INTRODUCTION

In plants, cell fate is generally determined through positional information. Exchange of non-cell-autonomous signals may provide the means by which cells assume their fate in relation to surrounding tissues. To this end, information molecules may cross the plasma membranes via secretion/internalization or follow a symplasmic route via plasmodesmata (PD). Cell-to-cell trafficking of macromolecules, such as RNA-protein complexes, is thought to occur through PD. Numerous studies on viral movement proteins (MPs) as well as endogenous non-cell-autonomous proteins have provided direct evidence for the involvement of a PD-based non-cell-autonomous protein (NCAP) signaling pathway. Here, using interaction and coexpression assays, we demonstrate that the microtubule-associated and viral movement protein binding protein MPB2C from Nicotiana tabacum, and its homolog in Arabidopsis, At MPB2C, are KN1/STM binding factors. Interaction between the MPB2C proteins and KN1/STM was mapped to the KN1 homeodomain, a region not essential for heterodimerization with BEL1. Expression of MPB2C in single cells prevented KN1 cell-to-cell movement. Furthermore, in vivo trichome rescue studies established that MPB2C negatively regulates KN1 association to plasmodesmata and, consequently, cell-to-cell transport. These findings are discussed in terms of the role played by MPB2C proteins in regulating the cell-to-cell trafficking of homeodomain proteins in plants.

MPB2C, a Microtubule-Associated Protein, Regulates Non-Cell-Autonomy of the Homeodomain Protein KNOTTED1

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Plasmodesmata establish a pathway for the intercellular trafficking of viral movement proteins and endogenous non-cell-autonomous proteins, such as the two closely related meristem-maintaining KNOTTED1-like homeobox (KNOX) proteins Zea mays KNOTTED1 (KN1) and Arabidopsis thaliana SHOOTMERISTEMLESS (STM). KNOX family members are DNA binding proteins that regulate the transcriptional activity of target genes in conjunction with BEL1-like homeodomain proteins. It has been shown previously, using in vivo transport assays, that the C-terminal domain of KN1, including the homeodomain, is necessary and sufficient for cell-to-cell transport through plasmodesmata. Here, using interaction and coexpression assays, we demonstrate that the microtubule-associated and viral movement protein binding protein MPB2C from Nicotiana tabacum, and its homolog in Arabidopsis, At MPB2C, are KN1/STM binding factors. Interaction between the MPB2C proteins and KN1/STM was mapped to the KN1 homeodomain, a region not essential for heterodimerization with BEL1. Expression of MPB2C in single cells prevented KN1 cell-to-cell movement. Furthermore, in vivo trichome rescue studies established that MPB2C negatively regulates KN1 association to plasmodesmata and, consequently, cell-to-cell transport. These findings are discussed in terms of the role played by MPB2C proteins in regulating the cell-to-cell trafficking of homeodomain proteins in plants.

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of viral MPs and HD proteins into the NCAP pathway. Based on these findings, we advance the hypothesis in vivo as a negative regulator of KN1 cell-to-cell movement. Movement assays provided evidence that MPB2C functions and STM but not with BEL1. MPB2C binding was mapped to the microtubules, and STM but not with BEL1. MPB2C binding was mapped to the microtubules, and STM but not with BEL1. MPB2C binding was mapped to the microtubules, and STM but not with BEL1.

Microinjection experiments have established that maize KN1 has the capacity to interact with PD to increase the size exclusion limit (SEL) and mediate its cell-to-cell trafficking as well as that of its own mRNA (Lucas et al., 1995; Kragler et al., 2000). Most viruses encode specialized MPs that have the capacity to interact with host proteins to regulate their intercellular transport through PD, and such microinjection studies provided direct evidence in support of the hypothesis that KN1 and tobacco mosaic virus (TMV) MP utilize common components of the NCAP pathway (Kragler et al., 1998b, 2000).

There is evidence that the regulation of movement of the TMV MP-RNA complex into neighboring cells depends on the interactions of TMV MP with endogenous proteins such as the NON-CELL-AUTONOMOUS PATHWAY PROTEIN1 (NCAPP1) (Lee et al., 2003), PD-located casein kinases (Lee et al., 2005), cell wall-modifying enzymes such as pectin methyl esterase (Chen et al., 2000), or the Ca^{2+}-sequestering protein calreticulin (Chen et al., 2005). Furthermore, within plant cells, the TMV MP association with microfilaments and microtubules appears to regulate the access of the TMV MP-RNA complex to the PD pathway (Heinlein et al., 1995; McLean et al., 1995; Boyko et al., 2000, 2007; Gillespie et al., 2002; Nelson and Citovsky, 2003; Wright et al., 2007).

Insight into the mechanism by which microtubules may negatively regulate TMV MP movement has been gained through the identification of MPB2C, an endogenous protein in Arabidopsis that interacts with the TMV MP. In situ labeling experiments demonstrated that At MPB2C exhibited properties equivalent to those of the non-cell-autonomous proteins. The specificity of the interaction between MPB2C and KN1/STM was supported by the failure of MPB2C to interact with a pumpkin (Cucurbita maxima) phloem NCAP, Cm PP16 (Xoconostle-Cazares et al., 1999) (Figures 1A and 1B). A similar negative result was obtained with Nt NCAPP1, a component of the NCAP pathway that mediates the delivery of Cm PP16 to PD (Lee et al., 2003).

A single Nt MPB2C-like gene was identified in the Arabidopsis genomic database (At MPB2C; At5g08120) with a similarity at the amino acid level of 62%. Yeast two-hybrid interaction assays demonstrated that At MPB2C interacted with a pumpkin (Cucurbita maxima) phloem NCAP, Cm PP16 (Xoconostle-Cazares et al., 1999) (Figures 1A and 1B). Both can form homodimers and specifically interact with Nt KN1 and STM.

A Functional KN1 Cell-to-Cell Movement Motif Is Essential for MPB2C–KN1 Interaction

The inability of MPB2C to dimerize with the HD protein BEL1 implies that MPB2C-KN1/STM heterodimer formation depends on motif(s) distinct from those found in BEL1, allowing a BEL1-like protein to bind to KN1/STM. To identify such motifs, we used three KN1 deletion constructs: KN1ΔN, lacking both the KNOX and ELK motifs; KN1ΔC, devoid of the ELK, NLS, and HD motifs; and KN1ΔHD, lacking the HD motif (Figure 1C). In yeast two-hybrid assays, both KN1ΔC and KN1ΔHD interacted with STM and BEL1 but did not interact significantly with At MPB2C or Nt MPB2C (Figure 1B). These results indicated that the HD motif was necessary for MPB2C binding. Thus, the KN1–MPB2C interaction requires the presence of the HD motif that is also responsible for DNA binding (Smith et al., 2002; Viola and Gonzalez, 2006) and cell-to-cell movement (Kim et al., 2005b). In agreement with the reported function of the KNOX motif to mediate an interaction with BEL1-like proteins (Bellaoui et al., 2001; Muller et al., 2001), no KN1ΔN heterodimer formation was observed with BEL1.

Protein overlay assays were next performed to further test for the interaction between KN1 and MPB2C. Here, TMV MP was included as a positive control, since we earlier demonstrated binding to MPB2C under the conditions used in these overlay assays (Kragler et al., 2003). To probe MPB2C binding to the KN1
region essential for cell-to-cell transport, we used a mutant KN1 protein, KN1M6, which is defective in cell-to-cell movement capacity (Lucas et al., 1995). KN1M6 harbors three Lys-to-Ala substitutions (from Lys-265 to -267 to Ala-265 to -267) in a basic amino acid stretch adjacent to the HD motif.

