Gene regulatory interactions at lateral organ boundaries in maize

Michael W. Lewis1, Nathalie Bolduc1,*, Kayley Hake1,2, Yadanar Htike1, Angela Hay1,5, Héctor Candela1,3 and Sarah Hake1,2,**

ABSTRACT

Maize leaves have distinct tissues that serve specific purposes. The blade tilts back to photosynthesize and the sheath wraps around the stem to provide structural support and protect young leaves. At the junction between blade and sheath are the ligule and auricles, both of which are absent in the recessive liguleless1 (lg1) mutant. Using an antibody against LG1, we reveal LG1 accumulation at the site of ligule formation and in the axil of developing tassel branches. The dominant mutant Wavy auricle in blade1 (Wab1-R) produces ectopic auricle tissue in the blade and increases the domain of LG1 accumulation. We determined that wab1 encodes a TCP transcription factor by positional cloning and revertant analysis. Tassel branches are few and upright in the wab1 revertant tassel and have an increased branch angle in the dominant mutant. wab1 mRNA is expressed at the base of branches in the inflorescence and is necessary for LG1 expression. wab1 is not expressed in leaves, except in the dominant mutant. The domain of wab1 expression in the Wab1-R leaf closely mirrors the accumulation of LG1. Although wab1 is not induced to lg1 expression in the leaf, LG1 is needed to counteract the severe phenotype of the dominant Wab1-R mutant. The regulatory interaction of LG1 and WAB1 reveals a link between leaf shape and tassel architecture, and suggests the ligule is a boundary similar to that at the base of lateral organs.

KEY WORDS: Maize, Leaf, Inflorescence

INTRODUCTION

Alteration of plant architecture has been a critical driver of crop domestication. Structural modifications that occurred often resulted from changes in branching architecture by altering the number, length or angle of branches. During maize domestication, axillary branch number and length decreased, leading to the maize underlay its regulation. Earlier reports showed that lg1 RNA levels increase in the dominant mutant Wab1-R (Foster et al., 2004). We cloned Wab1-R and found that it encodes a TCP transcription factor implicated in tassel branch angle, previously described as branch angle defective1 (bad1) (Bai et al., 2012). Using an antibody against LG1, we show that LG1 requires WAB1 in the tassel and is misexpressed in a pattern that is identical to that of WAB1 in the dominant mutant. Our results demonstrate that WAB1 regulates LG1 directly or indirectly and suggest that the ligule forms at a boundary similar to that found between lateral organs initiating from the meristem.

RESULTS

LG1 protein accumulation defines boundary regions in leaf and tassel

Maize plants that carry two different lg1 mutations were grown to assess their phenotypes in the leaf and tassel. The ligule and auricles were missing in the lg1 reference allele (lg1-R) (Fig. 1A-D), which carries a deletion (Moreno et al., 1997). In lg1-n2375, which contains a mutation in a highly conserved residue within the predicted DNA-binding domain (V206M) (personal communication, David Braun, University of Missouri), occasional patches of ligule were visible
(Fig. 1E). Tassels of both lg1 alleles were upright with reduced or small pulvini (Fig. 1F-J). Tassel branch angle as well as tassel branch number were reduced in lg1-R (Table 1A). The tassel branch number was not different for lg1-n2375 but the angle was significantly narrower (Table 1A).

We generated a LG1 antibody to follow its accumulation through time and in mutant backgrounds (Fig. 2). LG1 was detected in leaves and tassel branches of wild-type plants but absent in lg1-R and reduced in lg1-n2375 (Fig. 2E,F). In developing leaves, LG1 accumulated by Plastochron 7 (P7) at a region coincident with the preligule band (Fig. 2A,B). In P8 and later leaves, LG1 accumulation marked the differentiating ligule band and, later, the morphologically distinct ligule (Fig. 2C,D). In lg2 mutant leaves, the ligule and auricle are missing, except near the margin (supplementary material Fig. S1A). LG1 accumulation was only detected in the marginal domain in lg2 mutant leaves (supplementary material Fig. S1B-D). These data suggest that accumulation of LG1 is required for correct ligule differentiation and outgrowth.

