The miR165/166 Mediated Regulatory Module Plays Critical Roles in ABA Homeostasis and Response in Arabidopsis thaliana

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Abstract

The function of miR165/166 in plant growth and development has been extensively studied, however, its roles in abiotic stress responses remain largely unknown. Here, we report that reduction in the expression of miR165/166 conferred a drought and cold resistance phenotype and hypersensitivity to ABA during seed germination and post-germination seedling development. We further show that the ABA hypersensitive phenotype is associated with a changed transcript abundance of ABA-responsive genes and a higher expression level of ABI4, which can be directly regulated by a miR165/166 target. Additionally, we found that reduction in miR165/166 expression leads to elevated ABA levels, which occurs at least partially through the increased expression of BG1, a gene that is directly regulated by a miR165/166 target. Taken together, our results uncover a novel role for miR165/166 in the regulation of ABA and abiotic stress responses and control of ABA homeostasis.

Author Summary

Functions of miRNAs in plant development and stress responses have been extensively studied. However, little is known about how a miRNA may perform critical functions in both plant development and abiotic stress responses. One well-known miRNA, miR165/166, has critical roles in plant development. In this study, we show that this miRNA also has important functions in ABA and abiotic stress responses. Since the expression level of miR165/166 can be reduced to different extents using short tandem target mimicry (STTM), in the present work, we used STTM165/166 transformants with moderate developmental phenotype to examine its potential role in abiotic stress responses. Our results show that miR165/166 plays critical roles in drought and cold stress resistance as well as in...
ABA responses. Our work reveals that miR165/166-mediated regulatory module is linked with ABA responses and homeostasis through ABI4 and BG1.

Introduction

The phytohormone abscisic acid (ABA) plays critical roles in plant growth and development, such as seed maturation, seed germination, seedling growth, stomatal movement, as well as plant responses to abiotic and biotic stress, including drought, salinity, cold and pathogen infection [1–4]. The fluctuation of cellular ABA levels, which are determined by biosynthetic and catabolic pathways, allow plants to cope with physiological and environmental conditions [5–7]. De novo ABA biosynthesis from carotenoids is the primary pathway to produce ABA [7]. Many genes involved in this pathway have been identified, such as ABA1, ABA2, ABA3, NCED3 and AAO3 [8, 9]. An additional biosynthetic pathway occurs through hydrolysis of Glc-conjugated ABA (abscisic acid-glucose ester [ABA-GE]) to ABA by two glucosidases, AtBG1 and AtBG2, which localize to the ER and vacuole, respectively [10, 11]. Hydroxylation and conjugation are catabolic pathways that mediate the fine-tuning of ABA levels. Members of the cytochrome P450 family, CYP707A1 to CYP707A4, control the hydroxylation reaction, and ABA uridine diphosphate glucosyltransferase (UGT) catalyzes the conjugation of ABA with Glc to produce ABA-GE [12–17].

Plant responses to ABA is mediated by a network of signaling pathways. In the core pathway, ABA is perceived by the ABA receptors, PYRABACTIN RESISTANCE1 (PYR1)/PYR1-likes/REGULATORY COMPONENT OF ABA RECEPTORs (RCARs) [18, 19]. Once bound to ABA, PYLs will recruit PROTEIN PHOSPHOSTASE 2C (PP2C) [20] and form a PYR/RCAR-PP2C complex to inhibit the PP2C activity, thereby activating the SNF1-RELATED PROTEIN KINASE2 (SnRK2) kinases [21–23]. The activated SnRK2s phosphorylate downstream effector proteins including the AREB/ABF-type basic/region leucine zipper (bZIP) transcription factors, which control the expression of many ABA-responsive genes [24, 25]. Among these transcription factors, ABA INSENSITIVE 3 (ABI3), ABI4 and ABI5 are essential regulators in the control of seed germination and early seedling growth [26–32].

