Research Paper

MYB82 functions in regulation of trichome development in Arabidopsis

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Abstract

Trichome initiation and patterning are controlled by the TTG1–bHLH–MYB regulatory complex. Several MYB transcription factors have been determined to function in trichome development via incorporation into this complex. This study examined the role of MYB82, an R2R3-MYB transcription factor, in Arabidopsis trichome development. MYB82 was revealed to be a nuclear-localized transcription activator. Suppression of MYB82 function by fusion with a dominant repression domain (SRDX) resulted in glabrous leaves, as did overexpression of N-terminal-truncated MYB82. Overexpression of MYB82 genomic sequence, but not its cDNA sequence, led to reduced trichome numbers. Further investigation indicated that at least one of the two introns in MYB82 is essential to the protein’s trichome developmental function. An MYB-binding box was identified in the third exon of MYB82, which was inferred to be crucial for MYB82 function because the mutation of this box interfered with the ability of MYB82 to rescue the gl1 mutant. Protein interaction analysis revealed that MYB82 physically interacts with GLABRA3 (GL3). In addition, MYB82 and GL1 can form homodimers and heterodimers at R2R3-MYB domains, which may explain why their overexpression reduces trichome numbers. These results demonstrate the functional diversification of MYB82 and GL1 in trichome development.

Key words: MYB82, GL1, GL3, trichome, Arabidopsis.

Introduction

Trichomes are single-celled epidermal hairs that help protect plants against herbivores, transpirational water loss, and UV irradiation (Marricio and Rausher, 1997; Serna and Martin, 2006). In Arabidopsis, trichomes exist on most aerial plant parts, including rosette leaves, stems, cauline leaves, and sepals, but not on hypocotyls and cotyledons. Trichome morphology and density vary among different organs. Trichomes on rosette leaves contain three to four branches, whereas cauline and stem trichomes are less branched or unbranched, respectively. Trichome density on the abaxial side of leaves increases with plant transition from vegetative to reproductive growth (Telfer et al., 1997).

Trichome formation is controlled by programmed cell determination. The initiation and formation of trichomes has been extensively studied. The trichome developmental process is strictly controlled by transcription factors, which recognize specific DNA motifs in gene regulatory regions to activate or repress transcription, possibly through interaction with other proteins. Trichome initiation is regulated by a network under the control of a WD40–bHLH–MYB complex. In Arabidopsis, TRANSPARENT TESTA GLABRA1 (TTG1), a WD40 repeat protein, regulates trichome differentiation. Loss of function of TTG1 can also result in a lack of trichomes (Walker et al., 1999). GL3 and EGL3 are two functionally redundant bHLH transcription factors, both of which regulate trichome initiation and act as a bridge to mediate the interaction between MYB and TTG1 (Payne et al., 2000; Zhang et al., 2003). The R2R3-MYB transcription factor
GL1 is necessary for trichome initiation, and its mutation causes glabrous leaves (Oppenheimer et al., 1991). MYB23 is functionally equivalent to GL1 during trichome initiation, and they redundantly regulate trichome initiation at leaf edges (Kirik et al., 2005). In contrast to R2R3-MYB proteins, single-repeat R3-MYB proteins act as negative regulators of trichome development. These R3-MYB proteins consist of seven members: CAPRICE (CPC), TRIPTYCHON (TRY), ENHANCER OF TRY AND CPC 1 (ETC1), ETC2, ETC3, TRICHOMELESS1 (TCL1), and TCL2. CPC, TRY, ETC1, ETC2, and ETC3 function redundantly in trichome development (Esch et al., 2004; Kirik et al., 2004a,b; Schiefelbein et al., 2007; Wester et al., 2009). TCL1 plays an important role in trichome formation on stems and pedicels (Wang et al., 2007), and TCL2 functions redundantly with TCL1 in controlling trichome formation on inflorescences (Gan et al., 2011). It has been suggested that single-repeat R3-MYB proteins negatively regulate trichome development by competing with GL1 for binding to GL3/EGL3, resulting in disruption of (R2R3-MYB)–bHLH–TTG1 complexes (Payne et al., 2000; Bernhardt et al., 2003; Esch et al., 2003; Ishida et al., 2008).

