The maize brown midrib4 (bm4) gene encodes a functional folylpolyglutamate synthase

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SUMMARY

Mutations in the brown midrib4 (bm4) gene affect the accumulation and composition of lignin in maize. Fine-mapping analysis of bm4 narrowed the candidate region to an approximately 105 kb interval on chromosome 9 containing six genes. Only one of these six genes, GRMZM2G393334, showed decreased expression in mutants. At least four of 10 Mu-induced bm4 mutant alleles contain a Mu insertion in the GRMZM2G393334 gene. Based on these results, we concluded that GRMZM2G393334 is the bm4 gene. GRMZM2G393334 encodes a putative folylpolyglutamate synthase (FPGS), which functions in one-carbon (C1) metabolism to polyglutamylate substrates of folate-dependent enzymes. Yeast complementation experiments demonstrated that expression of the maize bm4 gene in FPGS-deficient met7 yeast is able to rescue the yeast mutant phenotype, thus demonstrating that bm4 encodes a functional FPGS. Consistent with earlier studies, bm4 mutants exhibit a modest decrease in lignin concentration and an overall increase in the S:G lignin ratio relative to wild-type. Orthologs of bm4 include at least one paralogous gene in maize and various homologs in other grasses and dicots. Discovery of the gene underlying the bm4 maize phenotype illustrates a role for FPGS in lignin biosynthesis.

Keywords: brown midrib, lignin, folylpolyglutamate synthase, folylpolyglutamate synthase, Zea mays, methylenetetrahydrofolate reductase.

INTRODUCTION

Maize brown midrib (bm) mutants, so named for the reddish-brown pigmentation of their midribs, affect lignin concentration and composition (Barriere et al., 2004, 2007; Vermerris et al., 2010). Lignin is a heteropolymer involved in the strengthening of stalks and contributes to the resistance of plants to some insects and pathogens (Santiago et al., 2013). Lignin accumulates in the secondary cell walls and is cross-linked with arabinoxylans through ferulate bridges. In maize, polymers of lignin are composed of H, G, and S lignin, which, respectively, are composed of the three different hydroxycinnamoyl alcohol subunits (monolignols), p-coumaryl (H), coniferyl (G), and sinapyl (S) alcohol (Barriere et al., 2007). Three of the six previously characterized bm mutants are known to be involved in the lignin biosynthetic pathway. bm1 and bm3 encode cinnamyl alcohol dehydrogenase (CAD) and caffeic acid O-methyltransferase (COMT), respectively. CAD catalyzes the synthesis of coniferyl and p-coumaryl alcohols, while
COMT catalyzes the synthesis of sinapyl alcohol (Vignols et al., 1995; Halpin et al., 1998). The recently cloned bm2 encodes a functional methylenetetrahydrofolate reductase (MTHFR) involved in the formation of the key methyl donor, S-adenosyl-L-methionine (SAM) (Tang et al., 2014). SAM links MTHFR with lignin biosynthesis by serving as a methyl donor for both COMT and caffeoyl CoA 3-O-methyltransferase (CCoAOMT) (Figure 1) (Tang et al., 2014).

In this study, we describe the characterization and cloning of a fourth bm gene, bm4, which encodes a functional polyglylutamate synthase (FPGS, EC# 6.3.2.17) that acts upstream of MTHFR in the lignin biosynthetic pathway (Figure 1). FPGS functions in one-carbon (C1) metabolism to catalyze the γ-linked polyglutamlylation of tetrahydrofolate (THF). In plants, C1 metabolism feeds into the biosynthesis of purines, thymidylate, serine, methionine, and formylmethionine (fMet) for which THF is required. Polyglutamlylated folates are the preferred substrates of folate-dependent enzymes and are the primary forms of folate found in living cells (Cossins and Chen, 1997; Mehrshahi et al., 2010). Thus, we hypothesize that FPGS-catalyzed polyglutamylation of THF stimulates the downstream synthesis of polyglutamlylated 5-methyl THF catalyzed by the bm2-encoded MTHFR (Figure 1) (Tang et al., 2014). It is therefore reasonable that a mutation in the FPGS gene (i.e., bm4) would alter lignin content and/or composition.

