TOPLESS mediates brassinosteroid control of shoot boundaries and root meristem development in Arabidopsis thaliana

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ABSTRACT

The transcription factor BR1-EMS-SUPPRESSOR 1 (BES1) is a master regulator of brassinosteroid (BR)-regulated gene expression. BES1 together with BRASSINAZOLE-RESISTANT 1 (BZR1) drive activated or repressed expression of several genes, and have a prominent role in negative regulation of BR synthesis. Here, we report that BES1 interaction with TOPLESS (TPL), via its ERF-associated amphiphilic repression (EAR) motif, is essential for BES1-mediated control of organ boundary formation in the shoot apical meristem and the regulation of quiescent center (QC) cell division in roots. We show that TPL binds via BES1 to the promoters of the CUC3 and BRAVO targets and suppresses their expression. Ectopic expression of TPL leads to similar organ boundary defects and alterations in QC cell division rate to the bes1-d mutation, while bes1-d defects are suppressed by the dominant interfering protein encoded by tpl-1, with these effects respectively correlating with changes in CUC3 and BRAVO expression. Together, our data unveil a pivotal role of the corepressor TPL in the shoot and root meristems, which relies on its interaction with BES1 and regulation of BES1 target gene expression.

KEY WORDS: BR signaling, BES1, EAR domain, TOPLESS, Organ boundary, Quiescent center, Quiescence

INTRODUCTION

Brassinosteroids (BRs) are steroid plant hormones with an essential role in plant growth and development (Clouse, 2011; Guo et al., 2013). In tight connection with environmental cues and other plant hormones, BRs control shoot and root growth and distinct developmental programs such as photomorphogenesis, organ boundary formation and vascular differentiation (Ibanes et al., 2009; Bell et al., 2012; Gendron et al., 2012; Wang et al., 2012). BR perception triggers a signaling cascade that ultimately leads to activation and accumulation of two homologous transcription factors: BR1-EMS-SUPPRESSOR 1 (BES1) and BRASSINAZOLE-RESISTANT 1 (BZR1). In the nucleus, BES1 and BZR1 modulate the expression of thousands of genes with a role in cell elongation, BR synthesis, and in the control of multiple cellular processes (He et al., 2005; Yin et al., 2005). Such a wide range of transcriptional effects relies on the ability of BES1 and BZR1 to interact with different families of transcription factors, which partly modify their DNA-recognition motif and switch their transcriptional activity from a repressor to activation function (Yin et al., 2005; Oh et al., 2012). Although early studies showed that BZR1 binds a conserved BRRE (CGTGC/TG) element in the promoters of BR biosynthetic genes (He et al., 2005), whereas BES1 activates gene expression by recognizing as a complex with the bHLH factor BES1-INTERACTING MYC-LIKE 1 (BIM1) an E-box (CANNGT) element in its target promoters (Yin et al., 2005), more recent studies have established that both factors have similar DNA binding and transcriptional activities (Sun et al., 2010; Yu et al., 2011). BES1 and BZR1 interact with the PHYTOCHROME-INTERACTING FACTOR (PIF) family of bHLH factors to co-regulate a large number of light- and BR-responsive genes (Oh et al., 2012; Bernardo-García et al., 2014), and are blocked by the DELLA repressors via a similar sequestration mechanism as PIFs (Bai et al., 2012; Gallego-Bartolome et al., 2012; Li et al., 2012). However, BES1 and BZR1 also play independent roles in other processes, such as BES1-mediated attenuation of abscisic acid (ABA) signaling (Ryu et al., 2014) and BZR1 negative regulation of immune signaling (Lozano-Durán et al., 2013).

BES1 and BZR1 share a conserved ERF-associated amphiphilic repression (EAR) motif in the C-terminal region, and recent studies show that the repressive function of these factors involves direct interaction with the co-repressor TOPLESS (TPL) (Oh et al., 2014; Ryu et al., 2014). TPL and its TOPLESS-RELATED (TPR) homologs belong to the family of Groucho/Tup1 transcriptional co-repressors (Long et al., 2006), which bind a wide range of transcription factors via their EAR motifs to repress downstream targets (Kagale and Rozwadowski, 2011; Causier et al., 2012). Repression by TPL/TPR has been associated with the recruitment of HISTONE DEACETYLASE 19 and 6 (HDA19 and HDA6), two closely related deacetylases that promote chromatin compaction and transcriptional inactivation (Long et al., 2006; Krogan et al., 2012), and SMLX transcriptional repressors (Szemenyei et al., 2008; Pauwels et al., 2010; Wang et al., 2015), in addition to playing a role in the central oscillator through interaction with PRR5, PRR7 and PRR9 (Wang et al., 2013). Likewise, TPL modulates BZR1-regulated cell elongation (Oh et al., 2014) and mediates antagonistic effects of BRs on ABA signaling, a response that is specifically controlled by BES1 (Ryu et al., 2014).