In wild-type tassels, LG1 was detected at the adaxial base of developing tassel branches near the junction with the rachis (Fig. 2G-J). Expression could be detected in young tassels (~1 mm, Fig. 2G) and persisted as the tassel grew (~3 mm, Fig. 2H). The accumulation did not spread far from the branch-rachis junction into the branch and was usually detected in one branch at a time through transverse serial sections (Fig. 2I,J). LG1 was also expressed at the junction of secondary tassel branches (Fig. 2J). Thus, LG1 accumulation marks two distinct boundaries in the maize plant, the junction between sheath and blade and the junction of tassel branches.

Table 1. Tassel measurements

<table>
<thead>
<tr>
<th></th>
<th>TBA</th>
<th>TBN</th>
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<td>A</td>
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<td>wt sibs</td>
<td>26.67°</td>
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<td>3.77</td>
<td>8</td>
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<td>lg1n-2375</td>
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<td>10</td>
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<td></td>
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<tr>
<td>B</td>
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<tr>
<td>wt sibs</td>
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</tr>
<tr>
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<td>10</td>
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<td>P&lt;0.01</td>
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<tr>
<td>C</td>
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<tr>
<td>wt sibs</td>
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<td>7</td>
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<td>Wab1-R/+</td>
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<td>14</td>
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<td>P&lt;0.001</td>
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TBA, tassel branch angle; TBN, tassel branch number.

LG1 accumulation in Wab1-R leaves explains the dominant phenotype

Prior work showed that lg1 is upregulated in Wab1-R mutants, which have a normal sheath but an abnormal ligular region and blade (Foster et al., 2004; Hay and Hake, 2004). In heterozygotes, ectopic auricle can be found in the blade, either as isolated patches or continuous with the auricle (Fig. 3A). In homozygotes, leaves are very narrow and ectopic auricle is replaced by sheath tissue that continues up into the blade (Fig. 3B).

In both Wab1-R homozygous and heterozygous leaves, the LG1 domain expanded into the blade but was still excluded from the sheath (Fig. 3C,D). LG1 accumulation was detected in younger leaves in Wab1-R compared with wild type (Fig. 3E,F). When examining transverse sections of wild-type plants, LG1 was detected in the adaxial epidermis in only one leaf in a section (Fig. 3E). We detected LG1 throughout the width of the leaf in Wab1-R (Fig. 3F). The timing and location of LG1 accumulation in Wab1-R is consistent with the phenotypic defects found in the mutant leaves (Foster et al., 2004; Hay and Hake, 2004) and suggests that WAB1 is a positive regulator of LG1.

Cloning of Wab1

To identify the gene responsible for Wab1-R, we combined positional cloning with isolation of an intragenic suppressor. Wab1-R was mapped to an interval containing two genes, one encoding a bHLH-containing TCP transcription factor that had previously been identified in a forward genetic screen for upright tassel branches (Bai et al., 2012), and the other encoding a bHLH transcription factor (Fig. 4A). Neither gene revealed any sequence differences when compared with the parent PF4902 and no polymorphisms were detected by Southern blot hybridization (supplementary material Fig. S2). To identify which gene was responsible for Wab1-R, we used EMS mutagenesis. A single revertant, wab1-rev, that had lost the Wab1-R phenotype and carried the PF4902 polymorphism was identified. Sequencing revealed a C389T mutation that resulted in a R130W substitution (Fig. 4A) in the highly conserved DNA-binding domain of the TCP gene (Martin-Trillo and Cubas, 2010). No sequence differences were detected in the other bHLH gene. The identification of an intragenic mutation that suppresses the dominant Wab1-R phenotype confirmed that wab1 encodes this TCP gene.

wab1-rev was made homozygous and grown to maturity to assess the inflorescence phenotype. Homozygotes had fewer, upright tassel branches (Fig. 5A,B). Following three back-crosses to A619, revertants had an average of 1.3 tassel branches compared with 5.8 in the normal siblings (Table 1B). The upright angle was similar to that identified in the branch angle