First, At MPB2C, Nt MPB2C, KN1, KN1M6, and TMV MP were expressed in *Escherichia coli*, isolated to near homogeneity, and quantified following SDS-PAGE (Figure 2A). Next, Nt MPB2C or At MPB2C was blotted onto a nitrocellulose membrane, which was then cut into strips and used for overlay assays. Incubating immobilized Nt MPB2C with BSA followed by KN1 immunodetection confirmed the specificity of the detection system; note the absence of signal (Figure 2B). Incubation of the immobilized Nt MPB2C with KN1 plus a 50-fold molar excess of BSA, or KN1, followed by KN1 immunodetection resulted in a clearly discernible signal.

To further confirm the specificity of KN1 binding to Nt MPB2C, we next performed competition assays with a 50-fold molar excess of At MPB2C or Nt MPB2C. As shown in Figure 2B, excess levels of either Nt MPB2C or At MPB2C greatly diminished the KN1 signal. Equivalent results were obtained when we performed reciprocal overlay experiments in which At MPB2C was used as the immobilized protein (Figure 2B).

To test whether a movement-impaired KN1 protein is still capable of MPB2C interaction, we reversed the overlay system and blotted equal molar amounts of TMV MP, KN1, and the movement-deficient mutant KN1M6 onto the membrane and then incubated it with recombinant At MPB2C. Immunodetection of bound MPB2C revealed strong signals at the positions of the TMV MP and KN1, whereas only a very faint signal was present at the position of KN1M6. Equal amounts of KN1 and KN1M6 were loaded, as indicated by equivalent signals detected with the KN1-specific antibody (Figure 2C, bottom panel). These results are consistent with our yeast two-hybrid findings and support the notion that a functional KN1 cell-to-cell movement motif is essential for a strong interaction with MPB2C.

**MPB2C Binds to RNA and Alters KN1 RNA Binding Capacity**

Previous microinjection and trichome rescue experiments established that KN1 binds and traffics its own mRNA to neighboring cells (Lucas et al., 1995; Kragler et al., 1998b; Kim et al., 2005b). To test whether MPB2C displays RNA interaction activity and could alter KN1 RNA recognition, we submitted the recombinant proteins to RNA binding assays. Immobilized and renatured BSA, At MPB2C, KN1, and TMV MP were incubated with labeled total *Arabidopsis* RNA harvested from 2-week-old seedlings. An RNA signal was detected at the positions of At MPB2C, KN1, and TMV MP (Figure 2D). Showing the specificity of the RNA binding assay, no RNA was detected associated with the negative control protein BSA.

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**Figure 1.** Protein Interaction Assays Showing Specific Interaction of KN1 with MPB2C.

(A) Yeast two-hybrid interaction assay using Nt MPB2C, Δ1-196 Nt MPB2C, KN1, and KN1ΔC fused to the GAL4 DNA binding domain (BD) and Nt MPB2C, KN1, and Cm PP16 fused to the GAL4 activation domain (AD). BD-empty and AD-empty strains express only the binding and activation domains, respectively. Note that BD-Nt MPB2C alone gives high background on the selective growth medium but shows no α-galactose activity (blue stain).

(B) Summary of the observed yeast two-hybrid interactions. The interaction according to the measured relative β-galactose activity and growth rate was characterized as high (+ +), with the maximum measured in the system, middle (+), with lower activity of the maximum, very low (+ /), with ~10-fold less than the maximum activity of the particular construct, or not above background (+). For an example with BD-KN1ΔC, see Supplemental Table 1 online.

(C) KN1 domain structure and deletion constructs used in yeast two-hybrid assays and their capacity to interact with MPB2C or BEL1.
Next, by adding excess quantities of At MPB2C or TMV MP to the assay, we tested the potential effect of At MPB2C on the KN1 RNA binding activity. High amounts (10-fold excess) of At MPB2C reduced specifically detectable RNA signals at KN1 and MPB2C, whereas excess TMV MP diminished all RNA signals (Figure 2D). Neither KN1 nor At MPB2C bound to double-stranded DNA, whereas TMV MP could bind, in vitro, double-stranded DNA (Figure 2D, right panel).

**KN1 Cell-to-Cell Trafficking Is Restricted by MPB2C**

In previous studies, a negative effect of transiently expressed MPB2C was reported on the cell-to-cell movement capacity of coexpressed TMV MP (Kragler et al., 2003). Consequently, we next examined whether MPB2C has a similar effect on the ability of KN1 to move through PD. Here, microinjection methods were used to test KN1 movement in the presence of MPB2C. KN1 and MPB2C were first expressed in and purified from *E. coli*, fluorescently labeled, and then introduced into mesophyll cells of *N. benthamiana* leaves. Movement capacity was tested by coinjection of 12-kD F-dextran or 11-kD rhodamine-dextran: an increase in PD SEL occurs during NCAP trafficking, and this allows for the codiffusion of the reporter dextrans.

In control experiments, the small membrane-impermeant fluorescent tracer, lucifer yellow CH, was first injected into target mesophyll cells to confirm their symplasmic connectivity (Table 1). A second test probe, acridine orange, which is membrane-impermeable in its protonated form and binds to DNA, callose, and cell wall material (Karabetsos et al., 1987; Alche and Rodriguez-Garcia, 1997; He et al., 2007), also moved readily through PD.
into neighboring cells. Green fluorescent nuclei became visible within seconds in the injected cells and after 30 s in neighboring cells (Table 1, Figure 3A).

A mixture of 11-kD rhodamine-dextran and 12-kD F-dextran was next injected to test for the presence of endogenous NCAP trafficking. Retention of both probes in the injected cells (Figures 3B and 3C) established that these mesophyll cells were not actively engaged in NCAP movement. To confirm the capacity of this tissue to traffic NCAPs, we next injected fluorescently labeled KN1. As expected, rhodamine-KN1 was observed to move from cell to cell in 90% of such injections (Figure 3D, Table 1). Rhodamine-KN1, similar to TRITC-labeled KN1 (Kragler et al., 1998b), induced an increase of the PD SEL, allowing 12-kD rhodamine-dextran to move into neighboring mesophyll cells (Table 1).

The potential for cell-to-cell movement by At MPB2C and Nt MPB2C, per se, was next tested by coinjection with 12-kD F-dextran. As shown in Table 1, both MPB2C proteins remained in the injected cells together with the 12-kD F-dextran. Thus, based on microinjection assays, MPB2C does not have the capacity to increase the PD SEL or to move from cell to cell. Subsequently, we determined whether MPB2C inhibits KN1 transport activity by injecting a mixture of rhodamine-KN1, At MPB2C, and 12-kD F-dextran into target mesophyll cells. In the presence of At MPB2C, rhodamine-KN1 and 12-kD F-dextran remained in the injected cells (Figures 3E and 3F). Equimolar mixtures of rhodamine-tagged KN1 and fluorescein isothiocyanate (FITC)-tagged MPB2C also persistently stayed in the injected cells (Table 1, Figures 3G and 3H). Microinjected At MPB2C often appeared in fluorescent punctae within the cytosol (Figure 3I), a similar phenomenon was earlier observed with the Nt MPB2C-DsRED fusion protein (Kragler et al., 2003). Consistent with a previously reported specific inhibitory effect of Nt MPB2C on TMV MP movement capacity, no increase in PD SEL was observed when TMV MP was microinjected in the presence of At MPB2C (Table 1). Finally, coinjection of MPB2C along with cucumber mosaic virus MP (CMV MP) did not block the MP-induced increase in SEL (Table 1). Together, these microinjection experiments indicated that At MPB2C has the capacity to interact with KN1 and TMV MP in the mesophyll cytoplasm to block their ability both to increase the PD SEL and to move cell to cell.