RESULTS
Mapping bm4 to a 105 kb interval on chromosome 9

Like all brown midrib mutants, bm4 mutants display a distinctive pigmentation phenotype relative to wild-type siblings (Figure 2b,g,i,k,m,o,q). The bm4 mutation also affects the accumulation and composition of lignin (Table 1). These results suggested a role for bm4 in lignin biosynthesis and provided the impetus to identify the gene underlying this mutant. Previously, the bm4 gene had been mapped to the distal end of the long arm of chromosome 9 (Burnham, 1947). Our fine-mapping experiments (Experimental Procedures) established that the bm4 gene is located in a 3 cm interval (198.5–201.2 cm) that encompasses physical positions 154.33–155.45 Mb of the maize reference genome (RefGen v2 [AGPv2] with gene annotations v5b.60). Subsequent mapping experiments narrowed the bm4 candidate region to an approximately 127 kb interval (155 454–156 566 kb) that contains eight genes. A third mapping population consisting of 10 000 F2 plants that was segregating for bm4 was generated by selfing an F1 derived from a cross between the inbred B73 and a mutant plant that carried bm4-ref. In this population, 1417 plants displayed the bm4 phenotype (Tables S1 and S2). The shortage of mutant plants relative to the expected 25% is probably a consequence of an early-stage necrosis phenotype that co-segregates with the bm4 phenotype in B73-derived populations segregating for bm4-ref (S. Hill-Skinner, unpublished observation). Because this necrotic phenotype was not observed in other populations segregating for bm4 mutant alleles, there is no evidence to suggest that it is directly caused by bm4 mutants. All bm4 plants were screened for recombination events within sub-regions of the candidate interval (154.33–155.45 Mb, RefGen v2 [AGPv2] with gene annotations v5b.60) using PCR-based genotyping. Of the 56 identified recombinants, two were found to have recombination breakpoints within a 105 kb interval (154 397.6–154 502.6 kb). This interval contains six genes (Figure S1).

RNA-Seq analysis and gene expression of six candidate genes in the bm4 fine-mapping interval

As part of a screen to determine whether any of the six genes in the candidate bm4 interval were differentially expressed between bm4 mutant and wild-type siblings, we conducted an unreplicated RNA-Seq experiment. Only one of these six genes showed significantly decreased expression based on Fisher’s exact test (Figures S1 and S2B). This gene, GRMZM2G393334 (154 454 066–154 460 083 bp, RefGen v2 [AGPv2] with gene annotations v5b.60), encodes a putative FPGS. Because FPGS also has a substrate that is upstream of the bm2-encoded MTHFR enzyme (Figure 1) (Tang et al., 2014), we selected GRMZM2G393334 as the bm4 candidate gene.

The expression of GRMZM2G393334 across tissues of young seedlings and, to a lesser degree, mature plants was visualized via qTeller (qTeller.com) (Figure S3). Based on these results, GRMZM2G393334 is expressed in a wide variety of tissues as expected for an enzyme involved in a central metabolic process. In addition, quantitative reverse transcription polymerase chain reaction (qRT-PCR) of GRMZM2G393334 was performed on RNA extracted from plants each of which was homozygous for one of five Mu-derived bm4 alleles or bm4-ref (Table S2). All the mutants accumulated less bm4 transcript (2–16%) than the non-mutant B73 inbred (Figure 3), thereby confirming the results of the RNA-Seq analysis.

Seq-Walking based whole genome Mu-flanking sequencing

Seq-Walking (Li et al., 2013) was conducted using DNA from bm4 mutant plants isolated from six separate Mu-tagging events in 2011 (Methods) (Table S2). The rationale for this experiment is that at least some of these plants would be expected to contain Mu insertions in the bm4 gene that are not present in non-mutant stocks. A Seq-Walking library was constructed from pooled DNA of all six Mu alleles. The library was sequenced using a Life Technologies’ PGM instrument. A total of 296 304 out of 544 689 reads (54.4%) remained after quality trimming. Of these trimmed reads, 249 456 (84.2%) could be mapped to the B73 reference
Figure 1. BM4 in connection with lignin biosynthesis.
FPGS (BM4) is connected to the lignin biosynthesis pathway through a series of polyglutamylated molecules and BM2. Chemical structures were downloaded from KEGG (http://www.genome.jp/kegg/). '—' indicates a series of steps that converts polyglutamylated THF to polyglutamylated 5,10-methylene THF (Cossins and Chen, 1997).
genome and 238,118 (80.4%) could be uniquely aligned to the reference genome. In total, seven Mu insertions were detected within the bm4 mapping interval in gene GRMZM2G393334 (Table S3). All but one of these insertion sites were represented by only a few reads (Table S3).