The WD40–bHLH–MYB complex regulates the expression of downstream genes to control trichome development. GLABRA2 (GL2), a homeodomain (HD-Zip) transcription factor, is required for trichome morphogenesis. The gl2 mutant produces abnormal trichomes (i.e. most of the trichomes do not expand, and possess only a single branch; Rerie et al., 1994; Masucci et al., 1996; Fyvie et al., 2000; Ohashi et al., 2002), TRANSPARENT TESTA GLABRA2 (TTG2), a WRKY transcription factor, shares functions with GLABRA2 in controlling trichome outgrowth. Mutation in TTG2 causes unbranched trichomes (Johnson et al., 2002). GL2 is directly regulated by GL1, GL3, and EGL3 (Morohashi et al., 2007; Zhao et al., 2008), and TTG2 is a direct target of GL1 (Ishida et al., 2007; Zhao et al., 2008).

This study focused on the function of MYB82 in trichome development and demonstrated that MYB82 functions in the plant cell nucleus as a positive regulator. Although MYB82 loss of function did not disrupt trichome development, MYB82 overexpression led to abnormal trichome development. On the other hand, overexpression of MYB82-SRDX (fused with a dominant repression domain) or an N-terminal R2R3-MYB domain caused glabrous leaves. MYB82 driven by the GL1 promoter was able to rescue the glabrous phenotype by the R2R3-MYB domain caused glabrous leaves. On the other hand, overexpression of MYB82-SRDX plasmid, the genomic sequence was fused with the minimal repression domain (DLELRL). MYB82/GL1 SRDX plasmid, the genomic sequence was fused with the minimal repression domain (DLELRL). GL1 regulatory sequences used in these experiments were described previously (Lee and Schiefelbein, 2001) and included a 1.4-kb 5‘-fragment and a 1.8-kb 3‘-fragment. A 5‘-GAL4+35S minimal promoter sequence was fused into the pOCA28 vector. The putative promoters of MYB82 were amplified from genomic DNA using primers Pro-MYB82-F and Pro-MYB82-R (Supplementary Table S2). The fused Promoter–GUS was cloned into the pOCA28 vector. Transgenic plants were subjected to GUS staining as described by He et al. (2014).

### Materials and methods

#### Plant materials

*Arabidopsis* ecotype Col-0 and its gl1 mutant were used for experiments. Plants were grown at 23 °C under a 16/8 h light/dark cycle or a 8/16 light/dark cycle.

#### Subcellular localization

Full-length cDNA of MYB82 was fused with that of the eGFP protein in a frame downstream of the 35S promoter in a pOCA30a binary vector. The resulting 35S:MYB82-eGFP plasmid was transformed into *Agrobacterium tumefaciens* strain EHA105. The transformed *Agrobacterium* was incubated, harvested, and resuspended in infiltration buffer (0.2 mM acetosyringone, 10 mM MgCl2, and 10 mM MES, pH 5.6) and then infiltrated into *Nicotiana benthamiana* leaves. After infiltration, plants were incubated at 24 °C for 48 h before observation. DAPI staining was used for visualization of cell nuclear DNA. GFP and DAPI fluorescence were observed under a confocal laser scanning microscope (Olympus, Tokyo, Japan).

#### Real-time quantitative RT-PCR

Total RNA (1 μg), extracted using Trizol reagent (Invitrogen), was used for oligo(dT)18-primed cDNA synthesis according to the reverse transcription protocol (Fermentas). The resulting cDNA was subjected to real-time quantitative RT-PCR using a SYBR Premix Ex Taq kit (Takara) on a Roche LightCycler 480 real-time PCR machine. For each reported result, at least three independent biological samples were subjected to a minimum of three technical replicates. The results were normalized using the internal control *ACTIN2*. The primers for quantitative RT-PCR are listed in Supplementary Table S2 (available at JXB online).