A class of single-stranded RNAs that are 20–22 nucleotides in length and are referred to as microRNA (miRNAs) can regulate gene expression at post-transcriptional levels through specific base-pairing to target messenger RNAs [33]. miRNAs play critical roles in plant development, such as phase transition, pattern formation and morphogenesis [34]. miRNAs also play crucial roles in biotic and abiotic stress responses [35–38]. Additionally, more and more evidence is revealing that miRNAs are involved in hormonal responses. miR159 targets several MYB transcription factors, such as MYB33, MYB65 and MYB101, which interact with GA-response elements and control anther development and flowering time under short days [39, 40]. Disruption of the miR159-mediated repression of MYB33 and MYB101 alters responses to ABA during seed germination [41]. The auxin response pathway is also regulated by miRNAs. Proper regulation of Auxin Response Factor 10 (ARF10), ARF16 and ARF17 by miR160 is required for both shoot and root development [42–44]. ARF6 and ARF8 are targeted and negatively regulated by miR167 [45, 46]. Expression of a miR167-resistant ARF6 or ARF8 gene results in ovule and anther development defects [47]. miR167 could also target IAA-Ala Resistant3 (IAR3), which converts an inactive form of auxin to bioactive auxin [48]. miR390 guides the generation of trans-acting siRNAs, which target ARF2, ARF3 and ARF4 that are required for the proper establishment of adaxial-abaxial identity of lateral organs and vegetative phase transition [49–52]. The NAC1 transcription factor is
targeted by miR164 and acts on lateral root development through regulating auxin responses [45, 53–56]. miR393 targets auxin receptor TIR1 and closely related F-box genes [46, 57]. In addition, miR319-mediated regulation of TCP4 is required for the biogenesis of jasmonic acid through the modulation of LIP OxYGENASE 2 (LOX2) [58].

miR165/166 is one of the most extensively studied miRNAs, which have been shown to be involved in plant development. miR165/166 targets the Class III homeodomain leucine zipper family of transcription factor genes, including PHBULOSA (PHB), PHVOLUTA (PHV), REVOLUTA (REV), ATHB-8 and ATHB-15, which are required for the promotion of adaxial identity of lateral organs [59–62]. Recent work revealed that REV could directly regulate the expression of auxin biosynthetic enzymes TAA1 and YUCCA5 (YUC5), which in turn influence free auxin levels, and this was shown to be required for the shade-avoidance response [63]. The cytokinin (CK) biosynthesis gene ISOPENTENYL TRANSFERASE 7 (IPT7) was found to be the direct target of PHB, and the direct activation of IPT7 by PHB was shown to control the root meristem differentiation regulatory network [64].

Here we present evidence for an important role for miR165/166 in the regulation of ABA and abiotic stress responses and the maintenance of ABA homeostasis. We show that disruption of miR165/166-mediated repression of its targets through reducing miR165/166 expression levels leads to a drought and cold resistance phenotype and ABA hypersensitivity during and after seed germination. We found that ABI4 acts downstream of a miR165/166-mediated pathway and could be directly regulated by a miR165/166 target. We also discovered that miR165/166-mediated negative regulation of its targets is essential for maintaining ABA homeostasis at least partly through modulating the expression of BG1, which converts inactive ABA to active ABA. Our study links the miR165/166-mediated regulatory module to the ABA regulatory network and demonstrates a critical role for the miRNA in ABA responses and homeostasis.

**Results**

**STTM165/166 displays a drought and cold resistance phenotype**

To determine whether the miR165/166 mediated network plays important roles in response to abiotic stress, the previously reported stable transgenic Arabidopsis STTM165/166-31nt plants [65], in which the expression of miR165/166 is dramatically reduced, were used in stress resistance tests.

We compared the phenotype of wild type and STTM165/166 plants under drought conditions. When water was withheld from 3-week-old plants for up to 2 weeks, wild type plants severely wilted and displayed injury and reduced growth. In contrast, STTM165/166 plants appeared much healthier and less affected by the limited water (Fig 1A). When the wilted wild type and STTM165/166 plants were re-watered, only a small proportion of the wild type plants survived and continued to grow. However, a substantial proportion of STTM165/166 plants recovered (Fig 1A and 1B). Altered sensitivity to drought stress in plants is often caused by an altered rate of water loss from leaves. Consequently, we analyzed the water loss rate and found that detached wild type leaves lost water at a faster rate than STTM165/166 leaves (Fig 1C).

Interestingly, STTM165/166 is also more resistant to freezing temperatures compared with wild type based on freezing survival assay and cold-induced electrolyte leakage assay (Fig 2A and 2B). Given that CBF genes play critical roles in freezing tolerance, we analyzed the expression of these genes to test whether miR165/166 mediated regulation of freezing tolerance occurs through modulating CBF factors. However, no substantial difference in the expression levels and patterns of CBF1-3 under cold treatment was detected between wild type and STTM165/166 plants (Fig 2C). The expression of known CBF downstream genes, such as
RD29A and COR15A, was also analyzed (Fig 2D) and we found that the transcript levels of these genes in STTM165/166 in response to cold stress are similar to that of wild type. These results indicate that miR165/166 may modulate freezing tolerance through CBF-independent factors.