Fig. 1. Loss of lg1 affects leaf and tassel development. (A) A normal maize leaf (+/+), contains proximal sheath (s) and distal blade (b) separated by ligule (arrow) and auricle (a). (B) lg1-R lacks ligule and auricle. (C-E) Close-up of leaves split at the midrib (C) normal. (D) lg1-R, (E) lg1-n2375. (F,G) Tassel branch profile of normal compared with lg1-R. (H-J) The pulvinus (arrow) is visible in normal but missing in lg1 mutants.
defective1 (bad1) mutant (Bai et al., 2012), although they did not
describe a change in tassel branch number. Following a cross of
wab1-rev to bad1, all F1 progeny had upright and fewer tassel
branches, demonstrating that the two mutations are allelic. No
visible changes were detected in the leaf. We refer to bad1 as
wab1-bad because Wab1-R was identified and named first (Hake
et al., 1999; Hay and Hake, 2004). The wab1-bad1 and wab1-
bad2 lesions affect the same highly conserved bHLH domain as
Wab1-R (Fig. 4A).

LG1 and WAB1 have overlapping expression patterns
We quantified wab1 and lg1 transcript accumulation in Wab1-R leaves
by RT-PCR. Expression of wab1 and lg1 increased in P9 and P10
Wab1-R primordia compared with wild type (Fig. 4B,C). At the P11
stage, where a leaf could be dissected into blade, ligule and sheath,
wab1 misexpression was detected in the ligule and blade but not the
sheath of Wab1-R leaves (Fig. 4B). In these same tissue samples, lg1
was increased in the Wab1-R blade and absent in the sheath (Fig. 4C),
suggesting that wab1 spatially regulates LG1 accumulation.

We carried out in situ hybridizations with wab1 in order to
determine its expression domain (Fig. 4D-I). We were unable to
detect wab1 in normal leaves (Fig. 4D,E) but did find expression at
the base of both spikelet pair and branch meristems (Fig. 4H,I).
From serial transverse sections of 1-2 mm tassels, a sharp zone of
expression was detected on the adaxial side of the branch meristem,
adjacent to the main rachis (Fig. 4H). This expression pattern was
transient and not detected at the base of more mature tassel branches.

As predicted from the quantitative (q) RT-PCR results, we found
strong expression in Wab1-R leaves (Fig. 4F,G). Expression was
visible in Wab1-R starting with a P4 leaf and continued into the next
few leaves. Expression was stronger towards the margins than the
midrib (Fig. 4G). Both the timing and position of wab1 expression
were consistent with the dominant Wab1-R mutant phenotype
(Foster et al., 2004; Hay and Hake, 2004) and similar to the
misexpression of LG1 in Wab1-R.

LG1 requires WAB1 in the tassel
Given the tassel branch angle phenotype in wab1-rev (Fig. 5A,B),
we measured the branch angle of Wab1-R-Dominant mutants,
segregating in the B73 background. Branch angle was 6° in
normal siblings compared with 25° in Wab1-R/+ heterozygotes
(Table 1C). Plant phenotypes were examined for a family that
segregated both gain- and loss-of-function mutants in the A619
background (Fig. 5C; supplementary material Fig. S3). The tassel
branch angle was greater in Wab1-R plants compared with both
normal siblings and loss-of-function mutants (Fig. 5C). qRT-PCR showed that wab1 expression levels were higher in tassels of Wab1-R mutants (Fig. 5D). Thus, the dominant Wab1 mutation causes a larger branch angle, whereas loss of wab1 function results in a small angle and fewer branches.

We examined wab1 mRNA levels in seedlings and tassels of wab1-rev plants. In the seedling, where wab1 was normally excluded, wab1 misexpression disappeared. In the tassel, where wab1 was normally expressed, wab1 levels were still high (supplementary material Fig. S4). Thus, the mutation in the DNA-binding domain did not interfere with the increased expression conferred by the dominant mutation in the tassel, but it did in the leaf. These results suggest that a functional WAB1 protein is needed to maintain high levels of wab1 expression in Wab1-R leaves, a zone where wab1 is normally absent.