PCR-based sequencing of Mu-tagging alleles

To confirm the Mu insertions detected via Seq-Walking and determine which are associated with particular bm4 mutant alleles, PCR primers were designed to amplify each insertion (Table S4). PCR was conducted on the original pre-pooled DNA samples used for Seq-Walking as well as DNA samples from the B73 inbred and a stock homozygous for the bm4-ref allele (Table S2). Strong PCR bands detected via gel electrophoresis were sequenced. These sequencing experiments confirmed the presence of a Mu1 insertion in the first intron of the candidate gene for the plant carrying the bm4-Mu 11-8050D allele that was not detected in other DNA samples, including B73 and the bm4-ref stock (Figure 4).

Subsequently, similar PCR-based analyses were conducted on the four mutants isolated from the 2013 mutant screen using a series of gene-specific primers designed based on the sequence of GRMZM2G393334 in combination with the MuTIR primer (Table S4 and Table S2). Allele-specific Mu1 insertions were detected in exon 1, intron 2, and exon 4 of GRMZM2G393334 in the bm4-Mu 13-7033E, bm4-Mu 13-7029B, and bm4-Mu 13-7064E alleles, respectively (Figure 4). These results confirm that GRMZM2G393334 is bm4.

Figure 2. Phenotypic characterization of bm4 mutant phenotypes. bm4 mutants display reddish coloring of their leaf midribs. Plants shown were grown in the greenhouse under 27°C daytime temperature and 24°C night-time temperature. (a, b) B73 wild-type and bm4-ref; (c, d) B73; (e, f) bm4-ref; (g, h) bm4-Mu 13-7027D; (i, j) bm4-Mu 13-7029B; (k, l) bm4-Mu 13-7033E; (m, n) bm4-Mu 13-7064E; (o, p) bm4-Mu 11-8034B; (q, r) bm4-Mu 11-8050D. Phenotypic appearance of the adaxial (a) and abaxial (b) sides of bm4-ref and B73 leaves. (g, i, k, m, o, q) Phenotypic appearance of the abaxial sides of bm4-Mu mutants. Phloroglucinol-hydrochloric acid staining of the adaxial (c) and abaxial (d) sides of B73 wild-type midrib tissue. Phloroglucinol-HCl staining of the adaxial (e) and abaxial (f, h, j, l, n, p, r) sides of bm4 mutant midrib tissue. Scale bars = 100 μm.
Table 1  Lignin characteristics of wild-type and mutant plants at different developmental stages

| Year | Stage | Genotype | Klason lignin | Biological replicates (n) | WT-MUT | S/G difference | WT-MUT |
|------|-------|----------|---------------|--------------------------|--------|----------------|--------|
| 2014 | PS 9  | WT       | 0.194 ± 0.011 | 1                        | 1.32   | 0.027*         | 1.32   |
|      |       | MUT      | 0.167 ± 0.005 | 2                        | 1.00   | 0.032*         | 1.00   |
| 2012 | PA 1  | WT       | 0.198 ± 0.008 | 2                        | 1.50   | 0.027          | 1.50   |
| 2010 | PS 2  | WT       | 0.194 ± 0.005 | 2                        | 1.22   | 0.032*         | 1.22   |
| 2012 | PS 1  | WT       | 0.196 ± 0.004 | 3                        | 1.45   | 0.049*         | 1.45   |
| 2014 | PS 9  | WT       | 0.192 ± 0.004 | 3                        | 1.21   | 0.032*         | 1.21   |

Klason lignin values are based on 2–3 technical replicates. Compositional values are based on one technical replicate. One biological replicate is a single, whole-plant sample. S/G = G (mol g⁻¹ dry wt) / C0 (mol g⁻¹ dry wt).

Klason lignin values are based on 2–3 technical replicates. Compositional values are based on one technical replicate. One biological replicate is a single, whole-plant sample. S/G = G (mol g⁻¹ dry wt) / C0 (mol g⁻¹ dry wt).

Most of the GRMZM2G393334 gene, including the entire coding region, was amplified and sequenced from a stock homozygous for the bm4-ref allele. Sequence comparisons to the corresponding sequence from the B73 reference genome revealed 11 substitutions (three transversions and eight transitions), a single six-base insertion, and two single-base deletions in the coding region. Each of the 11 substitutions was also detected in at least one of the NAM founder inbreds (McMullen et al., 2009), none of which display a bm4 mutant phenotype, indicating that these substitutions are not the causal mutation of bm4-ref. Although the six-base insertion was not detected in the NAM founders, it was detected in three of four inbreds (Q66, Q67 and B77) that contributed to our Mu-active stocks (Dataset S2). The two deletions were detected in neither the NAM founder inbreds nor the Mu parents (Datasets S1 and S2). In particular, the deletion in exon 14 is predicted to cause a frameshift and premature stop codon in the translated protein (Figure S4). However, because non-coding regions of the gene which were not sequenced could harbor a causal mutation and the frameshift and premature stop codon would only affect the C-terminus of the protein which is in any case outside of the conserved domain it is not possible to conclude whether the deletions in the reference allele are causative.