Deregulation of miR165/166 results in an ABA response phenotype

We also tested the response of STTM165/166 to ABA. Without ABA treatment, there was no significant difference in the seed germination and cotyledon greening between wild type and STTM165/166 (Fig 3A). However, when the wild type and STTM165/166 seeds were sown on MS medium supplemented with ABA, we found that STTM165/166 was hypersensitive to ABA during seed germination. A delay of cotyledon greening was also observed for STTM165/166 plants (Fig 3A, 3B and 3C and S1 Fig). We examined the expression of miR165/166 and its targets in STTM165/166 at this early developmental stage with or without ABA treatment by qRT-PCR analysis, and found that the levels of mature miR165/166 were indeed dramatically reduced (Fig 3D and S2 Fig), and all the five target RNAs examined were elevated to different extents (Fig 3E and S2 Fig). These results indicate that blocking the full function of miR165/166 disturbs ABA responses. We also tested the ABA response of mutants of miR165/166 target genes, but did not observe a significant difference with that of the wild type (S3 Fig).
The miR165/166 mediated regulatory module affects the expression of ABA-responsive genes

The ABA-related phenotype that results from the compromised miR165/166 function indicates that a miR165/166 mediated regulatory module may affect ABA responses. To establish the molecular link between a miR165/166 mediated regulatory module and an ABA mediated regulatory network, we first compared expression of ABA-responsive genes, such as RESPONSIVE TO DESSICATION 29A (RD29A), RD29B, RAB18, EM1 and EM6 in wild type and STTM165/166 plants. Interestingly, without ABA treatment, the transcript levels of these genes were upregulated to different extents in STTM165/166 plants (Fig 4A). However, the difference in the expression of these genes disappeared when exogenous ABA was applied (Fig 4B). When seedlings were treated with 50 μM ABA for different time periods, there were still no significant differences in the transcript levels of ABA-responsive genes between wild type and STTM165/166 under cold treatment (S4 Fig).

Targets of miR165/166 directly regulate the expression of ABI4

Since the expression of ABA-responsive genes was upregulated in STTM165/166 under normal conditions, we speculated that ABA signaling may be activated or endogenous ABA level is altered. We examined the expression of core components of ABA signaling pathway, such as
PYLs (PYR1, PYL1, PYL2, PYL4, PYL5), SnRK2s (SnRK2.2, SnRK2.3, SnRK2.6), ABI1, ABI2 and HAB1. No significant difference in the expression of these genes was found between wild type and STTM165/166 (S5 Fig). We also compared the expression of these genes in wild type and STTM165/166 seedlings treated with 50 μM ABA for different time periods, and no significant difference was detected (S6, S7 and S8 Figs). Since ABI3, ABI4 and ABI5 are central regulators in the control of ABA-responsive genes, we determined the effect of knockdown miR165/166 on the expression of these genes. We found that the expression of ABI4 was substantially increased in STTM165/166 under normal conditions (Fig 5A). We then tested the expression of ABI4 in PHB:PHB G202G-YFP lines expressing a miRNA-resistant version of PHB fused to GFP driven by the PHB promoter. Interestingly, we found that ABI4 transcripts accumulated to higher levels in the tagged lines compared with that of wild type (Fig 5B). Bioinformatic analysis revealed that a typical HD-ZIPIII binding consensus sequence exists in the ABI4 promoter region (Fig 5C), and this prompted us to determine whether ABI4 could be directly regulated by a miR165/166 targeted HD-ZIPIII. Thus, we conducted an EMSA assay,
and found that PHB protein could bind to the region containing the typical HD-ZIPIII binding consensus sequence (Fig 5D). This indicates that a miR165/166 target can directly modulate *ABI4* expression.

**ABA homeostasis is altered in STTM165/166**

We also examined the expression of genes involved in the ABA homeostasis pathway. We could not detect any significant difference in the transcript level of any gene involved in de novo ABA biosynthesis, such as *ABA1* and *NCED3*, between wild type and STTM165/166 (S9 Fig). In addition to genes involved in ABA de novo synthesis, genes required for ABA conjugation or deconjugation also affect ABA homeostasis. We then checked the expression of genes involved in this pathway. Interestingly, we found that the expression of *BG1* was dramatically elevated in STTM165/166 seedlings compared with that of wild type (Fig 6A), but the expression of *UGT* genes was not altered (Fig 6A). We also found that the upregulation of *BG1* in STTM165/166 was not limited to the seedling stage. The transcript level of *BG1* was also higher in STTM165/166 leaves and flowers compared with that of wild type (Fig 6B).