BR signaling is also crucial to the control of cell proliferation in the shoot and root meristems. In the shoot apical meristem (SAM), BRs specifically modulate limited growth of organ boundaries, a group of small rarely dividing cells that separate new forming organs from the meristem (Fletcher, 2002; Reddy et al., 2004;
BZR1 fusions to the fluorescent protein YFP revealed that this factor is depleted in the boundaries, whereas brz1-1D-CFP shows uniform distribution in the SAM and boundary cells (Gendron et al., 2012). BZR1 directly represses expression of the organ boundary identity CUP-SHAPED COTYLEDON1, 2 and 3 (CUC1-3) genes, with constitutive brz1-1D mutants found to display organ fusion defects indicative of impaired organ boundary separation (Bell et al., 2012; Gendron et al., 2012).

Reduced BR signaling is likewise required to maintain quiescence at the root stem cell niche (Gonzalez-Garcia et al., 2011; Heyman et al., 2013). BRs promote quiescent center (QC) cell division through a cell-autonomous pathway that is independent of auxin and ethylene signaling (Gonzalez-Garcia et al., 2011; Lee et al., 2015) and that is mediated by the R2R3 MYB transcription factor BRASSINOSTEROIDS AT VASCULAR AND ORGANIZING CENTER (BRAVO). BRAVO is specifically expressed in the QC and stele initials and maintains QC quiescence downstream from BRASSINOSTEROID INSENSITIVE 1 (BRI1) (Vilarrasa-Blasi et al., 2014).

While recent studies provided evidence of a function of TPL/TPR in BES1/BZR1-mediated control of cell elongation, it is at present unknown whether this family of co-repressors is also involved in the promotion of cell proliferation in response to BR signaling. Here, we show that mutation of the EAR domain in the protein encoded by bes1-D reverses both the organ boundary and QC defects of bes1-D overexpressors. Increased TPL gene dosage aggravates the organ fusion and QC cell division phenotype of bes1-D mutants, while overexpression of the protein encoded by tpl-1 largely overrides bes1-D effects. We show that TPL binds to conserved BRRE and G-box elements in the CUC3 and BRAVO promoters through complex formation with BES1, and that pTPL::TPL seedlings display similar organ fusion defects and increased QC division rates to bes1-D mutants. Together, these results unveil a pivotal role of the co-repressor TPL in BR-regulated expression in the root and shoot meristems, and demonstrate that this function is essential to organ boundary initiation and maintenance, and to the preservation of low QC cell division rates.

RESULTS

BES1-TPL interaction is required for BES1 transcriptional activity

BES1, BZR1 and BEH1-4 all contain a conserved EAR domain (LXLXL) in their C-terminal region. Since EAR domain proteins were identified in complexes with the co-repressor TPL (Kagale et al., 2010), we investigated whether BES1 directly interacts with TPL. We analyzed the interaction of these proteins in vitro in a yeast two-hybrid assay and in vivo using bimolecular fluorescence complementation (BiFC) and co-immunoprecipitation (co-IP) studies in Nicotiana benthamiana leaves. As shown in Fig. S1A, BES1 and TPL were observed to interact in yeast cells, and this interaction is fully dependent on the presence of an intact EAR domain. Fluorescence of the reconstituted split YFP protein was observed in the nucleus of leaf cells co-transfected with the BES1-eYFPN and TPL-eYFPN constructs, but not in cells expressing PIF4-eYFPN and TPL-eYFPN, which were used as negative controls (Fig. S1B). TPL-HA was also pulled down from leaf extracts co-expressing the BES1-GFP and TPL-HA proteins, after BES1-GFP immunoprecipitation. By contrast, a mutated version of BES1, in which the three Leu residues in the EAR domain were replaced by Ala (BES1-EARm-GFP), was unable to pull down TPL-HA (Fig. S1C), demonstrating that TPL and BES1 interact via the BES1 EAR domain.

To test whether this domain is required for BES1 function, we analyzed repressive activity of the wild-type and BES1-EARm proteins in transient assays, using the pDWF4::LUC construct as a reporter. N. benthamiana leaves were agro-infiltrated with the pDWF4::LUC construct alone, or in combination with 3SS constructs for BES1, bes1-D, BES1-EARm or bes1-D-EARm proteins, and leaf discs were used to measure LUC activity. (Note that we refer here to the protein encoded by bes1-D as bes1-D and, likewise, to the protein encoded by tpl-1 as tpl-1.) As shown in Fig. S2A, expression of the BES1 and bes1-D proteins efficiently repressed the DWF4 promoter, but this repressive effect was not observed for the BES1-EARm or bes1-D-EARm mutated proteins. Also, expression of the TPL co-repressor reduced LUC activity driven by the DWF4 promoter and enhanced the repressive effects of BES1 (Fig. S2B), in contrast to a partial reversal of BES1 inhibitory effects observed on expression of the mutant tpl-1 protein. These effects were not observed when TPL or tpl-1 was co-expressed with BES1-EARm, in support of a function of TPL in repressing DWF4 expression via interaction with the BES1 EAR motif (Fig. S2B).