#### Plasmid construction

For the 35S:MYB82-eGFP plasmid, MYB82 cDNA was fused in-frame to the 5‘-terminal of eGFP driven by the CaMV 35S promoter in a pOCA30a binary vector. For the 35S:MYB82/GL1-SRDX plasmid, the MYB82/GL1 genomic sequence was fused with the minimal repression domain (DLELRL). GL1 regulatory sequences used in these experiments were described previously (Lee and Schiefelbein, 2001) and included a 1.4-kb 5‘-fragment and a 1.8-kb 3‘-fragment. A 5‘-GAL4+35S minimal promoter sequence was synthesized and inserted into an upstream GUS gene in a binary vector. GAL4 DNA-binding domain (BD) and GAL4 activation domain (AD; AD domain containing nuclear-localized signal from SV40) sequences were amplified from pGBK7 and pGAD7T plasmids, respectively. The primer sequences are listed in Supplementary Table S2. Plasmid construction details are available upon request.

#### GUS reporter analysis

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#### Yeast two-hybrid assay

Fusions with the GAL4 activation domain and the GAL4 DNA-binding domain were performed in the pGBK7 and pGAD7T plasmids. Full lengths or fragments of GL3, MYB82, and GL1 were individually cloned into pGBK7 or pGAD7T plasmids. Growth was determined as described in the Yeast Two-Hybrid System user manual (Clontech).

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Full-length coding sequences of *MYB82* and *GL3* were cloned into binary N-terminal fragment of yellow fluorescent protein (nYFP) and C-terminal fragment of yellow fluorescent protein (cYFP) vectors, respectively. *Agrobacterium* strains transformed with indicated nYFP or cYFP vectors were incubated, harvested, and resuspended in infiltration buffer (0.2 mM acetosyringone, 10 mM MgCl₂, and 10 mM MES, pH 5.6) to identical concentrations (A₆₀₀=0.5). Equal volumes of an *Agrobacterium* culture containing nYFP (A₆₀₀=0.5) and cYFP (A₆₀₀=0.5) were mixed before infiltration into *N. benthamiana* leaves. After infiltration, plants were incubated at 24 °C for 48 h before observation.

### Results

**MYB82 is a nuclear-localized transcription activation factor**

To identify the subcellular localization of MYB82, its coding region was fused with an *ENHANCED GREEN FLUORESCENT PROTEIN* (eGFP) reporter gene under the control of the cauliflower mosaic virus (CaMV) 35S promoter. Tobacco epidermal cells transformed to transiently express MYB82-eGFP showed considerable fluorescent signal in cell nuclei, with no signal observed in other compartments (Fig. 1A). This result suggested that MYB82 is a nuclear-localized transcription factor.

MYB transcription factors function as transcription activators or repressors (Dubos et al., 2010). To clarify whether MYB82 is a transcription activator or a transcription represcor, this work performed transient transcription assays in tobacco leaves. The reporter plasmid contained five tandem copies of the GAL4-binding site upstream of the GUS reporter gene (Fig. 1B). Full-length MYB82 was fused to the GAL4 BD downstream of the 35S promoter as an effector plasmid (Fig. 1B). The GAL4 AD was fused to BD to generate GAL4-BD:AD as a positive effector. Compared with GAL4-BD, GAL4-BD:AD significantly stimulated expression of GUS. When GAL4-BD:MYB82 was coexpressed with the reporter, GUS activities were higher than those observed from GAL4-BD:AD coexpression with the reporter (Fig. 1B). These data demonstrated that MYB82 was able to activate transcription via its intrinsic activation domain.

To further confirm which domain functions as a transcription activation domain, the N-terminal R2R3-MYB domain (nMYB82) and C-terminal domain (cMYB82) were separately fused to GAL4-BD. Coexpression results indicated that the C-terminal domain was responsible for the transcription activation function. Taken together, these data suggested that MYB82 is a nuclear-localized transcription activation factor.