To examine the effect of the altered expression of these genes on ABA levels in STTM165/166, we measured the content of ABA by ELISA using an anti-ABA antibody [10]. We found that the ABA content in STTM165/166 plants was approximately 3 fold of that in wild type (Fig 6C). This indicates that regulation of the *BG1* gene mediated by the miR165/166 regulatory module contributes to changes in ABA content.
To determine whether the upregulated BG1 expression might contribute to the drought resistance and reduced water loss phenotypes of STTM165/166 plants, we generated STTM165/166 plants in bg1-2 mutant background by crossing STTM165/166 plants and bg1-2 mutant plants, and we found that the drought resistance and reduced water loss phenotypes of STTM165/166 plants were partially suppressed by bg1-2 (S10 Fig). These indicate that the upregulation of BG1 in STTM165/166 accounts at least partially for its abiotic stress phenotypes.

miR165/166 targets directly regulate the expression of BG1

Since the expression of BG1 was enhanced in STTM165/166, we next investigated its expression in PHB:PHB G202G-YFP lines to determine whether higher expression of PHB could also affect the expression of BG1. We found that the expression of BG1 was upregulated in the PHB:PHB G202G-YFP line (Fig 7A). To determine whether PHB is directly associated with the BG1 promoter, we first analyzed the sequence of the BG1 promoter and found that it contains a PHB recognition motif (Fig 7B). A ChIP assay was then performed using PHB:PHB G202G-YFP lines and this showed that one region of the promoter was highly enriched relative to the 35S:GFP control (Fig 7C). The enriched region contains the PHB recognition motif. Additionally, EMSA assay further confirmed that PHB protein could bind to the enriched region (Fig 7D). These findings indicate that BG1 is also a direct target of PHB.
Discussion

Unlike some miRNAs, such as miR160, miR167 and miR393, which directly target and regulate the expression of key components of the auxin response pathway, the miR165/166 targets themselves are not major components of hormone response pathways but they regulate the transcription of important components of hormone pathways. Recent work showed that REV could directly modulate auxin biosynthetic gene expression and is involved in the shade-avoidance response pathway [63], whereas PHB directly activates the CK biosynthesis gene IPT7 and is integrated into the root meristem differentiation regulatory network [64]. Here we provide evidence that the miR165/166-PHB module is involved in regulating ABA homeostasis. The expression of BG1 could be directly promoted by PHB. Therefore, upregulation of the miR165/166 target gene expression caused by compromised miR165/166 function results in the increased expression of BG1, which in turn further modulates ABA homeostasis.

Proper regulation of miR165/166 is important for normal ABA responses. Once miR165/166 is repressed, its repression on target genes will be released, and the upregulated expression of miR165/166 targets will directly promote the accumulation of ABF4, which in turn activates downstream ABA responsive genes. Meanwhile, the increased miR165/166 targets could also

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Fig 6. ABA content is altered in STTMM165/166 plants. (A) Quantitative RT-PCR analysis of the expression of genes involved in ABA conjugation and de-conjugation. (B) Quantitative RT-PCR analysis of BG1 expression in various tissues of wild type and STTMM165/166 plants. (C) Comparison of the ABA content between wild type and STTMM165/166 plants.

doi:10.1371/journal.pgen.1006416.g006
upregulate the expression of the BG1 gene, which at least in part contributes to the elevation of ABA content in STTM165/166. Thus, the ABA hypersensitivity phenotype of STTM165/166 during seed germination and post-germination stages might be attributed to both the higher levels of active ABA and stronger ABA response caused by higher expression of BG1 and ABI4, respectively.

Like the ABI3 and ABI5 transcription factors, ABI4 also plays a critical role in ABA responses, but compared with ABI3 and ABI5, how the activity of ABI4 is modulated is largely unknown. In this study, we found that HD-ZIPIII transcription factors, which are the direct targets of miR165/166, could directly bind to the ABI4 gene promoter and regulate its expression. Thus, miR165/166 is relevant to ABI4 in ABA responses. It has been observed that the expression of miR165/166 was altered under different abiotic stress conditions, such as cold, heat, salt and oxidative stress [66–70]. Regulation of miR165/166 expression may help plants to cope with environmental stresses. Given that miR165/166 is an important regulator in plant growth and development, the miR165/166 mediated regulatory module might help coordinate developmental programs with environmental cues to optimize plant growth and developmental processes under stress. miR165/166 is evolutionarily conserved in a wide range of plant
species and its function in plant development is also very conserved. Future studies will determine whether the role of miR165/166 mediated regulatory module in ABA response and homeostasis is conserved in other plant species.