To understand the origins of the six bm4 mutants for which Mu insertions could not be identified, the bm4 gene was amplified from DNA from mutant plants carrying these alleles. Based on the crossing strategy, these plants were expected to be heterozygous for a new bm4 allele derived from the Mu parent and the bm4-ref allele. As discussed above, the bm4-ref allele contains at least 29 polymorphisms relative to the B73-derived Bm4 allele (Datasets S1 and S2). Sequence analyses identified three substitutions in the coding region of the bm4-Mu 11-8034B/bm4-ref plant relative to the bm4-ref allele (Dataset S2), including a non-synonymous substitution in the conserved Mur_Liga_se_M domain of GRMZM2G393334, which may have an impact on protein function (Figure S4). Because this substitution is not present in any of the 27 founder inbreds of the NAM population (McMullen et al., 2009), it could potentially be causative. At all sites assayed, no polymorphisms were detected relative to bm4-ref in DNA from the other five bm4-Mu mutant plants, consistent with the hypothesis that these plants may carry maternally derived deletions of GRMZM2G393334, i.e. deletions that arose in the Mu-active stocks. Gene deletions have been identified previously from Mu stocks (Walbot, 2000).

**bm4 encodes a functional FPGS**

MET7 in yeast encodes an FPGS protein that is essential in methionine biosynthesis and met7 mutant strains are methionine auxotrophs (Masselet and De Robichon-Szulmajster, 1975). Expression of maize Bm4 (Figure S5) in
mutant MATa met7 strains successfully complemented the met7 methionine auxotrophy (Figure 5), thus demonstrating that maize bm4 encodes a functional FPGS.

**bm4 lignin concentration and composition**

Phloroglucinol–HCl staining reveals qualitative differences in lignin deposition in midrib tissues between bm4 mutant lines and non-mutant controls (Vermerris et al., 2010). Consistent with this previous study, we found that vascular tissue and epidermal cells of midribs from non-mutant plants (B73 in our case) stain much more heavily than do those of midribs of bm4 mutant plants that are homozygous for the bm4-ref allele (Figure 2c–f). These results indicate greater deposition of lignin in B73 midribs. Similar differences were observed between B73 and plants that carried some of the newly isolated bm4-Mu alleles or that were putatively hemizygous (Figure 2h, j, l, n, p, r).
Lignin concentration and composition of stalks was measured quantitatively from plants that were backcrossed into B73 and homozygous for the bm4-ref allele and non-mutant controls. Lignin concentration and composition were determined using Klason lignin and thioacidolysis, as previously described (Tang et al., 2014). Stalks were collected in 2010, 2012, and 2014. The 2010 experiment involved a comparison of bm4-ref mutants in a B73-like background (via two generations of backcrossing; Experimental Procedures) versus B73. These stalks were collected post-senescence (PS; approximately 5 months after planting). The 2012 and 2014 experiments involved comparisons of stalks from bm4-ref mutant and wild-type siblings, both of which were the products of three generations of backcrossing to B73. In the 2012 experiment, stalks were collected either post-anthesis (PA; approximately 2 months after planting) or PS from the same field. Stalks in the 2014 experiment were collected from the same field, but only PS. Probably as a consequence of the interest in using maize stover for animal feed, previous studies assayed lignin content in brown midrib mutants during the stage of development at which silage is harvested, i.e., after anthesis but before maturity (Barriere et al., 2004; Vermerris et al., 2010). Consistent with this prior literature, our analyses of lignin concentration revealed both PA and nearly all PS stalks assayed from plants homozygous for the bm4-ref allele accumulate approximately 10-14% less lignin than do wild-type siblings (Table 1) (Barriere et al., 2004; Vermerris et al., 2010). Similar to results obtained for bm2 (Tang et al., 2014), the ratio of S to G lignin is elevated in bm4-ref stalks relative to wild-type at both stages of development analyzed (Table 1).

Analysis of BM4 paralogs

BLASTP analysis of the protein sequence (AFW89831.1) encoded by the bm4 gene (GRMZM2G393334) revealed at least one potential paralog in the maize genome. The GRMZM5G869779 gene encodes three protein isoforms (DAA49397.1, DAA49396.1, and DAA49398.1), which respectively share 72, 72, and 69% identity with BM4 over 93, 93, and 56% of the full-length BM4 sequence (Table S5). Like bm4, GRMZM5G869779 is expressed across many young, and to a lesser degree, mature tissues (Figure S6).