**Function repression of MYB82 resulted in glabrous leaves**

Although the functions of MYB82 are unclear, its protein sequence is highly similar to GL1 (Supplementary Fig. S1), an R2R3-MYB subgroup-15 member (Dubos et al., 2010) and a key regulator of trichome initiation (Oppenheimer et al., 1991). This work speculated that MYB82 might be involved in regulation of trichome development. To confirm this hypothesis, first the expression pattern of MYB82 was determined. The upstream sequence of MYB82 was used to drive the GUS reporter gene (Pro*MYB82*:GUS), which allowed transcription regulation of MYB82 to be monitored. GUS staining suggested that Pro*MYB82*:GUS was mainly expressed in the trichomes of new leaves (Fig. 2A), which implied that MYB82 might function in the initiation of trichomes. This work then obtained a homozygous T-DNA insertion line for *MYB82*, which was generated by the deletion of seven C-terminal amino acids (Fig. 2B). Expression analysis revealed that the abundance of truncated transcripts in the mutant was similar to the level of full-length transcripts present in the wild type (Fig. 2C). Moreover, this mutant was not phenotypically different from wild-type plants. These results suggested that the MYB82 C'-terminal deletion may not affect this protein’s function. Therefore, this work used an artificial miRNA approach (Liang et al., 2012) to suppress *MYB82* expression. An *amiR-myb82* sequence was designed using WMD3 (http://wmd3.weigelworld.org), with an *AthmiR395a* backbone used to drive its expression (Liang et al., 2012).
The amiR-myb82 precursor was inserted into the downstream of the 35S promoter in a binary vector. Twenty transgenic plants were further analysed for MYB82 transcript levels (Supplementary Fig. S1). As expected, MYB82 mRNA abundance was decreased in amiR-myb82 transgenic plants, with GL1 mRNA unchanged (Fig. 2D); however, no obvious phenotypic difference was observed between amiR-myb82 and wild-type plants, implying that MYB82 may function redundantly with its closely homologous genes.

Based on the fact that fusion of a dominant repression domain to a transcriptional activator can convert the latter into a strong repressor by repressing target gene expression (Hiratsu et al., 2003), this work employed a dominant repression approach to investigate MYB82 function. Transgenic Arabidopsis plants (35S:MYB82-SRDX) expressing MYB82 fused with the dominant EAR repression domain (Hiratsu et al., 2004) were generated. The resulting 35S:MYB82-SRDX transgenic plants produced nearly glabrous leaves with a few trichomes in leaf margins (Fig. 2E), reminiscent of the phenotypes exhibited by the trichome defective mutant gl1. As a positive control, 35S:GL1-SRDX transgenic plants were also generated; as expected, 35S:GL1-SRDX transgenic plants produced completely glabrous leaves.

The MYB82 protein consists of one N-terminal R2R3-MYB DNA-binding domain and one C-terminal activation domain. This work hypothesized that overexpression of the N-terminal DNA-binding domain would confer a dominant negative effect by preventing endogenous MYB82 or homologous proteins from associating with their target DNA motif. When nMYB82 with a deletion of the C-terminal domain was constitutively expressed (35S:nMYB82), trichome initiation completely failed, even in leaf margins.

GL2, a downstream target gene of WD40–bHLH–MYB complex, is expressed in the trichome and required for trichome development. This work investigated whether these transgenic plants with less trichomes have low GL2 expression levels. As expected, the trichome number agreed well with GL2 transcript abundance in these transgenic plants (Supplementary Fig. S2). Taken together, MYB82 positively regulates trichome development.

