promoter, the β-glucuronidase (GUS) gene, and the NOS terminator (Sinha et al., 1993) was used as a control in plant transformations. All constructs were cloned into the binary vector pBIN19 (Bevan, 1984). The expression plasmids 35S-kn7, 35S-KNAT7, and 35S-GUS were transformed using the Agrobacterium-mediated root transformation method of Valvekens et al. (1988). Transformants were selected on medium containing 50 mg/L kanamycin. Primary transformants (T0) were allowed to self-cross, and the resulting T2 progeny were scored for segregation of kanamycin resistance. Kanamycin-resistant T2 seedlings were transferred to soil, and mature plants were examined for alterations in morphology. The presence of transgenes in T2 lines was confirmed using the polymerase chain reaction and/or DNA gel blot analysis.

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