### Table 1. Microinjection Studies on KN1 Movement in the Presence of MPB2C

| Injected Probes | Injections | Movement (%) | Comment                        |
|-----------------|------------|--------------|---------------------------------|
| Lucifer yellow CH | 20         | 20 (100)     | Extensive; cells symplastically connected |
| Acridine orange | 20         | 20 (100)     | Nuclei, extensive; cells symplastically connected |
| 12-kD F-dextran + 11-kD rhodamine-dextran | 20     | 1 (5)        | Both dyes remain in injected cells |
| Rhodamine-KN1   | 10         | 9 (90)       | Extensive                        |
| Rhodamine-KN1 + 12-kD F-dextran | 12     | 9 (75)       | Both extensive                   |
| FITC-Nt MPB2C   | 10         | 0 (0)        | Appears in punctae and cytosol   |
| FITC-At MPB2C   | 10         | 0 (0)        | Appears in punctae and cytosol   |
| Nt MPB2C + 12-kD F-dextran | 10   | 0 (0)        | No increase of PD SEL; dye remains in injected cells |
| At MPB2C + rhodamine-KN1 + 12-kD F-dextran | 10   | 0 (0)        | No increase of PD SEL; dye remains in injected cells |
| FITC-At MPB2C + rhodamine-KN1 | 12  | 0 (0)        | Appears in punctae and cytosol   |
| At MPB2C + TMV MP + 12-kD F-dextran | 24  | 0 (0)        | No increase of PD SEL; dye remains in injected cells |
| At MPB2C + CMV MP + 12-kD F-dextran | 18  | 15 (84)      | Extensive; increase of PD SEL    |

Fluorescent probes were microinjected into N. benthamiana mesophyll cells and distribution was evaluated within 5 min. Equimolar amounts were used in probes in which two proteins were combined and adjusted to a final concentration of 2 μg/μL.

*Acridine orange (molecular weight = 302).*

### Transient Expression of MPB2C Inhibits KN1 Cell-to-Cell Movement in Arabidopsis

In Arabidopsis, transiently expressed KN1 was earlier shown to move between epidermal cells as well as from mesophyll cells into epidermal cells in KN1 transgenic plants (Kim et al., 2002, 2003, 2005b). Thus, the biolistic bombardment system was next employed to further investigate the inhibitory effects of MPB2C on KN1 movement capacity in epidermal tissues. We transiently expressed GFP-KN1 and MPB2C-DsRED in Arabidopsis epidermal cells. Two to 3 d after bombardment, we inspected this tissue for cell-to-cell transport of the fluorescent fusion proteins.

Control experiments were first performed to determine whether DsRED, GFP-KN1, At MPB2C-GFP, or Nt MPB2C-DsRED could move through epidermal PD. Consistent with the findings of Kim et al. (2002), GFP-KN1 was transported from bombarded cells to neighboring cells, albeit at a low rate of ~10% (Figure 4, Table 2). Interestingly, in the presence of KN1, when the PD SEL should be increased, no movement of DsRED was detected (Figure 4B, Table 2). Also, Nt MPB2C-DsRED and At MPB2C-GFP remained in the bombarded cells (Table 2). Furthermore, both proteins were observed to be colocalized with GFP-KN1 in cytosolic punctae, and this association abolished KN1 cell-to-cell spread (Figures 4E to 4G, Table 2). Co-localization of At MPB2C fused to red fluorescent protein (RFP) was also observed with KN1 harboring GFP at the C-terminus (KN1-GFP; see Supplemental Figure 1 online). These results were equivalent to those obtained in microinjection studies and offered additional support for the hypothesis that MPB2C interacts with KN1. In microinjection and transient expression assays, MPB2C interaction with KN1 prevents KN1 from moving cell to cell.

### MPB2C Reduces the Trichome Rescue Efficiency of Non-Cell-Autonomous GL1-KN1HD Fusions in Transgenic Plants

The potential of At MPB2C to limit KN1 trafficking was further tested using the trichome rescue system developed by Kim et al.
For these experiments, we transformed transgenic gl1/ProRbcS:GFP-GL1-KN1HD trichome rescue lines and Arabidopsis wild-type control lines with a construct expressing a tap-tagged At MPB2C driven by the cauliflower mosaic virus (CaMV) 35S promoter. As an assay for cell-to-cell movement, the number of trichomes present on the adaxial surface of the third and fourth leaves was counted (Table 3). In Pro35S:AtMPB2C-TAG transgenic control lines, the number and distribution of trichomes did not change significantly compared with those in wild-type plants (Figure 5A). The trichome rescue line gl1/ProRbcS:GFP-GL1-KN1HD (Figure 5B) showed ~66% of the trichomes observed with the control lines (Table 3). The rescue line developed on average 21 ± 3.4 trichomes per leaf, while the trichome rescue lines harboring the Pro35S:AtMPB2C
developed on average 14 ± 7 trichomes per leaf (Table 3). A statistical Student’s t test analysis revealed a P value of 1.0E-4, suggesting that the difference of trichome numbers observed on the trichome rescue lines was statistically significant. Thus, trichome rescue plants ectopically expressing At MPB2C (Figures 5C and 5D) developed significantly fewer trichomes than the parent rescue plant. Two independent gl1 rescue lines highly expressing At MPB2C relative to the GL1-KN1HD construct (see Supplemental Figure 2 online) over three generations consistently developed fewer than five trichomes on the third or fourth leaf. Also, these lines maintained a limited number of trichomes on leaves appearing at later stages (Figure 5C; see Supplemental Figure 2 online). Furthermore, as exemplified by the plant shown in Figure 5D, two T1 lines had uneven distributions of trichomes over the leaf surface. The negative effect of At MPB2C overexpression on ProRbcS:GFP-GL1-KN1HD–mediated trichome rescue activity is consistent with the hypothesis that MPB2C limits the cell-to-cell movement of GL1-KN1HD.

MPB2C Expression Abolishes GFP-GL1-KN1HD Presence at PD

The subepidermal expression of GL1-KN1HD as a GFP fusion protein allowed us to ask whether the cellular distribution was altered due to the coexpression of At MPB2C. In ProRbcS:GFP-GL1-KN1HD lines, fluorescent signal was detected in spots in the region of the cell walls thought to resemble accumulation at PD (Figure 5E; see Supplemental Figure 3 online) (Kim et al., 2002) as well as in nuclei of epidermal and subepidermal cells (Figure 5G; see Supplemental Figure 3 online). To confirm the inhibition of GFP-GL1-KN1HD transport through PD by MPB2C, we examined the distribution of GFP-GL1-KN1HD in trichome rescue lines harboring Pro35S: At MPB2C-TAG. In plants with few or no trichomes, GFP-GL1-KN1HD fluorescent signal was detected neither in punctae at cell walls nor in nuclei of epidermal cells (Figure 5F; see Supplemental Figure 3 online). These lines showed fluorescent fusion protein exclusively in the nuclei of subepidermal cells, indicating stable expression of the GFP-GL1-KN1HD construct (Figure 5H).