MYB82 introns affected its function

Although GL1 positively regulates trichome initiation, GL1 overexpression reduces trichome number (Larkin et al., 1994). To investigate the effects of constitutive and ectopic expression of MYB82, MYB82 cDNA was inserted downstream of the 35S promoter in a binary vector. The 35S:MYB82c construct was transformed into wild-type Arabidopsis plants. Unexpectedly, no visible trichome-defective phenotype (Fig. 3) was observed in any of the 37 35S:MYB82c transformants although most of them contained high levels of MYB82 transcripts (Supplementary Table S1). It has been suggested that the second introns of GL1 and GaMYB2 contain a MYB-binding box required for gene function (Wang et al., 2004); however, the current work was unable to find a similar MYB-binding box in the two introns of MYB82. Considering the possibility that unknown cis-elements are
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Given that MYB82 displayed a function similar to GL1, this work investigated whether the MYB82 protein was able to complement the trichome defect of the gl1 mutant. Because 1.4-kb upstream and 1.8-kb downstream regions of the GL1 gene are necessary for its appropriate expression (Lee and Schiefelbein, 2001), these two regions were used for the GL1 promoter (Fig. 4). As a positive control, the GL1 promoter was used to drive GL1c or GL1g in the gl1 mutant (Fig. 4). In accordance with a previous report (Wang et al., 2004), pGL1:GLg, but not pGL:GLc, was able to rescue the gl1 mutant. pGL1:MYB82g and pGL1:MYB82c were constructed in a similar fashion. When these two constructs were separately introduced into the gl1 mutant, pGL1:MYB82g completely complemented the mutant, with leaf trichome densities comparable to the wild type, whereas pGL1:MYB82c partially complemented the gl1 mutant, with trichome densities lower than the wild type but higher than the gl1 mutant (Fig. 4).

Both pGL1:MYB82g and pGL1:MYB82c could rescue gl1 mutants

Analysis of MYB82 loss- and gain-of-function suggested that MYB82 could mediate Arabidopsis trichome development.

The MYB-binding box in the third exon of MYB82 was crucial for gene function

Although pGL1:MYB82c promoted trichome initiation in the gl1 mutant, pGL1:GL1c did not (Wang et al., 2004).
These results were confusing, because 35S:MYB82c had no effect on trichome phenotypes. The first intron of the GL1 gene contains an MYB-binding box required for GL1 expression, which explains why pGL1:GL1c could not rescue the gl1 mutant (Wang et al., 2004). However, no MYB-binding boxes are present in MYB82 introns. Speculating that an unidentified cis-element exists in exon sequences of MYB82, this work searched the complete MYB82 genomic sequence and found a perfect MYB-binding box in the third exon (Fig. 5). In contrast, no MYB-binding boxes exist in GL1 gene exons. This box is thus likely responsible for MYB82 gene function. To confirm this hypothesis, this work changed the MYB-binding box sequence without altering the amino acid sequence to generate mMYB82g and mMYB82c (Fig. 5) and then used pGL1:mMYB82g and pGL1:mMYB82c in a complementation assay of the gl1 mutant. As shown in Fig. 5, pGL1:mMYB82g partially complemented gl1, whereas pGL1:mMYB82c had no effect on gl1 trichome initiation. These results suggested that the MYB-binding box in the third exon of MYB82 is required for MYB82 function in trichome initiation.

**MYB82 was incorporated into the TTG1–bHLH–MYB complex**

The conserved signature motif ([DE]Lx2[RK]x3Lx6Lx3R) of MYB proteins is crucial for their interaction with the bHLH protein GL3 that functions in trichome initiation and anthocyanin synthesis (Zimmermann et al., 2004; Dubos et al., 2010). This motif also exists in the MYB82 protein (Supplementary Fig. S3). To verify whether MYB82 interacts with GL3, the MYB82 full-length coding region was fused to the BD domain of pGBK-T7, and GL3 was fused to the AD domain of pGAD-T7. Yeast two-hybrid assays suggested that MYB82 interacted with GL3 (Fig. 6A). To determine which region of the MYB82 protein is responsible for this interaction, the N-terminal region containing the MYB domain and the C-terminal region were separately fused with the BD domain. The N-terminal region was found to be sufficient for MYB82 interaction with GL3 (Fig. 6A). To confirm whether this interaction also occurred in plant cells, bimolecular fluorescence complementation assays were employed (Fig. 6B). nYFP was ligated to MYB82 and cYFP was ligated to GL3. When MYB82-nYFP was transiently coexpressed with GL3-cYFP, strong YFP fluorescence was visible in epidermal cell nuclei of N. benthamiana leaves. No YFP fluorescence was detected in negative controls (i.e. MYB82-nYFP coexpressed with cYFP or nYFP coexpressed with GL3-cYFP; Fig. 6B). These results suggested that MYB82 physically interacts with GL3 in plant cell nuclei.