We examined LG1 accumulation in the tassel to see whether it was affected by loss of WAB1 function. Ig1 levels disappeared in the wab1-rev mutant tassels compared with seedlings (Fig. 5E). LG1 immunolocalization confirmed an absence of protein accumulation in axils of tassel branches in wab1-rev mutants compared with Wab1-R/+ plants (Fig. 5F-I), consistent with the hypothesis that WAB1 positively regulates Ig1 in the tassel. We detected normal LG1 accumulation in the blade-sheath boundary of wab1-rev mutants (Fig. 5J,K; supplementary material Fig. S5), suggesting that WAB1 is not needed for Ig1 expression in the leaf. The combined increase of Ig1 in Wab1-R and loss of Ig1 expression in wab1-rev supports the hypothesis that WAB1 regulates Ig1.

**Genetic interactions of Wab1-R and Ig1-R**

To determine whether Ig1 and wab1 interact genetically, we examined the phenotype of double mutants in a segregating family. Tassel branch angles were similarly narrow between Ig1-R and the Ig1-R; Wab1-R/+ double mutant, suggesting that Ig1 acts epistatically to Wab1-R (Fig. 6A). These results are consistent with WAB1 being upstream of LG1.

We quantified blade width and length in the Ig1-R; Wab1-R double-mutant families. Ig1-R mutants were narrower than wild type at the auricle but not at the mid-blade point. The double-mutant leaves were narrower than either single mutant at both positions and significantly shorter (P<0.01) (Fig. 6B), suggesting a synergetic interaction.

These results highlight regulatory interactions between wab1 and Ig1 (Fig. 6C). In the context of the tassel, where wab1 is normally expressed, Ig1 is dependent on wab1, and Ig1-R is epistatic to Wab1-R. In the leaf, where wab1 is normally excluded, the double-mutant phenotype is synergetic, suggesting that these gene products have opposing effects on leaf shape and that the ectopic accumulation of LG1 counteracts some of the effects of wab1 in the leaf.

**DISCUSSION**

We show that LG1 protein accumulation is normally confined to a narrow band of cells at the blade-sheath boundary of the leaf and in the axil of tassel branches. In Wab1-R leaves, LG1 accumulates earlier and expands up into the blade when compared with wild type. We cloned Wab1-R and discovered it encodes a protein with a TCP bHLH domain that had recently been identified as a tassel...
branch angle mutant (Bai et al., 2012). *wab1* is expressed in tassel branch axils, overlapping with LG1 accumulation. In the absence of *wab1*, LG1 accumulation disappears. *wab1* is normally excluded from wild-type leaves but is ectopically expressed in *Wab1-R* mutant leaves, mirroring LG1 accumulation. Our data reveal a gene regulatory interaction that normally functions in the tassel but was recruited to the leaf in the *Wab1-R* mutant, leading to the dominant phenotype. Our data also suggest that the ligule functions as a boundary that separates tissue types and that creation of this boundary is correlated with correct medial-lateral growth.

**The nature of the dominant mutant phenotype**

The nature of the *Wab1-R* mutant is unknown. We did not detect any changes in the coding region compared with the progenitor nor did we identify any large polymorphisms, such as an insertion or deletion by Southern blot hybridization. Sequencing outside of the coding region was confounded by differences in the *Wab1-R* progenitor PF4902, compared with the reference genome. Given that *Wab1-R* arose following another tissue culture (Hake et al., 1999), it may have been caused by an epigenetic mutation (Manning et al., 2006) or a distal transposon, such as the transposon 60 kb upstream of *tb1* (Studer et al., 2011). *wab1* is normally silenced in leaves, but is expressed in *Wab1-R*. Another mutation, *wab2*, has a similar ectopic auricle phenotype when homozygous but no tassel phenotype. Future research into *wab2*, which may be a negative regulator of *wab1*, should lead to an understanding of what normally keeps *wab1* silent in leaves.