**KN1 Shows Altered Subcellular Distribution in the Presence of MPB2C**

To further confirm the potential of KN1 to interact with MPB2C, we investigated the subcellular distribution of KN1 and MPB2C fluorescent fusion proteins expressed after agroinfiltration (Figure 6). First, we established the subcellular distribution of KN1-GFP alone. At all stages examined, KN1-GFP appeared in the cytosol and in the nuclei of ~80% of cells (Figures 6A and 6B). In weakly expressing cells up to 36 h after infiltration, KN1-GFP

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**Figure 4.** Cell-To-Cell Movement of Transiently Expressed KN1 Is Impaired by MPB2C in Arabidopsis Leaf Epidermal Tissue.

Two-week-old Arabidopsis C24 plants were bombarded with gold particles coated with plasmids expressing fluorescent proteins driven by the CaMV 35S promoter. Confocal images of fluorescent fusion proteins coexpressed in single epidermal cells were taken at 1 to 2 d after bombardment. (A) KN1-GFP–emitted fluorescent signal (green) is present in cells adjacent to the bombarded cell at 2 d after bombardment. (B) to (D) Coexpression of KN1-GFP and DsRED. KN1-GFP is found in neighboring cells (B), whereas DsRED remains in the expressing cell (C). (D) shows a merged image. (E) to (G) Cell coexpressing KN1-GFP and Nt MPB2C-DsRED. KN1-GFP remains in the bombarded cell and appears in stationary punctae (E). Red channel image shows the presence of Nt MPB2C-DsRED in the same cell (F). In the merged image (G), colocalization of KN1 and Nt MPB2C fluorescent fusion proteins is visible (yellow). N, nucleus. Stars indicate cells in which fluorescent proteins moved. Bars = 80 µm.
was detected in the cytosol and nucleus. In highly expressing cells, KN1-GFP accumulated at the nuclear envelope and at endoplasmic reticulum (ER)-like structures, which collapsed after heat treatment (Figure 6A). At later time points, KN1-GFP appeared mainly as an evenly distributed protein in the cytosol and formed, in addition, fluorescent aggregates of varying sizes (Figure 6B).

In contrast with KN1-GFP, At MPB2C-GFP and At MPB2C-RFP were not observed in nuclei and appeared transiently at static filaments and later in punctate arrays, suggesting an association with the cytoskeleton (Figures 6C and 6D). At MPB2C-RFP punctae did not colocalize with ER-GFP or the F-actin marker Talin-GFP (see Supplemental Figure 1 online). In the later stages of expression, or in highly expressing cells, we observed that At MPB2C-GFP generally formed large aggregates. In coexpression experiments after 1 d, At MPB2C-GFP punctae colocalized with its ortholog Nt MPB2C-DsRED (see Supplemental Figure 1 online).

Next, we asked whether MPB2C induces changes in KN1 cellular distribution. Within 2 d after agroinfiltration, KN1-GFP and Nt MPB2C-DsRED became visible in small punctae and at microtubule-like structures (Figures 6E and 6F). This colocalization pattern was transient, and at later stages, KN-GFP and Nt MPB2C-DsRED2 appeared together in small punctae (Figures 6G to 6I). Comparable results were also obtained with KN1-GFP coexpressed with At MPB2C-mRFP1 in Arabidopsis epidermal cells after particle delivery (see Supplemental Figure 1 online). Combined with the reported altered cellular distribution of TMV MP due to overexpressed MPB2C (Kragler et al., 2003), these findings suggest that MPB2C has the potential to induce KN1 accumulation at microtubules in vivo.

The STM KNOX HD Mediates MPB2C Interaction

To test whether STM, similar to KN1, colocalizes and interacts with At MPB2C, we employed the bimolecular fluorescence complementation system (Walter et al., 2004). This split yellow fluorescent protein (YFP) system tests for in vivo interaction of fusion proteins consisting of N- and C-terminal truncated YFP and interaction partners. Once the fusion partners interact, high levels of YFP fluorescence can be detected in the cells.

First, we expressed in N. benthamiana epidermal cells split YFP fusion proteins (NYFP-STM D HD and CYFP-STM D HD) harboring a mutant form of STM lacking the C-terminal ELK and HD

Table 2. Coexpression after Particle Delivery and Cell-to-Cell Movement of KN1-GFP in the Presence of RFP Fusion Proteins in Arabidopsis

| GFP Construct | RFP Construct | No. of Cells | Neighboring Cells (%) | Comment | Neighboring Cells (%) | Comment |
|---------------|---------------|--------------|-----------------------|---------|-----------------------|---------|
| None          | DsRED         | 193          | n/a                   | n/a     | 0 (0)                 | Nucleus, cytosol |
| GFP           | DsRED         | 84           | 70 (83)               | Nucleus, cytosol | 0 (0)                 | Nucleus, cytosol  |
| GFP           | Nt MPB2C-DsRED| 137          | 110 (80)              | Nucleus, cytosol | 0 (0)                 | Punctae, microtubules, aggregates |
| GFP-KN1       | DsRED         | 124          | 16 (13)               | Nucleus, cytosol | 0 (0)                 | Nucleus, cytosol  |
| GFP-KN1       | Nt MPB2C-DsRED| 209          | 0 (0)                 | Punctae, microtubules, aggregates | 0 (0)                 | Punctae, microtubules, aggregates |
| At MPB2C-GFP  | Nt MPB2C-DsRED| 128          | 0 (0)                 | Punctae, microtubules, aggregates | 0 (0)                 | Punctae, microtubules, aggregates |
| None          | KN1-mRFP1     | 94           | n/a                   | n/a     | 9 (10)                | Cytosol, nucleus |

DNA encoding fluorescent fusion protein constructs was coated on gold particles and delivered into Arabidopsis epidermal cells. Two- to 4-week-old soil-grown plants were used, and fluorescent fusion protein distribution was analyzed at 2 to 3 d after bombardment using a confocal microscope. When two constructs were combined, an approximately equimolar mixture was used to coat the gold particles. Exclusively, cells were evaluated showing high levels of detectable red and/or green fluorescence. n/a, not applicable.

Table 3. At MPB2C Overexpression Alters Trichome Recovery Mediated by GFP-GL1-KN1HD in Transgenic gl1 Trichome Rescue Plants

| Genotype (Number of T1 Lines)a | Total No. of Trichomes (No. of Leaves Evaluated)b | Average No. per Leaf | Relative Changec | Comments |
|--------------------------------|--------------------------------------------------|----------------------|------------------|----------|
| Wild-type Col-0 (10)           | 638 (20)                                         | 32 ± 3.9             | 100%             | All plants with normal trichome distribution |
| Wild-type Col-0/Pro35S:AtMPB2C (7) | 442 (14)                                         | 32 ± 2.7             | 100%             | All plants with normal trichome distribution |
| gl1/ProRbcS:GFP-GL-KN1HD (45)  | 1475 (90)                                        | 21 ± 3.4             | 66%              | All plants with >15 trichomes per leaf |
| gl1/ProRbcS:GFP-GL-KN1HD/Pro35S:AtMPB2C (21) | 8439 (596)                                     | 14 ± 7               | 44%              | Fifty-two plants (T2) show fewer then 3 trichomes per leaf; two plants (T1) show irregular trichome distribution across one leaf |

a Number indicates the number of T1 lines representing independently transformed plants except for gl1/ProRbcS:GFP-GL-KN1HD, which was a stable T6 line.