**MYB82 and GL1 formed homodimers and heterodimers**

Many transcription factors, including bHLH and bZIP transcription factors, function as homo- or heterodimers (Murre et al., 1989; Ferre-D’Amare et al., 1994; Vinson et al., 2002). The Phosphate Starvation Response 1 (PHR1) protein containing a single MYB repeat has been shown to function as a dimer (Rubio et al., 2001). Two closely related R2R3-MYB

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**Fig. 5.** Effect of the MYB-binding box of MYB82 on trichome development. Schematic presentations of constructs are depicted on the left; red letters indicate the wild-type and mutated MYB-binding box; arrows indicate the GL1 promoter; bars and lines indicate MYB82 exons and introns, respectively; red bar indicates a mutated MYB-binding box.

**Fig. 6.** Interactor of the MYB82 protein. (A) Interaction of MYB82 with GL3 in yeast; interaction was indicated by the ability of cells to grow on synthetic dropout medium lacking Leu/Trp/His/Ade and containing 5 mM 3AT; full-length MYB (MYB82 and GL1), N-terminal truncated MYB (nMYB), and C-terminal truncated MYB (cMYB) were cloned into pGBK-T7; full-length GL3 was cloned into pGAD-T7. (B) Interaction of MYB82 with GL3 in plant cells; fluorescence was observed in nuclear compartments of Nicotiana benthamiana leaf epidermal cells, resulting from complementation of the N-terminal portion of YFP fused to MYB82 (MYB82-nYFP) with the C-terminal portion of YFP fused to GL3 (GL3-cYFP).
proteins, MYB21 and MYB24, were recently confirmed to form homo- and heterodimers (Song et al., 2011). Given their similar protein sequences and functions, dimeric interaction likely exists between MYB82 and GL1. To verify this possibility, this work performed a yeast two-hybrid assay. As expected, both MYB82 and GL1 were able to form homodimers and heterodimers (Fig. 7). This work also determined the domain responsible for the interaction, finding that the N-terminal MYB domain is necessary and sufficient for dimer formation (Fig. 7A and B).

Discussion

Most R2R3-MYB proteins have been characterized using genetic approaches and have been found to be involved in the control of plant-specific processes such as primary and secondary metabolism, cell fate and identity, developmental processes, and responses to biotic and abiotic stresses (Dubos et al., 2010). A particularly interesting entity is the WD40–bHLH–MYB transcription complex, which has specific functions determined by different MYB proteins. For instance, the complex regulates anthocyanin biosynthesis in vegetable tissues when MYB75/90/113/114 is incorporated (Gonzalez et al., 2008); when GL1/MYB23 is recruited, the complex regulates trichome initiation and branching (Kirik et al., 2005; Zhao et al., 2008). In roots, WER is present in the complex that controls root hair patterning (Lee and Schiefelbein, 1999). Here, it is suggested that MYB82 joins in the complex and positively regulates trichome development.