Analysis of BM4 homologs

As discussed above, the bm4 gene encodes a functional FPGS. This enzyme has received significant attention because of its importance in human pathology (Galpin et al., 1997; Rotts et al., 1999; Christoph et al., 2012). In plants, FPGS is most often reported to be involved in the polyglutamylation of folates in C1 metabolism. These polyglutamylated folates are the preferred substrates of folate-dependent enzymes (Cossins and Chen, 1997; Mehrshahi et al., 2010). Homologs of FPGS have been identified in various plant species. Among the grasses, FPGS proteins fall into two clades, the first of which contains the protein encoded by bm4 (Figure 6 and Table S5). The Oryza sativa, Brachypodium distachyon, and Setaria italica protein sequences in the first clade share 86, 85, and 84% sequence identity with BM4 over 89, 89, and 100% of BM4, respectively. The Sorghum bicolor, O. sativa, B. distachyon, S. italica, and paralogous Zea mays (two isoforms) protein sequences in the second clade share 73, 70, 74, 73, and 72% sequence identity with BM4 over 89, 90, 94, 96, and 93% of BM4, respectively. The three FPGS genes of Arabidopsis thaliana share 50-62% sequence identity with BM4 (Figure 6 and Table S5). The proteins encoded by these three genes accumulate in the mitochondria, chloroplast, or cytosol, respectively (Ravanel et al., 2001).

DISCUSSION

Six maize loci have been defined by brown midrib mutant phenotypes. Five of six of these mutants have shown to result in decreased lignin content of stalks (Halpin et al., 1998; Barriere et al., 2004, 2007; Guillaumie et al., 2008; Vermerris et al., 2010; Mechin et al., 2014; Tang et al., 2014). Three of these genes have been previously cloned.

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only one of these genes, GRMZM2G393334, showed by fine-mapping experiments contains six genes (Figure approaches in combination with Seq-Walking analysis of metabolism (Cossins and Chen, 1997; Mehrshahi glutamylation of THF as part of one-carbon (C1) synthase (FPGS) as demonstrated in yeast complementation experiments (Figure 3). FPGS is involved in the polyglutamation of THF as part of one-carbon (C1) metabolism (Cossins and Chen, 1997; Mehrshahi et al., 2010).

FPGS has been shown to play multiple roles in plants. The two known isoforms of FPGS of Oryza sativa appear to play roles in seed development (Anukul et al., 2010). The three isoforms of FPGS of Arabidopsis thaliana accumulate in the mitochondria, chloroplast, and cytosol (Ravenel et al., 2001). There is evidence that the mitochondrial FPGS is necessary for proper nitrogen utilization early in Arabidopsis seedling development (Jiang et al., 2012). In addition, the plastidial FPGS is necessary for post-embryonic cell expansion and meristem maintenance in developing roots (Srivastava et al., 2011). Double FPGS mutants in Arabidopsis have been shown to display embryo and seedling lethal phenotypes (Mehrshahi et al., 2010). In contrast, our own studies show the maize bm4 mutant does not exhibit any pronounced defects in seedling development, including roots (Figure S7).

We are unaware of any prior reports of FPGS affecting lignin biosynthesis. A role for this enzyme in this pathway is, however, consistent with the fact that polyglutamylated THF is converted by a series of steps to polyglutamylated 5,10-methylene THF, which is used by bm2-encoded MTHFR to generate 5-methyl THF (Cossins and Chen, 1997; Mehrshahi et al., 2010). Polyglutamylated 5-methyl THF acts as a substrate for the synthesis of methionine, which is used as a substrate for the generation of SAM, which in turn serves as a methyl donor for the lignin biosynthetic enzymes COMT and CCoAOMT (Figure 1) (Tang et al., 2014).

Consistent with the hypothesis that bm4-encoded FPGS works upstream of bm2-encoded MTHFR is the finding that both proteins are predicted to localize to the cytoplasm (Table S6). In addition, mutants in both genes display similar lignin phenotypes. Both mutants accumulate reduced concentrations of lignin in their stalks relative to wild-type. Notably, both mutants also exhibit increased ratios of S to G lignin in stalks relative to wild-type (Table 1) (Tang et al., 2014). Finally, the bm4 and bm2 genes exhibit similar expression patterns across tissues (Figure S8). Vermerris et al. (2010) have reported that bm2-bm4 double mutants exhibit further reductions in lignin accumulation relative to the single mutants and wild-type along with severe defects in plant growth. These studies were conducted using the reference alleles of bm2 and bm4. The double mutant phenotype could be most easily explained if these reference alleles are leaky mutants, such that two partial defects in a common biochemical pathway would result in a more extreme phenotype than either partial defect alone. Our results indicate that the bm4-ref allele is leaky, but do not provide evidence for the bm2-ref allele being leaky (Figure 3).