**LG1 is downstream of WAB1**

Grasses are characterized by a distinct leaf morphology that includes an enclosing sheath, a photosynthetic blade, two auricles and a ligule.
fringe. The first sign of a preligule band is a zone of division that occurs in a P6-P7 leaf primordium. These divisions are parallel and perpendicular to the long axis of the leaf. At about P7-P8, divisions occur that are periclinal to the surface, causing growth out of the plane of the leaf (Sharman, 1941; Sylvester et al., 1990). The periclinal divisions initiate the actual ligule and do not occur in the lg1-R leaf, leading to a failure of ligule and auricle formation (Sylvester et al., 1990). Previous work, in which RT-PCR (Foster et al., 2004; Moreno et al., 1997) and whole-mount in situ hybridization (Moon et al., 2013) was used, has shown that lg1 is expressed at the ligule. We used an antibody to follow the timing of LG1 accumulation at a cellular resolution. LG1 protein is visible in a band of ~20 cells coincident with the first divisions. The band of LG1 accumulation narrows such that not all dividing cells accumulate LG1 protein. Accumulation is strongest on the adaxial epidermis, consistent with the formation of the ligule on the adaxial side of the leaf. Accumulation outside the adaxial domain may be required for development of the auricle.

In Wabi-R, the pattern of LG1 accumulation correlates well with the dominant mutant phenotype (Foster et al., 2004; Hay and Hake, 2004). LG1 is detected in Wabi-R starting at the P4 stage, the same stage at which ectopic wab1 is detected and when the phenotype first manifests as a narrow leaf primordium. Both LG1 accumulation and wab1 expression extend throughout the leaf width and distally into the blade. The increase in width at the auricle compared with mid-blade in Wabi-R mutants is consistent with the zone of increased LG1 expression.

In the inflorescence, LG1 protein accumulates in the axes of tassel branches early in their development. This pattern overlaps that of wabi and is dependent on wab1. In the wabi loss-of-function mutant, fewer branches form and LG1 protein fails to accumulate. Branches that do form are upright. In the gain-of-function mutant, an increase of LG1 and wab1 mRNA occurs with a concomitant increase in tassel branch angle. Unlike the leaf, where wab1 is normally excluded, the increase in wabi and LG1 in the tassel is confined to their normal regions of expression, affecting only tassel branch angle.

Given that LG1 still accumulates in leaves of wabi-rev plants, WAB1 is sufficient to turn on lg1 in the leaf but is not necessary. We hypothesize that in wild type an unknown transcription factor, perhaps a different TCP, turns on lg1 in the leaf.

TCP expression in boundaries
The narrow leaf phenotype of Wabi-R is consistent with a role in restricting growth suggested in studies of other TCP genes. teosinte branched1 (db1) is expressed in maize lateral branches and suppresses elongation of the branch (Doebly et al., 1997; Hubbard et al., 2002). Cycloidea is expressed in the dorsal part of Antirrhinum floral meristems, which leads to the zygomorphic floral form (Luo et al., 1996). cinnamata mutants show extra growth at the margins, revealing a lack of growth restraint (Nath et al., 2003). BRC1, the closest Arabidopsis thaliana gene to wab1, is expressed in axillary meristems to promote growth arrest (Aguilar-Martineze et al., 2007).

In contrast to the expression domain of BRC1 and db1 within the lateral meristem, wab1 is expressed in the boundary between lateral organs and the meristem. Rather than repressing growth of the lateral organ, wab1 expression may repress growth in the axil. The reduction in branch number seen in wabi loss-of-function mutants suggests that this boundary expression is required for branch initiation.