b Leaf trichomes appearing on the adaxial side on the third and fourth leaves of T2 plants (≥10) were counted.

c Percentage of trichomes calculated against Col-0 plants transformed with Pro35S:AtMPB2C.
motifs (amino acids 252 to 382). High fluorescence levels were detected in these cells, confirming that the STM<sub>D</sub>HD constructs were functional and that the remaining KNOX motif was sufficient to mediate STM<sub>D</sub>HD homodimerization (Figure 7A). As with KN1-GFP (Figures 6A and 6B), the STM<sub>D</sub>HD constructs appeared at ER-like structures and in the cytosol. By contrast, coexpressed NYFP-STM<sub>D</sub>HD and CYFP-At MPB2C emitted weaker YFP signals exclusively in the cytosol that was excluded from nuclei (Figure 7B). Similar to At MPB2C (Figures 6C and 6J), coexpression of CYFP-At MPB2C together with full-length STM fused to NYFP (NYFP-STM) appeared in small mobile and highly fluorescent punctae (Figure 7C), which formed larger aggregates at 2 to 3 d after infiltration (Figure 7D).

In the split YFP system, the intensity of the YFP signal reflects the capacity of two proteins to interact. Thus, we scanned the tissues with fixed confocal settings and measured the relative fluorescent signal intensities in cells expressing the YFP constructs (Figures 7E to 7J). Compared with cells expressing the two STM<sub>D</sub>HD constructs (Figures 7A and 7E), very low YFP signals could be detected in cells coexpressing NYFP-STM<sub>D</sub>HD.
and CYFP-At MPB2C (Figure 7F). High fluorescence levels were detected again in cells expressing full-length STM and At MPB2C split YFP fusion constructs (Figures 7G and 7H).

The fluorescence signals emitted by the split YFP fusion proteins were measured on a linear scale and compared with each other (Figures 7I and 7J). Coexpressed STMΔHD fusion proteins yielded similar high levels of fluorescent signals as did NYFP-STM expressed together with CYFP-At MPB2C. Supporting the notion that the HD mediates interaction, NYFP-STMΔHD coexpressed with CYFP-At MPB2C showed an approximately fivefold weaker signal (Figures 7I and 7J).

**MPB2C Promoter Is Active in Young Tissues**

The MPB2C-mediated downregulation of KN1 trafficking through PD implies that, in wild-type Arabidopsis plants, At MPB2C should be coexpressed or expressed in neighboring tissues where KN1-related proteins, such as STM and KNAT1, are produced. To test this prediction, we examined At MPB2C promoter activity in Col-0 plants transformed with ProAtMPB2C:GUS (for β-glucuronidase) constructs. Two to 3 d after germination, ProAtMPB2C:GUS–driven GUS production was detected in the vascular tissues of cotyledons, leaf primordia, and the area of

**Figure 6. Colocalization and Intracellular Distribution of KN1 and MPB2C Fluorescent Fusion Proteins.**

Confocal images of N. benthamiana source leaves expressing fluorescent fusion proteins at 1 to 3 d after agroinfiltration. (A) After 36 h, KN1-GFP is detected in the nuclei and at the nuclear envelope (N1). Also, a cellular distribution similar to that in ER-associated proteins (ER-GFP) is observed in high-expressing cells. In low-expressing cells, no association with the nuclear envelope is detected (N2). After heat treatment (2 min of high fluorescent light), the KN1-GFP–tagged ER-like structures collapse and appear as large bodies outside the nucleus (insets).

(B) High levels of KN1-GFP appear as soluble protein in the cytosol and as aggregates (arrows) at 72 h after infiltration.

(C) and (D) Images exemplifying the cellular distribution of At MPB2C-GFP (C) and At MPB2C-RFP (D). Green and red fluorescent punctae and filaments are detected aligned with arrays previously shown to resemble microtubules (Kragler et al., 2003).

(E) to (I) Tissue coexpressing KN1-GFP and Nt MPB2C-DsRED after 36 h.

(E) Nt MPB2C-DsRED appears at thin filaments (arrowheads) and in small punctae.

(F) The same cell shows the expression of Nt MPB2C-DsRED colocalizing with KN1-GFP in the merged image. Triangles indicate KN1-GFP not colocalizing with Nt MPB2C-DsRED. Note that the majority of detected KN1-GFP and Nt MPB2C is present at filamentous structures resembling microtubules (arrowheads).

(G) Cells coexpressing KN1-GFP after 48 h.

(H) Cells coexpressing At MPB2C-mRFP after 48 h.

(I) Merged image of (G) and (H). Green signal emitted by GFP fused to KN1 is detected with At MPB2C-mRFP in punctae. Blue indicates chloroplast autofluorescence. N, nucleus. Bars = 40 μm.
Figure 7. At MPB2C Interaction with STM Depends on the Presence of the HD in Split YFP Interaction Assays.

Confocal images of *N. benthamiana* source leaves expressing split YFP constructs after agroinfiltration. **(A)** Cells expressing NYFP-STMΔHD and CYFP-STMΔHD. Two days after agroinfiltration, high YFP fluorescence signals were present in the cytosol and in association with ER-like structures. Insets show magnified regions with fluorescent signals in ER-like structures and the cytosol. **(B)** Cells expressing NYFP-STMΔHD and CYFP-At MPB2C at 2 d after agroinfiltration. Relatively low YFP signals were detected exclusively in the cytosol of epidermal cells. Insets show magnified regions indicated by rectangles with nucleus (4',6-diamidino-2-phenylindole [DAPI]-stained) and cytosol. Note that no yellow fluorescent signal was detected in nuclei (N). Blue indicates DAPI staining, and green indicates YFP fluorescence. **(C)** and **(D)** Cells expressing NYFP-STM and CYFP-At MPB2C. **(C)** One day (24 h) after agroinfiltration, high YFP fluorescence signals were present in mobile punctate structures (arrowheads) and the cytosol. **(D)** After 2 d (48 h), large fluorescent punctae appeared and no fluorescent signals were detected. Note that the YFP signal in the cytosol disappeared and no YFP signals were detected in nuclei.
the shoot apical meristem (Figures 8A and 8B). In later developmental stages, these plants showed GUS staining in carpels and ovules (Figures 8C and 8D). Here, GUS activity was detected in the funiculus and integuments (Figure 8D). In roots, ProAtMPB2C:GUS plants showed weak GUS activity in a limited number of epidermal cells in proximity to the root apical meristem (Figure 8E).

Consistent with the promoter–GUS activity observed in Arabidopsis wild-type lines, RT-PCR assays (Figure 8F) indicated that AtMPB2C mRNA is either not produced or only weakly produced in cauline leaves and root tissues. Thus, the presence of MPB2C transcripts correlates with the staining patterns observed with the corresponding promoter–GUS constructs. Collectively, the observed AtMPB2C expression pattern suggests that the gene is active in tissues neighboring or overlapping those with STM and KNAT1 function (Lincoln et al., 1994; Long et al., 1996). At MPB2C mRNA is produced in distinct plant parts, such as meristems, carpels, and developing ovules, in which STM-related interaction partners like the BEL1-like proteins function (Modrusan et al., 1994; Reiser et al., 1995; Cole et al., 2006).