Due to the involvement of FPGS in a key metabolic process, it was initially surprising that bm4 mutant plants are viable even though they exhibit little bm4 expression relative to non-mutants (Figure 3). We hypothesize that the bm4 homolog GRMZM5G8689779 provides sufficient FPGS activity to avoid lethality. Consistent with this hypothesis, GRMZM5G8689779, like bm4, is expressed in many tissues (Figure S6).

In Arabidopsis thaliana, there are three known isoforms of FPGS. Each isoform is localized to the mitochondria, chloroplast, or cytosol. All forms act to polyglutamylate THF, but do so in a compartment-specific manner (Ravenel et al., 2001). Polyglutamylation is thought to lock folates in the given compartment, thus directing them towards specific biosynthetic processes (Appling, 1991; Mehrshahi et al., 2010). The putative cytosolic FPGS isoform is hypothesized to act upstream of the bm2-encoded MTHFR (Ravenel et al., 2001). More recent literature suggests some functional overlap exists among the various Arabidopsis isoforms (Mehrshahi et al., 2010). It is possible that the
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maize FPGS isoforms behave in a similar fashion, because three of four subcellular localization predictions place BM4 in the cytoplasm (Table S6). However, subcellular localization of homologous FPGS proteins proved inconclusive. THF that is not polyglutamylated may diffuse into the cytosol and supply minimum levels of THF necessary for survival. Alternatively, the BM4 paralog may provide some baseline level of polyglutamylated THF to the pathway upstream of MTHFR. Other explanations may involve compensatory biochemical pathways. Due to the complex nature of carbon metabolism, it is possible that other yet discovered processes and enzymes may lead to polyglutamylated THF. The effect of bm4 mutants on folate accumulation remains to be determined.

EXPERIMENTAL PROCEDURES

Phenotyping bm4 mutants

Mutant bm4 plants are easily distinguishable from non-mutants by the reddish-brown pigmentation of their leaf midribs (Figure 2b). This dark pigmentation is visible in leaf midribs approximately 1 month after planting and persists through maturity. This pigmentation is most obvious on the abaxial side of the leaf (Figure 2b,g,i,k,m,o,q).

Generation of bm4 Mu-tagged alleles

To assist in the identification of the bm4 gene, new mutant alleles of bm4 were isolated by screening large populations of plants derived from two separate crosses of Mu-active lines (female parents) by stocks homozygous for bm4-ref in 2011 (approximately 230 000 plants) and 2013 (approximately 138 000 plants), respectively. In combination, 10 F1 plants that displayed the typical bm4 phenotype (Figure 2b) were identified: six in the 2011 screen and four in the 2013 screen (Table S2).

Primer design

SNPs (single nucleotide polymorphisms) and Indel Polymorphisms (IDPs) for fine mapping the bm4 gene were identified from RNA-Seq data (below). KASP primers to detect these SNPs were designed by LGC Genomics (www.lgcgenomics.com/). IDP primers and gene-specific primers were designed using the online primer design software, Primer 3 (http://biotools.umassmed.edu/bioapps/primer3_www.cgi).

bm4 fine mapping

The bm4 gene was initially mapped on chromosome 9 to an interval (198.5–201.2 cm, 154.33–155.45 Mb, maize RefGen v2 [AGPv2]) with gene annotations v5b.60) defined by the flanking Taqman probes SNPT3210 and SNPT6527 (Table S7), which were identified via comparisons between two genetic maps: MaizeGDB’s IBM 2008 Neighbor 9 Map and ISU’s IBM 2009 Integrated Map (Fu et al., 2005; Lawrence et al., 2008). Subsequently, fine mapping was conducted in 2009 using markers IDPbm4-4 and KASP000 (Table S7), which narrowed the mapping interval (154 438 813–154 565 293 bp, RefGen v2 [AGPv2] with gene annotations v5b.60) to one containing eight candidate genes. Additional fine-mapping experiments were conducted in 2013 using an F2 population segregating for bm4 and consisting of 10 000 plants derived from the cross between a plant that carried the bm4-ref mutant and the inbred line B73 (Table S2). Leaf tissue for DNA isolation was collected from 1417 mutant plants approximately 30 days after planting when the bm4 phenotype (Figure 2b) could be scored. Recombinants in the mapping interval were identified using PCR-based IDP markers IDP154337900 and IDP154765138 (Table S7 and Table S1). Identified recombinants were then genotyped using various IDP and KASP markers within the mapping interval (Table S7 and Table S1).