To confirm these results in vivo, we generated 3SS::bes1-D-GFP and 3SS::bes1-D-EARm-GFP transgenic lines, and two bes1-D-EARm lines (L13 and L33) were further characterized (Fig. S3A). As expected, overexpression of the bes1-D-GFP protein phenocopied the bes1-D mutant, with a decreased response to the biosynthetic inhibitor brassinazole (BRZ), and the characteristic bent petioles and curled leaves of adult bes1-D plants (Fig. S3B-D). However, none of these phenotypes was recapitated in bes1-D-EARm-GFP lines, nor in the stronger overexpressor (Fig. S3B-D), indicating that the EAR domain is essential for BES1 function.

BR biosynthetic gene expression confirmed that mutation of the EAR domain abolishes the ability of bes1-D to repress CPD, DWF4 and ROT3 genes (Fig. S3E). IAA19 and PRE5 gene activation was also impaired in bes1-D-EARm lines, suggesting that the EAR domain is not only essential for bes1-D repressive activity but for the transcriptional activation of its target genes. Together, these results establish that the EAR domain is essential for BES1 transcriptional activity, with mutation of this domain inactivating bes1-D function.

Loss of TPL function abolishes the constitutive BR response phenotype of bes1-D mutants

TPL and the four TPR Groucho/Tup1 co-repressors were identified by isolation of the temperature-sensitive tpl-1 mutant, which shows severe apical-basal axis defects and fused cotyledons and, at restrictive temperatures, the replacement of the shoot by an apical root (Long et al., 2006). The tpl-1 mutation has a semi-dominant character due to the dominant-negative effect of the N176H substitution over the rest of the TPL/TPRs proteins (Long et al., 2006). Inactivation of all five TPL/TPR genes is indeed required to recapitate the tpl-1 phenotype, identical phenotypic alterations being also observed in lines ectopically expressing tpl-1 (Wang et al., 2013).

To obtain additional genetic evidence for BES1 and TPL interaction, we generated double tpl-1 OX;bes1-D and TPL::bes1-D lines by crossing plants overexpressing the mutant tpl-1 protein (tpl-1 OX) or which expressed an extra copy of the TPL gene (pTPL::TPL), respectively, into the bes1-D mutant background. As shown in Fig. 1A,B, overexpression of tpl-1 abolished the BRZ-insensitive phenotype of the constitutive bes1-D mutants, with tpl-1 OX;bes1-D seedlings showing shorter hypocotyls than bes1-D or the wild type (WT), and a similar growth inhibition response to BRZ as WT.
Expression of this mutant protein caused by itself the inhibition of hypocotyl elongation, and a hypersensitive response to BRZ, indicative of a function of TPL in BR-dependent promotion of hypocotyl growth. 

BES1 and BZR1 promote plant growth via direct activation of multiple cell wall remodeling and auxin signaling genes, including *IAA19*, *SAUR15* and *PRE5* (Sun et al., 2010; Oh et al., 2012). Expression of these gene targets was significantly reduced in *tpl-1* OX plants, the *tpl-1* protein also suppressing activation of these genes in the *bes1-D* background (Fig. 1C). Moreover, as reported for the *tpl;tpl1:tpl4* triple mutant (Oh et al., 2014), *bes1-D* caused a milder repression of the BR biosynthetic *DWF4*, *ROT3* and *CPD* genes in *tpl-1* OX seedlings than in the WT background (Fig. 1E).

Notably, *tpl-1* overexpression rescues the bent petioles and curly leaf phenotype of adult *bes1-D* plants, with *tpl-1* OX lines showing smaller and more compact rosettes because of their shorter petioles (Fig. 1D). Upon flowering transition, *tpl-1* OX inflorescences were also smaller and more compact than WT, and more detailed phenotypic studies showed that their compact aspect is associated with defects in pedicel elongation. By contrast, *bes1-D* inflorescences were larger than those of WT (Fig. 1E), and had bigger flowers as a result of increased expansion of sepals and petals (Fig. S4). All these phenotypes were rescued by *tpl-1*, the inflorescences of *tpl-1* OX;*bes1-D* plants being identical to those of *tpl-1* OX plants (Fig. 1E, Fig. S4). Together, these results indicate that impaired TPL function interferes with BES1 transcriptional activity, and abolishes not only BES1 repressive function but also its ability to activate gene expression.