**DISCUSSION**

Intercellular trafficking of HD transcription factors, such as KN1, STM, and KNAT1, is likely to act as an important developmental signal in plants. HD protein trafficking is thought to occur via PD and should be under strict control to ensure the proper separation of differentiation domains. Developmental modifications in PD are known to affect free GFP diffusion and to regulate selective KN1 transport (Itaya et al., 1998; Oparka et al., 1999; Kim et al., 2002, 2003, 2005a, 2005b). However, almost nothing is known about the potential PD transport regulators suggested to exist for KN1 or STM. Here, we show that MPB2C is an RNA and HD motif binding protein that functions as a component in the regulation of KN1 trafficking.

**KN1 Subcellular Distribution**

Our observation that ectopically expressed KN1 is not located exclusively to the nucleus by default is not surprising. STM, the Arabidopsis homolog of KN1, had also been reported to be cytoplasmic upon ectopic overexpression in epidermal leaf cells (Cole et al., 2006). In other studies, however, coexpressed STM and KNAT1 fluorescent fusion proteins had been reported to be located to nuclei (Hackbusch et al., 2005). Cole et al. (2006) suggested that this inconsistency might be an artifact. However, in our experiments, despite an often observed accumulation of KN1-GFP at the nuclear surface, single confocal sections revealed true nuclear localization, with visible exclusion from the nucleoli, of the construct in most cells of agroinfiltrated and particle-bombarded tissues. Kuijt et al. (2004) examined the subcellular localization of three rice (Oryza sativa) KNOX class I family members. They reported complex and heterogeneous patterns of intracellular localization varying between tissues and different KNOX class I members. Intriguingly, highly motile punctate structures were also detected with Os KN1, which is the closest relative to maize KN1 in rice (Kuijt et al., 2004). The described localization patterns coincided, except for the transient reticulate structure, with the observed patterns displayed by KN1-GFP. These various intracellular localization patterns detected with KNOX proteins might be caused by a tight regulatory mechanism imposed by KNOX binding partners such as the OVATE proteins, BLH proteins, and MPB2C.

**MPB2C as a Molecular Regulator of HD Protein Transport**

The microtubule-associated NtMPB2C was originally described as a specific TMV MP–interacting partner inhibiting the cell-to-cell trafficking of TMV MP but not that of the CMV MP (Kragler et al., 2003). As it seems unlikely that plants evolved a conserved MPB2C protein to limit the spread of one distinct class of viruses, we probed the MPB2C interaction with other plant endogenous NCAPs. Interaction assays indicated that both MPB2C orthologs from N. tabacum and Arabidopsis specifically bind to KN1 and STM. Intriguingly, MPB2C does not bind to other NCAPs, such as SHR, LFY, or Cm PP16. MPB2C seems to recognize specifically non-cell-autonomous class I KNOX proteins, represented by KN1 and STM, and not other HD proteins such as BEL1 that are suggested to be cell-autonomous (Kim et al., 2005b). Thus, MPB2C may regulate the intracellular distribution of an NCAP subclass and seems to be part of a pathway controlling KN1/STM availability for translocation across cell borders. Indeed, abundant MPB2C interferes with the cell-to-cell transport activity of KN1 in microinjection assays, in transient expression assays, and should be under strict control to ensure the proper separation of differentiation domains. Developmental modifications in PD are known to affect free GFP diffusion and to regulate selective KN1 transport (Itaya et al., 1998; Oparka et al., 1999; Kim et al., 2002, 2003, 2005a, 2005b). However, almost nothing is known about the potential PD transport regulators suggested to exist for KN1 or STM. Here, we show that MPB2C is an RNA and HD motif binding protein that functions as a component in the regulation of KN1 trafficking.

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and in trichome rescue assays. These observations are in agreement with the previously suggested function of MPB2C as a microtubule-associated TMV MP binding protein with the capacity to interrupt cell-to-cell transport by enhancing the microtubular association of TMV MP (Curin et al., 2007).

At present, we cannot exclude the possibility that the observed inhibition of cell-to-cell transport is a secondary effect of the high expression levels of MPB2C. However, this scenario seems unlikely, as in our experiments, KN1 and STM interact directly with MPB2C via their HD. Also, the endogenous promoter activity pattern of MPB2C in Arabidopsis suggests that MPB2C functions within or in the proximity of meristematic tissues, where STM and BP/KNAT1 are expressed and moving from cell to cell.

KN1 and STM colocalize in the cytosol with MPB2C in a punctate manner previously shown to coincide with microtubules (Kragler et al., 2003). A similar pattern was observed with subsets of OVATE family proteins interacting with distinct BLH and KNOX proteins (Hackbusch et al., 2005). However, a function of OVATE regarding cell-to-cell transport was not reported. MPB2C, although of similar size, harbors no motifs related to OVATE family members and seems to have a distinct function directed specifically toward regulating the trafficking of KNOX proteins. For other KNOX motif binding proteins, such as BLH proteins, a negative role on KN1 cell-to-cell transport seems unlikely. This notion finds support based on the following: (1) BLH proteins bind to the KNOX motif of KN1 dispensable for cell-to-cell transport, and (2) BLH proteins facilitate the nuclear import of KNOX proteins (Cole et al., 2006).

Considering that HD proteins function to define cell identity, it is logical to assume that mechanisms exist to control both HD protein levels in the appropriate (expressing) tissues and their cell-to-cell transport to neighboring tissues. Support for this notion is derived from the failure of MPB2C to interact with mutant KN1 and STM proteins lacking a functional HD transport motif, such as KN1M6, KN1ΔHD (Lucas et al., 1995; Kim et al., 2005b), and STMΔHD. Also, in transgenic trichome rescue plants, MPB2C inhibits the KN1ΔHD-mediated cell-to-cell transport of GL1 toward PD and, consequently, to the epidermis (Figure 5; see Supplemental Figure 3 online). Therefore, we conclude that MPB2C negatively controls KN1 trafficking activity by binding to the HD motif.

Sequence analysis of MPB2C cDNAs and predicted amino acid sequences indicates that no significantly related genes are found in other kingdoms than plants and that the gene is present only once per plant genome. As discussed for OVATE proteins (Hackbusch et al., 2005), MPB2C seems to provide a link for HD proteins to the microtubules. Here, as suggested for the TMV MP pathway (Curin et al., 2007), MPB2C could constitute the entry point for an HD protein sequestration pathway operating with the help of proteasomes to degrade excess cytosolic KN1 (Figure 9).

In tobacco and Arabidopsis, endogenous MPB2C levels are very low (Kragler et al., 2003) (Figure 8) and at the time of trichome initiation may not be sufficient to block KN HD transport from cell to cell, thus allowing trichome rescue in the ProRbcS:GFP-GL1-KN1HD line. On the other hand, in transgenic trichome rescue plants, high levels of MPB2C blocked KN1HD-mediated transport. However, in wild-type plants, class I HD proteins are expressed in a limited number of cells and endogenous MPB2C might contribute sufficiently to modulate non-cell-autonomous KNOX protein trafficking. MPB2C could restrict the number of KN1/STM macromolecules available to enter the PD pathway in the shoot apical meristem. By this means, MPB2C may ensure

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**Figure 8. Promoter Activity of At MPB2C in Arabidopsis.**

(A) to (E) Seedling and flower tissues of ProAtMPB2C:GUS plants stained for GUS activity. (A) to (C) The promoter drives GUS production in the vasculature of cotyledons (A), tissue associated with leaf primordia, and apical meristem (B) and carpels (C). (D) Weak GUS activity in ovules of ProAtMPB2C:GUS plants. (E) Root tips of wild-type (control) and ProAtMPB2C:GUS plants. (F) RT-PCR of At MPB2C and Actin as a control. Note the very low levels of At MPB2C transcripts relative to Actin in wild-type Arabidopsis Col-0 plants.
that transport-competent HD transcription factors are not distributed extensively across multiple cell layers. As depicted in the model presented in Figure 9, MPB2C may directly regulate the HD protein levels available for intercellular transport.