RNA-Seq analysis

RNA-Seq was performed on an F2 population of 200 plants segregating for bm4 from a bm4-ref by B73 cross (Table S2). Plants were initially genotyped 21 days after planting and phenotyped 32–38 days after planting (Figure 2). Of the 200 plants, midrib tissue was collected from 50 genotyped bm4-ref mutants and 50 wild-type plants 41 days after planting. About 1 inch of tissue was collected from the second youngest leaf of each plant sampled and immediately frozen under liquid nitrogen. Midribs of the bm4-ref plants and wild-type plants were pooled separately and pools were ground under a stream of liquid nitrogen. RNA was extracted from the ground samples using Qiagen’s RNeasy Plus Mini kit.

RNA-Seq libraries were prepared by the Iowa State University DNA Facility and sequenced using Illumina’s GAII Sequencing technology. Single-end reads of length 75 bp were generated. After sequencing, raw reads were subjected to quality trimming according to the previously described method (Tang et al., 2014). Fisher’s exact test was used to test the null hypothesis that the proportions of reads of a given gene among the total reads in genomic space are not different between the bm4 mutants and wild-type siblings. Only genes with at least 40 total reads from both genotypes were used to perform Fisher’s exact test. False discovery due to multiple testing was controlled (Benjamini and Hochberg, 1995). Genes with adjusted P-values (q-values) smaller than 0.001% and absolute value of log2 mutant/wild-type fold change > 1 were declared to be differentially expressed. Note that this comparison did not include biological replication. Both biological and technical variations could contribute to the differential expression between two samples. We, therefore, only used the results of this analysis in prioritizing candidate genes within the candidate interval.

Expression analysis using qTeller

The online tool qTeller (qTeller.com) was used to visualize the expression pattern of selected genes across various tissues. The data supplied by qTeller originates from RNA-Seq experiments conducted in various labs within the plant science community. Additional information on the datasets and in-house analysis can be found on the qTeller website: www.qteller.com.

qRT-PCR

One-month-old midribs from plants homozygous for five of the bm4-Mu alleles, bm4-ref, and B73 (Table S2) were collected according to the method described above for RNA-Seq analysis. Single pools of 3-4 midribs from separate plants were prepared for each genotype. RNA was extracted from each pool using Qiagen’s RNeasy Plus Mini kit and reversed transcribed with Bio-Rad’s iScript cDNA Synthesis kit. Thus, one cDNA library was prepared for each genotype. Two technical replicates of each cDNA sample were run with bm4 gene-specific primers and two technical replicates of each cDNA library were run with GAP primers. Quantitative real-time PCR was performed on a Roche Light Cycler 480II instrument using Bio-Rad’s iQ SYBR Green Supermix.
Relative expression for each sample was quantified using the 2^(-ΔΔCT) method (Yuan et al., 2006). A single expression value was calculated for each genotype by average across all technical replicates.

\[ \text{Sample}_{i} = \frac{\text{Sample}_{j}}{2^\left(\Delta \text{Ct} - \text{Ct}_{	ext{ref}}\right)} \]

and Bm4 insert were digested using the restriction enzymes SaI-HF and XbaI (New England BioLabs) following NEB’s suggested conditions. The digested Bm4 coding sequence and shuttle vector were isolated by gel electrophoresis using Bio-Rad Low Range Ultra Agarose and SYBR Gold (Life Technologies) and purified using Qiagen’s Gel Purification Kit. Purified insert and vector were ligated using NEB’s T4 DNA ligase following the manufacturer’s recommended reaction conditions. \(\text{MAT}_{\text{Bm4}}\) met7 mutant yeast were transformed with either cloned p413-ADH/Bm4 vector or empty p413-ADH vector using the high-efficiency LiAc/SS Carrier DNA/PEG transformation method developed by the Gietz laboratory (http://home.cc.umanitoba.ca/~gietz/method.html) (Gietz and Woods, 2002). Gibco-BRL 10 mg/ml \(\cdot\) herring (AdipoGen). All \(\text{MAT}_{\text{Bm4}}\) met7 vectors were transformed with p413-ADH, and \(\text{MAT}_{\text{Bm4}}\) met7 transformed with p413-ADH/Bm4 strains were plated on YPD and SDC–Media. SDC–Medias. SDC–His and –Met medias were generated using Clontech –His and –Met–Trp amino acid dropout medias, respectively (http://www.clontech.com/). Other media ingredients used included Difco Bacto peptone, Bacto yeast extract, Bacto tryptone, Bacto agar, agar Noble, and yeast nitrogen base without amino acids. Additionally, Fisher dextrose, Acros LjAC dehydrate, and Sigma Trp and PEG350 were also used. \(\text{MAT}_{\text{Bm4}}\) met7-derived yeast strains were cultured in media containing 200 \(\mu\)g/ml \(\cdot\) G418 (AdipoGen). All \(E.\) coli strains were incubated at 37°C for 1–2 days and all yeast strains were incubated at 30°C for 5–3 days.