Lateral organ boundaries and the ligule
Support for the idea of a boundary between lateral organs and the shoot apical meristem is well-supported by analysis of boundary genes (Aida and Tasaka, 2006). Whether boundary genes function at the ligule has not been determined. However, LATERAL ORGAN BOUNDARY (LOB) regulates brassinosteroid (BR) function, and manipulation of BR ameliorates the lob defect (Bell et al., 2012; Gendron et al., 2012). BR has a well-documented role in the ligule in rice. Mutants that fail to perceive BR have upright leaves with small auricles, whereas addition of BR to leaves causes the blade to lean out because of expanded auricle cells (Wada et al., 1981; Yamamura et al., 2000).

We propose that the ligule functions as a boundary. The mature sheath and blade contain different epidermal cell types, distinct venation and unique abaxial-adaxial patterning (Candela et al., 2008; Russell and Evert, 1985; Sylvester et al., 1990). At this boundary, reorientation of growth occurs with the ligule growing out of the plane of the leaf. LG1 or a gene downstream may act as an organizer of tissue polarity (Green et al., 2010). In mutants without the ligule, such as Liguleless narrow (Moon et al., 2013) and Wabi-R homozygotes, a lack of integrity is documented with proximal identity (sheath) spreading into distal regions (blade). Boundaries are also needed for lateral growth; mutants that lack ligules are narrower. Interestingly, leaves of dominant Kn1 mutants with ectopic ligule and auricle in the blade are wider than those of their normal siblings (Freeling and Hake, 1985; Ramirez et al., 2009), suggesting that the ectopic boundary formation supports additional medial-lateral growth.

The role of LG1 and WAB1 in plant architecture
Identifying the tissue-specific regulation of LG1 accumulation provides insight into its role in plant architecture. Quantitative trait mapping identified a region upstream of lg1 as a QTL for domestication in rice (Ishii et al., 2013; Zha et al., 2013). In maize, comparisons of ear and tassel expression showed that lg1 is normally excluded from ear primordia but is expressed in the highly branched ear of a ramosa1 mutant (Eveland et al., 2013). We identified a LG1 regulator that normally functions in the tassel. In the absence of wab1, tassel branches are upright and few, and lg1 is not expressed. In Wabi-R tassels, the increase in wabi leads to an increase in LG1 and a larger branch angle. wabi itself might also play a role in natural variation. Both wabi and lg1 map to QTL for tassel branch number (Brown et al., 2011; Mickelson et al., 2002).

In Wabi-R leaves, the gene module is redeployed, with ectopic wab1 and expanded LG1 accumulation that affects leaf width and proximal-distal patterning. We speculate that this gene module is utilized in other examples of morphological variation — similar to the story of KNOX and CUC genes, and their roles in leaf diversity (Bharathan et al., 2002; Blein et al., 2008; Floyd and Bowman, 2010).

MATERIALS AND METHODS

Plant materials
Wabi-R arose from anther tissue culture following a cross of PF4902 and HF1. Sequencing revealed the parent was PF4902. Potential alleles Wabi-DC and Wabi-RM (Hay and Hake, 2004) carry the same polymorphisms as Wabi-R and PF4902 and are, thus, assumed to be pollen contaminants and not independent alleles. wabi-bad1 was introgressed into A619 four times (Bai et al., 2012). The lg1-R allele was obtained from the Maize Genetics Stock Center and introgressed at least seven generations into W23. The lg1-n2375 line was obtained from the Maize Genetics Stock Center and introgressed twice into B73.

For expression and phenotypic analysis of young plants, seedlings were grown in the greenhouse. Dissected parts were fixed in FAA overnight or frozen in liquid nitrogen. For screens of mature plant phenotypes and/or large populations, plants were grown at the Gill Tract summer field in Albany, CA. For mature plants, leaf phenotypes were scored at the leaf above the ear. Tassels were measured at or just prior to dehiscence.
**Recombinant mapping, revertants and genotyping**

Families segregating 1:1 for Wab1-R/+;+/- were screened for recombination between umc2372 and bmc1329. Recombinants were further tested with primers within this interval. A total of 1300 individuals were examined.