**MPB2C May Function as a Chaperone**

Interestingly, the wide diversity of functions performed by the tubulin-based cytoskeleton and its associated factors, in conjunction with the high degree of structural conservation of interacting cytoskeletal factors observed across all kingdoms, suggest that a microtubule-associated protein, such as MPB2C, is present in nonplant organisms. However, an MPB2C-like protein could not be found in other kingdoms, which would facilitate a functional prediction for plants. In a hypothetical scenario, KN1 could associate with MPB2C at the cytoskeleton. Here, KN1, as suggested for TMV MP (Kragler et al., 2003, Curin et al., 2007), might rapidly enter the proteasome-dependent degradation pathway. By this means, MPB2C could regulate two aspects: (1) the quality and amount of KN1 present in the shoot apical meristem, and (2) the pace of KN1-mRNA cell-to-cell transport to neighboring tissues.

**Figure 9. Model of MPB2C Regulating KN1 Transport.**

A hypothetical model depicting MPB2C as a KN1 transport-controlling factor. KN1 is produced in the cytosol; there, a decision is made between nuclear import (right panel), cell-to-cell transport via PD (left panel), and MPB2C-mediated association to microtubules (bottom panel). MPB2C binding to KN1 depends on a functional HD motif, which also constitutes the KN1 cell-to-cell transport signal. Once a KN1-mRNA complex enters the PD translocation pathway, the KN1 HD transport motif is modified or occupied. By this means, a KN1-mRNA complex escapes nuclear import and gains access to adjacent cells. However, aberrant or unbound KN1 molecules, not immediately entering the PD pathway, could be recognized by MPB2C. In such a scenario, KN1 could associate with MPB2C at the cytoskeleton. Here, KN1, as suggested for TMV MP (Kragler et al., 2003, Curin et al., 2007), might rapidly enter the proteasome-dependent degradation pathway. By this means, MPB2C could regulate two aspects: (1) the quality and amount of KN1 present in the shoot apical meristem, and (2) the pace of KN1-mRNA cell-to-cell transport to neighboring tissues.
**METHODS**

**Plant Materials**

*Nicotiana* sp and *Arabidopsis thaliana* plants were grown in controlled environmental chambers under light intensity in the range of 800 to 1000 \( \mu \text{mol} \cdot \text{m}^{-2} \cdot \text{s}^{-1} \) and temperatures of 22°C for 12 h of light for *Nicotiana* species and 16 h of light for *Arabidopsis*.

**Cloning, Expression, and Purification of Recombinant Proteins**

Specific primers were designed based on the cDNA sequences of Nt MPB2C (GenBank accession number AAL95696) and the genomic sequences of At MPB2C (The Arabidopsis Information Resource accession number At5g08120) and used in PCR to clone the respective cDNAs or genomic fragments into TOPO or pENTR/D-TOPO vectors (Invitrogen) for further cloning.

*Escherichia coli* cDNA RT-PCR cDNA fragments of At MPB2C were obtained from total RNA isolated from 2-week-old *Arabidopsis* Col-0 seedlings as template. *Escherichia coli* cDNA PCR cDNA fragments of Zm KN1, Nt NCAPP1, Cm PP16, At LFY (a gift from D. Weigel, Max Planck Institute for Developmental Biology), At AP1 (a gift from E. Meyerowitz, California Institute of Technology), At AP3 (a gift from J. Bowman, University of California-Davis), and At SHR (a gift from P. Benfey, Duke University) were obtained from plasmid templates harboring the appropriate cDNAs and cloned via PCR into the yeast two-hybrid vectors pGAD424 or pGADT7 for activation domain fusions and pGBT9 or pGBK7 for binding domain fusions (Matchmaker Systems; Clontech). KN1 deletion mutants were produced with the QuickChange site-directed mutagenesis kit (Stratagene) using the pGADT9-KN1 yeast shuttle vector as a template and verified by sequencing.

For His-tagged At MPB2C and Nt MPB2C protein expression vectors, *Saccharomyces cerevisiae* NcoI/BamHI cDNA fragments were cloned into the *Escherichia coli* cDNA pET30a. His-tagged MPB2C proteins were purified to near homogeneity via Ni-column purification (Amersham) following the supplier’s protocols. Conditions for the renatured blot overlay assay are based on previously described assays (Kragler et al., 2000, 2003). In short, proteins were transferred onto nitrocellulose membranes (Protein 2-μm membranes; Amersham), washed twice with water, washed three times with overlay buffer containing 2% BSA (Sigma-Aldrich) for 2 h, and incubated for 24 h at 10°C with overlay buffer (300 μL/cm²) containing 0.5 μg/mL purified KN1, MPB2C, or BSA (Sigma-Aldrich). For competition experiments, an ~50-fold molar excess of purified protein was added to the overlay buffer. After incubation, the strips were washed five times for 2 min each time with overlay buffer avoiding BSA and treated with 2% (v/v) digluteraldehyde (Sigma-Aldrich) for 1 min at room temperature. After washing five times with 1× PBS containing 5% BSA, bound recombinant proteins were detected following standard protein gel blot procedures using purified rabbit polyclonal antibodies (1:500) directed against KN1 or At MPB2C. Bound antibodies were detected with secondary anti-rabbit IgG conjugated with ALP or HR (1:10,000) followed by nitroblue tetrazolium/5-bromo-4-chloro-3-indolyl phosphate (Roche) color-staining reaction or the Amersham ECL Plus Western blotting detection system (Amersham) by exposure to x-ray film (Fuji) following protocols supplied by the manufacturer. RNA overlay assays and 5' labeling with [32P]-ATP of total RNA from 2-week-old *Arabidopsis* seedlings were done as described (Yoo et al., 2004).