**Phloroglucinol–HCl staining**

Midribs from 90-day-old \(\text{bm4}\) mutants and B73 plants were hand-sectioned and stained for approximately 1 min with phloroglucinol–HCl. Phloroglucinol–HCl was prepared as a 2× solution of 2% phloroglucinol in 95% ethanol and hydrochloric acid. Stained sections were viewed using a Nikon Eclipse E800 microscope with SPOT RT slider camera attachment (Diagnostic Instruments Inc.) and imaged using SPOT v. 4.0.6 software (Diagnostic Instruments Inc.).

**Characterization of \(\text{bm4}\) lignin concentration and composition**

Entire \(\text{bm4}\)-ref and wild-type stalks were collected for lignin analysis from field-grown \(F_2\) plants derived from two-three successive rounds of backcrossing the \(\text{bm4}\)-ref allele into the B73 inbred. Stalks were collected either post-anthesis (PA; approximately 2 months after planting) or post-senescence (PS; approximately 5 months after planting). Stalks were cut at the first aboveground node and stripped of all leaves, ears, and tassels before air-drying for several weeks. Dried stalks were then processed through a Wiley mill with a 2 mm filter and the resulting stover was finely ground for 10 sec in a coffee grinder.

Approximately 300 mg of ground stover was analyzed for lignin concentration via Klassen lignin as described previously (Tang et al., 2014). The Klassen lignin analyses from 2010, 2012, and 2014 are based on one, two, and nine biological replicates per genotype, respectively and three, three, and two technical replicates per sample, respectively. For lignin composition, 10 mg of stover was subjected to thioacidolysis and analyzed by GC-MS, also described previously (Tang et al., 2014). The minor peaks associated with maize H-lignin are not detected using this method. Thioacidolysis analyses for 2010, 2012, and 2014 are based on one, two, and nine biological replicates per genotype, respectively. All thioacidolysis assays are based on one technical replicate per sample.
Identification of BM4 homologs

Homologs of maize BM4 were identified using NCBI’s BLASTP algorithm with the full-length BM4 protein sequence. Homologs with E-values near zero were selected for inclusion in the FPGS phylogenetic tree, which was constructed using the free tool Jalview following the previously published method (Tang et al., 2014).

Subcellular localization

Subcellular localization predictions of proteins were conducted using online software psORT, ipSORT, TARGETP, and MULTICO2 (HiRes) separately with default parameters for plant analyses.

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CONFLICT OF INTEREST

The authors have no conflict of interest to report.

SUPPORTING INFORMATION

Additional Supporting Information may be found in the online version of this article.

Figure S1. Fine mapping indicates bm4 is located in a 105 kb interval.

Figure S2. RNA-Seq expression of 6 genes in the bm4 fine mapping interval.

Figure S3. qTeller results for bm4 gene expression across different maize tissue types.

Figure S4. Amino acid and conserved domain analysis of bm4 alleles bm4-ref and bm4-Mu 11-8034B.

Figure S5. Bm4 sequence design for yeast complementation.

Figure S6. Expression pattern of bm4 versus expression pattern of paralog GRMZM5G869779.

Figure S7. Comparison of bm4-ref and B73 seedling roots.

Figure S8. Expression pattern of bm4 versus expression pattern of bm2.

Table S1. bm4 fine mapping scores.

Table S2. Summary of bm4 alleles.

Table S3. Seq-Walking targets in the bm4 fine mapping interval.

Table S4. Primer information for bm4 sequence and qRT-PCR analyses.

Table S5. Homologs of BM4.

Table S6. Subcellular localization prediction for BM4 and protein homologs in other grasses.

Table S7. Markers used for bm4 fine mapping.

Dataset S1. SNP information for the bm4 gene across various lines.

Dataset S2. SNP information for bm4-Mu alleles and their progenitors.

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