The wab1- rev allele was identified following EMS mutagenesis of Wab1-R. Pollen from 20 homozygotes introgressed into B73 was treated with ethylmethane sulfonate (EMS) (Neuffer, 1982). A 1% solution of EMS in paraffin oil was stirred overnight. A further dilution was made with 1 ml of pollen, 1 ml of 1% EMS and 14 ml of paraffin oil. After 40 min of shaking, pollen was applied to silks of inbred A619 with a paintbrush. Five thousand plants were screened for normal-appearing plants in the Gill Tract field (2011). All normal plants were screened for a CAPS marker in the TCP gene with primer set P1 and P2 (supplementary material Table S1), followed by Dral digestion. One of the normal plants carried the Pf4902 polymorphism and it was again crossed to A619. Southern blotting was performed as previously described (Kerstetter et al., 1994). 15 μg of genomic DNA from Wab1-R homozygotes and their progenitor (PF4902) was digested with seven enzymes (supplementary material Fig. S2) and blotted with a probe created using primers P1 and P2 (supplementary material Table S1).

The identification of wab1-bad1 plants was confirmed by sequencing analysis with primer set P3 and P4. Both alleles of lg1 were identified by phenotype. Sequencing of the BHLH gene within the mapping interval used P5/P6 and P7/P8 primer combinations (supplementary material Table S1).

**In situ hybridization**

*In situ* hybridization was performed as described (Jackson, 1991) with modifications (Bortiri et al., 2006), except that tissue was fixed for 16-18 h instead of 1 h. Two different wab1 probes were generated, corresponding to the 5'-end of wab1 cDNA but excluding the conserved TCP domain (P9/P10 and P11/P12, supplementary material Table S1). The two RNA probes were synthesized by using a DIG RNA labeling mix (Roche) and mixed prior to hybridization after verifying that individual probes generated the same pattern.

**Expression analysis**

Quantitative real-time PCR (qRT-PCR) was performed as described (Bolduc and Hake, 2009). The primer sets used for wab1 were P13/P14, for lg1 P15/P16 and for the gap run control P17/ P18 (supplementary material Table S1). For each experiment, at least three biological replicates and two technical replicates were assayed on a BioRad CFX instrument, and averaged – except for those shown in Fig. 4B,C, which come from two biological replicates pooling four individuals each. Normalization against a *gapdh* gene and relative fold enrichment were calculated by using the Normalized Expression mode (ΔΔCq) (Helleman et al., 2007) integrated in the instrument software.

**Antibody creation and immunolocalization**

The antibody against full-length LG1 was created as described (Chuck et al., 2010). Sequence encoding full-length LG1 protein was cloned into pENTR (using P19/P20, supplementary material Table S1) and, subsequently, into pDEST15 or pDEST17 (Invitrogen) to generate the N-terminal fusion proteins. The LG1 protein used for immunization of guinea pigs (Cocalico Biologicals) was produced in *E. coli* and purified by using a N-terminal HIS-tag. The serum was affinity purified against full-length LG1 expressed as a GST-tagged N-terminal fusion protein.

Maize plants were grown and sampled as described above and fixed in FAA under vacuum infiltration, dehydrated through an ethanol series into Histoclear and embedded in Paraplast plus. Tissue was sectioned to 10 μm using a Leica microtome. Localization was performed as previously described (Jackson, 1991). Primary anti-LG1 (guinea pig) was used at a 1:500 dilution, and guinea pig *α*-alkaline-phosphatase-conjugated secondary antibody was used at a 1:5000 dilution (Abcam). The alkaline phosphatase color reaction was stopped in water and the slides were mounted in aqueous mounting medium for imaging.

**Statistical analysis**

Unpaired Student’s *t*-test using mean, standard deviation and number was used to determine significance between populations. Standard deviations are shown in graphs throughout the paper.

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**Competing interests**

The authors declare no competing financial interests.

**Author contributions**

Y.H. carried out experiments. K.H. designed and carried out experiments. S.H., M.W.L., N.B., A.H. and H.C. designed and carried out experiments and wrote the manuscript.

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**Supplementary material**

Supplementary material available online at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.111955/-/DC1

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