**Transient Expression and Microinjection Assays**

Fluorescent labeling of MPB2C and KN1 with reactive rhodamine or FITC (Molecular Probes) and microinjection assays with recombinant proteins were performed on mesophyll cells of 3- to 4-week-old *N. benthamiana* source leaves as described previously (Fujivara et al., 1993; Noueiry et al., 1994; Kragler et al., 2000). Infiltration assays on *N. benthamiana* leaves were performed with LBA4404 or AGL1 Agrobacterium tumefaciens strains harboring the appropriate binary vectors grown at 28°C in selective Luria-Bertani medium to an OD₆₀₀ of 0.8, harvested, and resuspended in infiltration solution to obtain a final OD₆₀₀ of 1.6, as described (Yoo et al., 2004). Coexpression of fluorescent proteins was achieved by coinfiltration of a 1:1 mixture (OD₆₀₀ of 3.2) of AGL1 agrobacterial strains harboring the appropriate binary vectors. Transient expression of fluorescent fusion proteins in *Arabidopsis* was achieved by particle pressure delivery, using a BioList PDS-1000-He apparatus (Bio-Rad), of plasmid DNA coaxed onto 1-μm gold particles (Bio-Rad). Images of expressed fluorescent proteins or microinjected proteins were obtained with a Leica SP1 or SP4 confocal microscope. GFP, FITC, acridine orange, and lucifer yellow CH as well as mRFP1, DsRED, and rhodamine fluorescent probes were excited at 476/488 nm and 568 nm, respectively. GFP, FITC, lucifer yellow CH, and acridine orange were detected at 500

**Yeast Two-Hybrid Interaction Assays and in Vitro Binding**

The MPB2C interaction assays were performed following an established protocol (Kragler et al., 1998a). In short, the interaction mapping was conducted with the Saccharomyces cerevisiae strains H70c (MATa) or AH109 (MATα, GAL-MEL1) and the mating partner strains PCY3 (MATa) or Y187 (MATα, GAL-MEL1). To test for interaction of the activation domain and binding domain fusion proteins, the transformed strains were crossed and tested for His/ade auxotrophy and β-galactosidase and/or α-galactosidase activity on selective media. All transformed and diploid strains were selected and grown at 30°C on the appropriate selective synthetic complete medium supplied with 2% glucose or galactose and, if high unspecific activity of the binding domain fusion occurred, supplied with 5 to 20 mM 3-amino-1,2,4-triazole to limit the background growth on His-lacking medium.

KN1, KN1M6, TMV MP, and CMV MP proteins were expressed in *E. coli* and purified as described (Lucas et al., 1995; Kragler et al., 1998b). His-tagged At/NT MPB2C were purified to near homogeneity via Ni-column purification (Amersham) following the supplier’s protocols. Conditions for the renatured blot overlay assay are based on previously described assays (Kragler et al., 2000, 2003). In short, proteins were transferred onto nitrocellulose membranes (Protein 2-μm membranes; Amersham), washed twice with water, washed three times with overlay buffer containing 2% BSA (Sigma-Aldrich) for 2 h, and incubated for 24 h at 10°C with overlay buffer (300 μL/cm²) containing 0.5 μg/mL purified KN1, MPB2C, or BSA (Sigma-Aldrich). For competition experiments, an ~50-fold molar excess of purified protein was added to the overlay buffer. After incubation, the strips were washed five times for 2 min each time with overlay buffer avoiding BSA and treated with 2% (v/v) digluteraldehyde (Sigma-Aldrich) for 1 min at room temperature. After washing five times with 1× PBS containing 5% BSA, bound recombinant proteins were detected following standard protein gel blot procedures using purified rabbit polyclonal antibodies (1:500) directed against KN1 or At MPB2C. Bound antibodies were detected with secondary anti-rabbit IgG conjugated with ALP or HR (1:10,000) followed by nitroblue tetrazolium/5-bromo-4-chloro-3-indolyl phosphate (Roche) color-staining reaction or the Amersham ECL Plus Western blotting detection system (Amersham) by exposure to x-ray film (Fuji) following protocols supplied by the manufacturer. RNA overlay assays and 5' labeling with [32P]-ATP of total RNA from 2-week-old *Arabidopsis* seedlings were done as described (Yoo et al., 2004).
to 520 nm (green channel), mRFP1, DsRED, and rhodamine at 610 to 630 nm (red channel), and chloroplast fluorescence at 680 to 710 nm (blue channel). All tissues/cells harboring green and red fluorescent probes were also scanned in sequential mode, switching between the 476/488-nm and 568-nm laser excitations and according to detection channels to ensure specific identification of red and green fluorescent probes in their appropriate channels. The images were assembled using ImageJ 1.32 freeware (http://rsb.info.nih.gov/ij/) and Canvas 8 (Deneba Systems).

Transgenic Arabidopsis Lines, Expression Constructs, and Assays
All transgenic Arabidopsis lines were produced using the flower-dipping/silwet agroinfiltration method (Clough and Bent, 1998) using binary vector harboring AGL1 agrobacteria grown in selective Luria-Bertani medium. Transgenic gfp plants harboring ProRbcS:GFP-GL1-KN1HD (a gift from D. Jackson) were selected on germination plates containing hygromycin (50 μg/mL). Plants transformed with pEarleyGate 103 (Pro35S:AtMPB2C-GFP) or pEarleyGate 205 (Pro35S:AtMPB2C-TAP) vectors (Earley et al., 2006) were screened for BASTA resistance by spraying twice at 2 to 3 weeks after germination with 200 mg/L BASTA solution (Ralfsfeisen Warehouse). Genomic PCR fragments containing genomic 495-bp up-stream sequences of At MPB2C (ProAtMPB2C) from the start codons were made using FK231 (5'-CACCTTTCTTGCAGTGTAAGC-3') and FK250 (5'-TCTAGTGGTTACAAACT-3') primers and cloned into pENTR-TOPO vector (Invitrogen). The binary vector used to produce the plant expression vector ProAtMPB2C:GUS via gateway recombination was pKGWFS7 (Karimi et al., 2002).

RT-PCR analysis was done as described (Kragler et al., 2003) using the primers FK227 (5'-CACCTTAGTAGGAGGACGCAAC-3') and FK228 (5'-ATAATTAGTGAAGGCTAGTGATTG-3') for At MPB2C, FK296 (5'-GGAAGAAATGCTTCTCAAC-3') and FK398 (5'-GACTCTGGAGCCGC-3') for At MPB2C-TAP, FK259 (5'-GTATAGTTCATCCATGCTCT-3') and FK296 (5'-GGAAGAAATGCTTCTCAAC-3') for At MPB2C:GFP, and FK346 (5'-ATGACCATCGTGAAGACAGA-3') and FK347 (5'-AGGGCAACGCGCTGATTTACTGA-3') for At MPB2C-TAP:GUS. To standardize the expression levels, we used FK424 (5'-GGAAGAGCTGTACGTAAC-3') and FK425 (5'-GTGAGACTCTTGCACTGC-3')-directed against an Actin cDNA (The Arabidopsis Information Resource accession number At3g18780).

Accession Numbers
Sequence data from this article can be found in the Arabidopsis Genome Initiative or Genbank/EMBL databases under the following accession numbers: Nt MPB2C (AAL95696), At MPB2C (At5g08120), Zm KN1 (AAP76321), At BEL1 (At5g41140), At STM (At1g62360), At LFY (At5g1850), At SHR (At4g37650), At AP1 (At1g69120), At AP3 (At3g54340), Nt NCAPP1 (AF307094), and Cm PP16-1 (AF079170).

Supplemental Data
The following materials are available in the online version of this article.
Supplemental Figure 1. Subcellular Distribution of At MPB2C and Nt MPB2C, GFP-KN1, ER-GFP, and Talin-GFP Expressed in Epidermal Cells.
Supplemental Figure 2. Comparison of the Relative At MPB2C and GL1-KN1HD Expression Levels with Trichome Numbers in Pro35S:AtMPB2C Transgenic Trichome Rescue Lines.
Supplemental Figure 3. Confocal Images of GL1-GFP-KN1HD Signals Detected in Leaves of Arabidopsis Trichome Rescue Lines.

Supplemental Table 1. Example for the Yeast Two-Hybrid Interaction Categorization as Shown in Figure 1B.

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MPB2C, a Microtubule-Associated Protein, Regulates Non-Cell-Autonomy of the Homeodomain Protein KNOTTED1

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