**Increased TPL dosage results in organ fusion defects**

Lines with an increased TPL dosage due to expression of an extra TPL gene copy (*pTPL::TPL*) displayed similar organ fusion defects to *bes1-D* mutants (Fig. 2A,C). Fusion of the cauline leaves and pedicels to the main stem and fused sepals and stamens (Fig. 2A,C) were observed in both *bes1-D* and *pTPL::TPL* lines, suggesting that an excess of TPL or BES1 function interferes with proper organ boundary formation. Similar defects were previously reported in *bzr1-1D* mutants (Gendron et al., 2012), indicating that BES1 and BZR1 redundantly control organ boundary formation.

Boundary cells are characterized by expressing a specific set of genes (Tian et al., 2014), including the *CUC1-3* boundary identity genes. This NAC-type family of transcription factors restricts cellular proliferation and differentiation, and plays a pivotal role in organ separation during both the vegetative and reproductive stages (Takada et al., 2001; Vroemen et al., 2003). *CUC1-3* have overlapping functions in boundary maintenance, as indicated by
A few percent of bes1-D (6%) and pTPL::TPL (11%) plants displayed floral patterning defects, such as extra petals, or a reduced number of petals of dissimilar size (Fig. 2D, Table S1). A related phenotype has been described for a mutant of *EARLY EXTRA PETALS 1 (EEP1)*, which encodes a microRNA (MIR164c) that post-transcriptionally regulates CUC1 and CUC2, with eep1 mutants failing to repress CUC1 and CUC2 expression in the second whorl (Laufs et al., 2004; Baker et al., 2005). Although *tpl-1*OX rescued the patterning defects of *bes1-D* plants, penetrance of these alterations was not increased in the *TPL::bes1-D* background (Table S1), suggesting that *TPL* controls petal initiation also via BES1-independent pathways, most likely via regulation of auxin signaling (Szemenyei et al., 2008).

**Fig. 2.** TPL and BES1 regulate postembryonic organ separation and cooperatively repress CUC3 expression. (A–D) Defects in organ boundary formation and maintenance observed in *pTPL::TPL* plants (*TPL* in the figure): pedicel fusion to the stem (A), fused stamens (B), partially fused sepals (C), flowers with three or five petals and petals of different size (D). Arrowheads indicate fused organs. (E) *pCUC3::GUS* expression in the inflorescence and branch junctions of *tpl-1*OX, WT, *pTPL::TPL*, *bes1-D* and *pTPL::TPL::bes1-D* plants. First primary inflorescences were collected for each genotype and used for staining. (F) Detail showing the boundary-associated pattern of *pCUC3::GUS* expression in WT, TPL and TPL::bes1-D inflorescences.

The lack of phenotype of single loss-of-function mutants (Vroemen et al., 2003; Laufs et al., 2004; Hibara et al., 2006; Burian et al., 2015). Likewise, incomplete penetrance of their organ fusion defects suggests that other pathways converge on the control of boundaries (Johnston et al., 2014; Colling et al., 2015; Hepworth and Pautot, 2015).

As for *cuc* mutants, sporadic organ fusion defects such as pedicel-stem fusions (Fig. 2A), fused stamens (Fig. 2B) and partially fused sepals (Fig. 2C) were observed in both *bes1-D* and *pTPL::TPL* plants. Penetration of this phenotype was similar in *pTPL::TPL* and *bes1-D* plants (2–4%, see Table 1), but was notably increased in the double *TPL::bes1-D* background (11% and 18%, see Table 1), suggesting a cooperative function of the BES1 and TPL proteins in mediating these alterations. Expression of the *tpl-1* mutant protein, on the other hand, rescued the organ fusion phenotype of *bes1-D* plants, none of these defects being observed in *tpl-1*OX or *tpl-1*OX::*bes1-D* plants (Table 1).

**Table 1.** Percentage of flowers that contain stamen-stamen or pedicel-stem fusions

<table>
<thead>
<tr>
<th>Genotype</th>
<th>n</th>
<th>Fused stamen (%)</th>
<th>Pedicel-stem fusion (%)</th>
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<td>Col-0</td>
<td>151</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td><em>pTPL::TPL</em></td>
<td>147</td>
<td>3 (2)</td>
<td>3 (2)</td>
</tr>
<tr>
<td><em>bes1-D</em></td>
<td>138</td>
<td>6 (4.3)</td>
<td>3 (2.2)</td>
</tr>
<tr>
<td><em>TPL::bes1-D</em></td>
<td>148</td>
<td>27 (18.2)</td>
<td>17 (11.5)</td>
</tr>
<tr>
<td><em>tpl-1</em>OX</td>
<td>164</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td><em>tpl-1</em>OX::<em>bes1-D</em></td>
<td>110</td>
<td>0 (0)</td>
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TPL regulates organ separation via BES1-mediated CUC3 gene repression