Materials and Methods

Plant materials and growth conditions

All Arabidopsis plants used in this study are in the Columbia-0 (Col-0) ecotype. Plants were grown in soil at 23°C under a 16h light/8h dark cycle. STTM165/166, PHB:PHB G202G-YFP lines, bg1-2 and ab14-1 have been described previously [10, 65, 71, 72].

Plasmid construction

To construct GST-PHB, the DNA of PHB was amplified using the genomic DNA of PHB:PHB G202G-YFP lines as template. The PCR products were purified and digested with EcoRI and inserted into the corresponding sites of the pGEX4T-1 vector.

Germination assay

To measure the rate of germination, seeds were harvested and stored under identical conditions. Seeds were surfaced sterilized and stored at 4°C for 3 days. Seeds were plated on MS plates containing 1% sucrose and 0.3% phytogel, and germinated at 22°C in a 16-h/8-h light/dark condition.

Freezing tolerance assay

Electrolyte leakage assay was performed as previously described [73] to determine the freezing tolerance of plants in this study. In brief, 3-week-old plants grown in soil were subjected to cold acclimation at 4°C for 7 days before freezing treatment. At each temperature point, three replicates were performed. A fully developed rosette leaf was placed in a small tube containing 100 ul deionized water, and a small ice chip was then added to each tube. Incubate the tube in a freezing bath (model 1187, VWRScientific) with temperature at 0°C. The temperature was reduced by 1°C every 30 min until -11°C was reached. At each temperature point, the tubes were removed from the freezing bath and placed on ice. Transfer the leaves and solutions to large tubes with 25 ml deionized water. Shake the tubes overnight and measure the conductivity of solutions. Then autoclave the tubes at 121°C around 20 min, and shake the tubes for another 3 hours before measuring the conductivity. Finally, calculate the ratio of conductivity before and after autoclaving.

For freezing survival assay, 12-day-old seedlings grown on MS plates containing 1% sucrose and 0.8% agar were subjected to cold acclimation at 4°C for 7 days. The freezing treatment was conducted in a freezing chamber with the following program: the temperature was set at 4°C and reduced to 0°C within 30 min and then the temperature was reduced 1°C every 1 hr until -7°C was reached. Transfer the plates at 4°C for 12hr in the dark and recover the seedlings at 23°C for 5 days.

ABA treatment

For ABA treatment, seedlings were grown in ½ MS liquid medium for one week were treated with 50 μm ABA for the indicated times as described previously [74].
Real-time RT-PCR analysis

For the examination of mRNA expression level, total RNA was extracted using the RNaseasy mini kit (Qiagen) according to the manufacturer's instructions, and reversely transcribed using the High-Capacity cDNA Archive Kit (Applied Biosystems). Quantitative real-time PCR was performed using the SYBR Green PCR master mix kit according to the manufacturer's instructions. Actin mRNA was used as an internal control. Relative gene expression level was calculated from 2-ΔΔCt values. Primers used for qPCR are listed in S1 Table.

Mature miRNA quantification

Mature miRNA quantification was performed according to TaqMan Small RNA Assays protocol (Applied Biosystems). Arabidopsis SnoR101 was used as an internal control. TaqMan Gene Expression Master Mix (Applied Biosystems) was used to perform qRT-PCR.

Chromatin Immunoprecipitation (ChIP) assays

ChIP assays were conducted as previously described [75]. Briefly, 2.0 g materials and the anti-GFP (Abcam) antibody were used for ChIP assay. The precipitated DNA was dissolved in 100 ul of TE buffer, and 2 ul was used for ChIP real-time PCR. Three independent biological replicates were performed, and a representative result is presented. Primer pairs used for ChIP enrichment test are described in S1 Table.