R2R3-MYB transcription factors have a modular structure consisting of an N-terminal DNA-binding domain (the MYB domain) and an activation or repression domain usually located at the C-terminus. MYB82 is an R2R3-MYB family member. Transient expression assays indicated that the MYB82 protein was localized in the plant cell nucleus (Fig. 1A) and contained an activation domain in its C-terminus (Fig. 1B). MYB82 showed high sequence similarity with GL1 (Supplementary Fig. S1), implying a role in trichome development. Similar to GL1 overexpression, elevated expression of MYB82 caused reduced trichome numbers. In addition, both pGL1:MYB82g and pGL1:MYB82c promoted trichome formation in the gl1 mutant. These results demonstrate that MYB82 function is nearly equivalent to that of GL1. Because MYB82 is a transcription activation factor, the addition of the dominant repression domain (SRDX) to this protein almost completely suppressed trichome initiation; this result is similar to that obtained using 35S:GLI-SRDX transgenic plants (Fig. 2B). Overexpression of N-terminal truncated protein, which may competitively suppress the association of paralogous MYB-related proteins with target gene cis-regulatory elements, caused completely glabrous leaves. This result suggests that MYB82 is able to promote expression of trichome development-associated genes.

In addition to protein function similarity to GL1, MYB82 also displayed functional divergence. This work found that 35S:MYB82g and 35S:MYB82c have different effects on trichome development. Further analysis suggested that at least one intron is required for MYB82 under the control of the 35S promoter to affect trichome development. The first intron of GL1, similarly to WER and GaMYB2 genes, contains an MYB-binding box required for functional complementation of the gl1 mutant (Wang et al., 2004). No MYB-binding box was found in the introns of MYB82, although it is still possible that unidentified cis-regulatory elements are present. When MYB82 driven by the GL1 promoter was used to rescue the gl1 mutant, pGL1:MYB82g showed complete function complementation of the gl1 mutant, whereas pGL1:MYB82c only partially complemented the
gl1 mutant. In contrast, pGL1:GLIg can complement the gl1 mutant, whereas pGL1:GLc has no contribution to mutant trichome initiation (Wang et al., 2004). The phenotypic difference between pGL1:MYB82c and pGL1:GLc in the gl1 mutant background suggested that the exons of MYB82 contain cis-regulatory elements that are absent from GL1 exons. As expected, MYB82 contains a perfect MYB-binding box in the third exon. Mutation of this MYB-binding box disrupted pGL1:mMYB82c complementation of the gl1 mutant. Although MYB82 is a paralogue of GL1, MYB82 has evolved distinct cis-regulatory elements that directly affect its functions. Taken together, MYB82 shows functional divergence from GL1 in regard to trichome development.

R2R3-MYB subgroup 15 consists of three members: GL1, MYB23, and WER (Dubos et al., 2010). MYB82 and GL1 protein sequences are highly similar to one another. Subgroup-15 members have been confirmed to be incorporated into the WD40-bHLH–MYB complex (Zimmermann et al., 2004). The current work’s protein interaction analysis suggested that MYB82 also interacts with the bHLH transcription factor GL3, implying that MYB82 is involved in trichome development through participation in the WD40–bHLH–MYB transcription complex.

A contradictory phenomenon is the observation that overexpression of positive regulators of trichome development, GL1 and MYB23, as well as MYB82, often cause trichome number reductions (Larkin et al., 1994; Kirik et al., 2001). The current work revealed that MYB82 and GL1 can form homodimers or heterodimers at the N-terminal R2R3-MYB domain. It has been confirmed that, in the WD40–bHLH–MYB complex, MYB interacts with bHLH at its MYB domain (Grotewold et al., 2000). It is therefore very likely that overexpression of the R2R3-MYB protein results in increased production of MYB homodimers or heterodimers, which may competitively lead to fewer WD40–bHLH–MYB complexes, and, consequently, to a reduction in trichome numbers.

## Supplementary material

Supplementary data are available at JXB online.

- **Supplementary Fig. S1.** Expression levels of MYB82 in amIR-myb82 transgenic plants.
- **Supplementary Fig. S2.** Expression levels of GL2 in different transgenic plants.
- **Supplementary Fig. S3.** MYB proteins containing the conserved signature motif ([DE]Lx[RK]x[Lx]x[Lx]x[R]).
- **Supplementary Table S1.** Expression and phenotype analysis of transgenic plants.
- **Supplementary Table S2.** Primer sequences.

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