To assess whether the fusion defects in *bes1-D* and *pTPL::TPL* lines were associated with downregulation of the CUC genes, we examined the spatial pattern of CUC3 expression in these plants. A *pCUC3::GUS* reporter line (Kwon et al., 2006) was crossed into the *tpl-1*OX, *pTPL::TPL*, *bes1-D* and *TPL::bes1-D* backgrounds and GUS expression was analyzed by staining of the inflorescences (Fig. 2E,F). During floral transition the SAM is converted to an inflorescence meristem. This process involves the formation of meristem-organ boundaries between the central inflorescence meristem and the floral primordia, and organ-organ boundaries that separate the four concentric whorls and adjacent organs within a whorl. CUC3 is reported to be expressed in each of these boundaries (Vroemen et al., 2003) and, in agreement with previous reports, GUS expression in WT inflorescences was restricted to the adaxial side of the pedicel axis and to the boundaries between floral primordia in the SAM. In floral buds, it formed a ring at the bases of sepals and petals and marked the boundaries between ovule primordia in the gynoecium (Fig. 2F). Notably, *tpl-1*OX increased CUC3 expression in all these boundary regions, while GUS expression was reduced in both *pTPL::TPL* and *bes1-D* plants. Moreover, *TPL::bes1-D* plants showed an additive inhibition of GUS expression, indicating that TPL and bes1-D synergistically suppress the CUC3 gene (Fig. 2E,F).

In paraclade junctions between primary and secondary stems CUC3 expression was restricted to the bases of the cauline leaf and the emerging axillary shoot (Fig. 3B). GUS activity was strongly reduced in *bes1-D* mutants, correlating with defective axillary branch separation (Fig. 3A,B). Reduced GUS expression was likewise detected in *pTPL::TPL* lines, in contrast to *tpl-1*OX which showed an expanded area of CUC3 expression (Fig. 3B). Also, increased TPL dosage resulted in stronger CUC3 inhibition and more severe cauline leaf-branch fusions in *TPL::bes1-D* plants, whereas *tpl-1*OX alleviated the fusion defects of *bes1-D* mutants (Fig. 3C). Similar trends in CUC3 expression were observed by RT-qPCR analyses of young seedlings, with reduced CUC3 transcript levels detected in *bes1-D*, *pTPL::TPL* and *TPL::bes1-D* lines, whereas in the *tpl-1*OX*::bes1-D* and *bes1-D*::EArm backgrounds expression levels were similar to the WT (Fig. 3E). In these analyses, CUC3 levels in *tpl-1*OX seedlings were slightly lower than in the WT, which was likely to be due to the delayed leaf differentiation in this genotype. Altogether, these results demonstrate that TPL and BES1 act in concert to repress CUC3 expression, with impaired TPL function in *tpl-1* overexpressors abolishing *bes1-D*-mediated suppression of CUC3.
factors. To test if TPL binds the same CUC3 promoter elements as BES1, we performed chromatin immunoprecipitation (ChIP) assays using both 35S::BES1-GFP plants and transgenic lines expressing the pTPL::TPL construct in the bes1-D mutant background. BES1-GFP ChIP-PCR studies confirmed that BES1 binds the CUC3 and DWF4 promoters with similar affinities, and associates with the same CUC3 promoter region as BZR1 (Fig. 3D) (Gendron et al., 2012). These two promoter fragments were also enriched by TPL-HA, although binding to the BES1 recognition sites was less efficient than for BES1-GFP (Fig. 3D), consistent with an indirect association of TPL with DNA. Together, these results demonstrate that BES1 recruits the TPL protein to the DWF4 and CUC3 promoters, pointing to a pivotal function of the TPL-BES1 module in the control of organ boundary maintenance through direct repression of the CUC1-3 genes.

TPL modulates root meristem organization through BES1-mediated suppression of BRAVO

Reduced BR signaling is crucial to the control of cell cycle progression in the root stem cell niche and to the correct organization of the meristem, whereas increased BR signaling promotes cell elongation and differentiation in the root transition-elongation zone (Gonzalez-Garcia et al., 2011; Chaiwanon and Wang, 2015). The BAS1 and SOB7 BR catabolic enzymes are expressed in the root cap and reduce availability of bioactive BRs in the adjacent stem cell niche (Chaiwanon and Wang, 2015). In the QC, BR signaling targets the BRAVO and ETHYLENE RESPONSE FACTOR 115 (ERF115) factors, which regulate QC quiescence in opposite ways (Heyman et al., 2013; Vilarrasa-Blasi et al., 2014). BRAVO is expressed in the QC and stele initials and acts as a cell-specific repressor of QC division (Vilarrasa-Blasi et al., 2014). BRAVO is a repression target of BES1 and BZR1, with reduced expression of this gene in bes1-D and bzr1-1D mutants leading to ectopic activation of QC division (Vilarrasa-Blasi et al., 2014). BRAVO is a repression target of BES1 and BZR1, with reduced expression of this gene in bes1-D and bzr1-1D mutants leading to ectopic activation of QC division (Vilarrasa-Blasi et al., 2014). BRAVO also physically interacts with and inactivates BES1, this negative-feedback loop enabling high levels of BRAVO expression in QC cells, at the same time that prevents its suppression as a result of fortuitous activation of BR signaling (Vilarrasa-Blasi et al., 2014).