Electrophoretic Mobility Shift Assay (EMSA)

GST-PHB recombinant fusion protein was expressed in the E. coli BL21 strain and purified using Glutathione sepharose 4B beads (GE Healthcare). The oligonucleotides were labeled with α-32P-dATP using T4 Polynucleotide Kinase (NEB), the 32P-labeled probes were incubated in 20 ul reaction mixtures containing 20 mM Tris-HCl (pH7.5), 300 mM NaCl, 5 mM MgCl2, 0.1% NP-40, 0.5 mM DTT for 20 to 60 min at room temperature, and separated on 6% polyacrylamide gels in Tris-glycine buffer (50 mM Tris, 380 mM glycine, 2 mM EDTA, pH 8.0). The oligonucleotides used for EMSA are listed in S1 Table.

Measurement of endogenous ABA levels

ABA content was measured with a Phytodetek ABA test kit (Agdia, Inc., Elkhart, IN) following the manufacturer's instructions.

Supporting Information

S1 Fig. The phenotype of wild type and STTM165/166 plants grown on MS medium supplemented with 0.1 μM ABA. Seedlings were photographed 7 days after stratification. (TIF)

S2 Fig. Quantitative RT-PCR analysis of the expression of both mature miR165/166 and its targets of 2-day-old seedlings grown on the MS medium containing 1.0 μM ABA. Three independent experiments were performed, and values are means ± standard deviation. Values are means ± standard deviation. (TIF)

S3 Fig. The phenotype of wild type and phb-13phv-11 plants grown on MS medium supplemented with 1.0 μM and 2.0 μM ABA. Seedlings were photographed 9 days after stratification. (TIF)
S4 Fig. Comparison of the expression of ABA-responsive genes in wild type and STTM165/166 seedlings treated with 50 μM ABA with a time course. Transcript abundance of RD29B and RAB18 was analyzed using qRT-PCR. Three independent experiments were performed, each with three replicates. Values are means ± standard deviation. (TIF)

S5 Fig. Comparison of the expression of core components of the ABA signaling pathway in wild type and STTM165/166 seedlings. Transcript abundance of genes involved in ABA signaling pathway was analyzed using qRT-PCR. Three independent experiments were performed, each with three replicates. Values are means ± standard deviation. (TIF)

S6 Fig. Comparison of the expression of core components of the ABA signaling pathway, PYLs, in wild type and STTM165/166 seedlings treated with 50 μM ABA for different time periods. Transcript abundance of PYLs was analyzed using qRT-PCR. Three independent experiments were performed, each with three replicates. Values are means ± standard deviation. (TIF)

S7 Fig. Comparison of the expression of other core components of the ABA signaling pathway, ABI1, ABI2 and HAB1, in wild type and STTM165/166 seedlings treated with 50 μM ABA for different time periods. Transcript abundance of ABI1, ABI2 and HAB1 was analyzed using qRT-PCR. Three independent experiments were performed, each with three replicates. Values are means ± standard deviation. (TIF)

S8 Fig. Comparison of the expression of other core components of ABA signaling pathway, SnRK2.2, SnRK2.3 and SnRK2.6, in wild type and STTM165/166 seedlings treated with 50 μM ABA for different time periods. Transcript abundance of SnRK2.2, SnRK2.3 and SnRK2.6 was analyzed using qRT-PCR. Three independent experiments were performed, each with three replicates. Values are means ± standard deviation. (TIF)

S9 Fig. Comparison of the expression of genes involved in de novo ABA biosynthesis in wild type and STTM165/166 seedlings. Transcript abundance of genes involved in de novo ABA biosynthesis was analyzed using qRT-PCR. Three independent experiments were performed, each with three replicates. Values are means ± standard deviation. (TIF)

S10 Fig. Comparison of the phenotypes of wild type, STTM165/166 and STTM165/166 in bg1-2 background under drought conditions. (A) Drought resistance test. 3-week-old plants (upper panel) were grown under the same conditions but without irrigation for 12 days (middle panel), and then re-watered for 3 days (lower panel). (B) Quantification of survival rates. Thirty plants of wild type and STTM165/166 were used in each experiment, and the survival rate was calculated from the results of four independent experiments. (C) Water loss assay. Aerial parts of 3-week-old plants were detached and weighed at the indicated time points. Water content at any time point was calculated as percentage of the fresh weight at time zero. Data were derived from four independent experiments (±SD). (TIF)

S1 Table. Primers and oligonucleotides used in this study. (XLSX)
Acknowledgments

We thank Rebecca Ann Stevenson for technical assistance and Dr. Jianhua Zhu for helpful discussion. We thank Dr. Yuhai Cui for seeds of PHB:PHB G202G-YFP lines.

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Role of mir165/166 in ABA Response and Homeostasis