To assess whether TPL function is required for BR-mediated control of cell progression in the root meristem, we examined QC cell division in pTPL::TPL and tpl-1 OX roots. As shown in Fig. 4, expression of an extra TPL copy notably increased the number of plants with a divided QC, two QC cell layers being observed in 25% of pTPL::TPL roots as compared with 5% in WT roots. By contrast, no QC cell divisions were observed in any of the tpl-1 OX roots analyzed. Moreover, pTPL::TPL expression greatly increased the frequency of divided QC cells in bes1-D plants, a double QC layer or partially duplicated cells being seen in 90% of TPL::bes1-D roots (Fig. 4). Lines expressing bes1-D-EARm, on the other hand,
displayed a WT behavior, indicating that the EAR domain is required for BES1 promotion of QC cell division (Fig. 4A,C). To further prove that TPL and *tpl-1* OX effects on QC division depend on BR signaling, we tested whether altered QC division in these genotypes could be rescued by the brassinosteroid 24-epibrassinolide (BL) or BRZ application. As shown in Fig. 4B,C, increased QC division rates were observed in *tpl-1* OX roots upon BL treatment, although divided cells were still less frequent than in the WT, while the increased QC division phenotype of TPL roots was partially rescued by the inhibitor BRZ. Hence, altogether these results are consistent with a cooperative action of BES1 and TPL in promoting QC cell division.

We next analyzed whether TPL effects on QC cell division correlate with suppressed BRAVO expression by crossing *pBRAVO::GFP* reporter lines into the *pTPL::TPL* and *tpl-1* OX backgrounds. Unfortunately, *pBRAVO::GFP* was silenced in *tpl-1* OX lines and we were unable to examine *tpl-1* effects on the expression of this gene. However, a notable decrease in GFP activity was observed in *pTPL::TPL* lines, providing evidence that an increased TPL dosage leads to BRAVO suppression (Fig. 5A). Owing to increased QC division, these plants displayed disorganized root meristems (Fig. 5A), and this phenotype was reverted by BRZ application (Fig. 5A,B). Western blot studies of *pBRAVO::GFP* and *pBRAVO::GFP;TPL* roots confirmed that TPL causes a similar reduction in BRAVO expression as seen in the WT in response to BL. In addition, BL further suppressed BRAVO expression in *pTPL::TPL* roots (Fig. 5C), suggesting an additive effect of TPL and BL in BRAVO suppression.

Finally, we tested whether TPL is recruited to the BRAVO promoter by performing ChIP-PCR studies on TPL, *bes1-D* lines.

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Fig. 4. TPL regulates QC cell division. (A,B) Microscopy images of mPS-PI stained 6-day-old root tips of the indicated genotypes, grown in long-day conditions on MS medium (A) and MS medium supplemented with 0.4 nM BL or 1 µM BRZ (B). Arrows mark QC position. The 35S::*bes1-D-EARm* line is L33. (C) Quantification of QC cell divisions expressed as percentage (*n*>50 seedlings for each genotype).
Altogether, our results demonstrate that interaction with TPL via its conserved EAR domain is essential for BES1 function in promoting QC cell division, and show that BL effects on QC division depend to a large extent on direct repression of the BRAVO gene by BES1. Thus, these data unveil a novel cell-specific function of TPL in the root stem cell niche.

**DISCUSSION**

BES1 is a pivotal factor in BR signaling, with dual roles as transcriptional activator and repressor. Here, we show that the BES1 EAR domain is essential for its transcriptional activity, and that this conserved domain mediates interaction with the co-repressor TPL, consistent with recent reports (Oh et al., 2014; Ryu et al., 2014).

Notably, overexpression of the mutant tpl-1 protein caused derepression of BES1/BZR1-repressed targets, such as DWF4, ROT3 and CPD, and impaired activation of the induced PRE5, IAA19 and SAUR13 targets (Fig. 1C,E), suggesting that TPL is also required for BES1/BZR1 transcriptional activation functions. This effect was more evident in tpl-1 OX;bes1-D plants, in which tpl-1 partially suppressed constitutive activation of these targets, in particular of PRE5. tpl-1 OX plants in fact showed shorter hypocotyls and petioles than WT and displayed a hypersensitive response to BRZ, while tpl-1 suppressed the BRZ-insensitive phenotype of bes1-D mutants, suggesting that the dominant-negative function of tpl-1 impairs the BR response.

Recent determination of the TOPLESS domain (TPD) crystal structure showed that the N176H substitution in tpl-1 is not relevant in dimerization or EAR binding (Ke et al., 2015). Although the molecular basis for the dominant nature of this mutation is not well understood, our finding that tpl-1 interferes with BES1 target gene activation suggest that TPL is implicated both in BR-repressed and -activated gene expression. Related findings were also obtained by fusion of the bes1-D-mEAR protein to SRDX, TPL or HDA19 (Ryu et al., 2014), which restitutes constitutive BR signaling activity of the protein and leads to elongated hypocotyl growth on BRZ, thus further supporting of a function of TPL in BES1/BZR1 target gene activation. A role for TPL in shoot meristem maintenance has been previously reported through its interaction with the WUSCHEL (WUS) homeodomain and RAMOSA1 zinc-finger transcription factors (Kiefer et al., 2006; Sablowski, 2007; Yadav et al., 2011; Gavallotti et al., 2010). Here, we provided biochemical and genetic evidence for a function of the BES1-TPL complex in direct suppression of the CUC3 and BRAVO genes, which act as cell-specific repressors of cell proliferation in the meristem boundaries and the root QC. We showed that increased TPL dosage causes similar organ fusion and QC division alterations as the constitutive BR response bes1-D mutation. Moreover, TPL and bes1-D have synergistic effects in inhibiting boundary formation and QC quiescence, whereas tpl-1 expression abolishes bes1-D defects. Our findings show that BES1 recruits TPL to the CUC3 and BRAVO promoters to repress boundary and QC cell-specific expression of these genes.

Comparative analyses of BR-responsive gene expression and organ boundary-specific transcriptomes (Tian et al., 2014) provided evidence of a significant overlap between boundary-enriched transcripts and BR signaling-repressed genes (Fig. S5). Most of the BR-repressed transcription factors were reported as BES1 and/or BZR1 direct targets, suggesting that BES1 and BZR1 modulate the expression of other boundary-specific regulators in addition to CUC genes. Interestingly, similar comparative studies of the QC cell transcriptome showed that the only transcription factors targeted by BZR1 and repressed by BL were the BRAVO, MONOPOLE and BES1 genes. BRAVO contains a G-box and several BRRE elements in its 2.1 kb upstream region (Fig. 5D), and significant enrichment was observed for a promoter fragment including the G-box and one of the BRRE elements, previously shown to be recognized by BES1 (Vilarrasa-Blasi et al., 2014), indicating that TPL is recruited to this promoter region by BES1 (Fig. 5E). Additionally, ChIP-PCR experiments on pTPL:TPL and pTPL:bes1-D seedlings grown on BRZ showed that BRZ impaired TPL binding to the BRAVO and CUC3 promoters in pTPL:TPL plants, but not in the BRZ-insensitive TPL:bes1-D background (Fig. 5F), establishing that BES1 is required for TPL recruitment to these promoters.
PLETHORA genes (PLT1, BABY BOOM/PLT4) (Chiawanon and Wang, 2015), supporting a key function of BRAVO downstream of BES1/BZR1 in the root QC.

Reduced division of boundary cells is crucial to the separation of young organs from the central meristem, and to the maintenance and organization of the meristem. Boundary cells express a specific set of genes that restrict cell division and auxin efflux carrier activity while promoting meristematic gene expression (Hepworth and Pautot, 2015). These cells, similar to the root QC, function as a type of organizing center, regulating the patterning and development of adjacent organs (Zádánková and Simon, 2014; Yu and Huang, 2016), thus highlighting a pivotal role of TPL in the organization of the shoot and root meristems. Consistent with this function, TPL is expressed at higher levels in the SAM and root meristem zone, and in young actively dividing tissues (Fig. S6). Moreover, our results provide evidence for a prevalent function of the BES1/BZR1-TPL module in coordinating the balance between cell proliferation and differentiation in both the root meristem and shoot boundary domains, therefore allowing organogenesis to the maintenance of meristem activity.

A further intriguing question is why TPL activity is required for the activation function of BES1 and BZR1. Groucho/Tup1 co-repressors are believed to function as binding scaffolds for histone deacetylases and chromatin remodeling complexes (Long et al., 2006; Zhu et al., 2010; Krogan et al., 2012), but their exact mechanism of action is not yet understood. Although genetic evidence suggests that TPL acts through HDAl9 (Long et al., 2006), high-throughput yeast two-hybrid approaches failed to identify HDAl9 as a direct TPL interactor (Causier et al., 2012), whereas interaction of these proteins was observed in plant extract pulldown experiments (Zhu et al., 2010). This would indicate that additional factors bridge TPL and HDAl9 and, in fact, yeast two-hybrid studies showed that TPL/TPR directly bind PKR1, a homolog of the PICKLE [PKL; ENHANCED PHOTOMORPHOGENIC 1 (EPP1)] chromatin remodeling factor (Causier et al., 2012). Interestingly, PKL was recently shown to associate with PIF3 and BZR1, which recruit this chromatin-remodeling factor to the promoters of the IAA19 and PRE1 genes (Zhang et al., 2014). Thus, it is possible that TPL forms chromatin modification complexes with opposite transcriptional outputs depending on its interaction with BES1 or the BES1-PIF heterodimer, an important task for the future being the identification of such complexes.

**MATERIALS AND METHODS**

**Plant materials and growth conditions**

*tpl*-1 35S::TPL (Wang et al., 2013), *pCUC3::GUS* (Kwon et al., 2006) and *pTPL::GUS* (Tao et al., 2013) genotypes are in the Col-0 background. *tpl*-1 35S::TPL plants were crossed to the *bes1*-D mutant (introgressed into Col-0; Banes et al., 2009) to obtain TPL::bes1-D and *tpl*-1 35S::GUS::Bes1-D, respectively.

Seeds were surface-sterilized for 15 min in 70% (v/v) ethanol and 0.01% (v/v) Triton X-100, followed by two washes of 2 min each in 96% (v/v) ethanol. Air-dried seeds were then sown on half-strength MS agar plates with 1% sucrose and stratified for 3 days at 4°C in the dark. BL (24-epibrassinolide, Sigma-Aldrich) and brassinazole (BRZ, Tokyo Chemical Industry) treatments were performed at 1.0 μM and 0.8 μM, respectively. Hypocotyls were measured using ImageJ (NIH) software.

**Plasmid constructs**

Full-length coding regions for the *Arabidopsis* BES1, TPL and PIF4 proteins were amplified with primers BES1-F/BES1-R, TPL-F/TPL-R and PIF4-YFP-F/PIF4-YFP-R, respectively (Table S2). The *bes1*-D mutant ORF was amplified from an *Arabidopsis bes1*-D mutant cDNA using primers BES1-F and BES1-R. To obtain the BES1-EARm and *bes1*-D-EARm constructs, primers BES1-F and BES1-EARm-R (Table S2) were used to introduce the EAR mutation into the corresponding ORFs, using as a template wild-type and *bes1*-D DNA, respectively. The PCR-amplified fragments were cloned into pENTR/D-TOPO (Invitrogen) and used for subsequent LR reactions.

BES1, BES1-EARm, *bes1*-D and *bes1*-D-EARm full-length coding regions were cloned by LR clonase (Invitrogen) recombination into pGWB5 (Nakagawa et al., 2007) to obtain the 35S::BES1-GFP, 35S::BES1-EARm-GFP, 35S::bes1-D-GFP and 35S::bes1-D-EARm-GFP constructs.

The TPL coding region was inserted by LR clonase recombination into pGWB14 (Nakagawa et al., 2007) to create the 35S::TPL-HA binary vector. The DWF4 promoter region was amplified using primers pDWF4-F and pDWF4-R (Table S2) and cloned into LucTrap-3 (Calderón-Villalobos et al., 2006) to obtain the pDWF4::LUC reporter plasmid.

**Transgenic plants**

35S::BES1-GFP and 35S::bes1-D-EARm-GFP constructs were transformed into the *Agrobacterium tumefaciens* strain GV3101. Arabidopsis transformation was performed through the floral dip method. Homozygous *Arabidopsis* lines were identified by kanamycin resistance and lines with appropriate expression of the transgene selected by western blot immunodetection using an anti-GFP antibody (Roche, 11 814 460 001).

**Bimolecular fluorescence complementation assay (BiFC)**

The TPL, PIF4 and BES1 coding sequences were inserted by LR reaction (Invitrogen) into pBiFC binary vectors containing the N-terminal and C-terminal YFP fragments (YFPN43 and YFPFC43, respectively). Plasmids were transformed into the *N. benthamiana* leaves. The p19 protein was used to suppress gene silencing. Two days after infiltration, leaves were observed under a Leica TCS SP5 laser scanning confocal microscope.

**Co-immunoprecipitation**

*N. benthamiana* leaves were co-infiltrated with *Agrobacterium* cultures bearing the 35S::BES1-GFP, 35S::BES1-EARm-GFP and 35S::TPL-HA plasmids in the appropriate combinations. After 48 h, leaves were homogenized in protein extraction buffer: 20 mM Tris-HCl pH 7.5, 5 mM MgCl2, 75 mM NaCl, 2.5 mM EDTA, 25 mM β-glycerophosphate, 0.1% Nonidet P-40, 10 mM NaF, 0.05% sodium deoxycholate, 5 mM β-mercaptoethanol, 10 µM MG-132, 1 mM PMSF and protease inhibitors (Roche). Extracts were cleared by centrifugation at 13,000 g for 15 min at 4°C, and 1 ml of the supernatant was incubated at 4°C for 3 h with 50 µl anti-GFP magnetic beads (μMACS Epoitope Tag, Miltenyi Biotec). Beads were bound using a magnet and washed five times with 500 µl extraction buffer. Immunocomplexes were eluted by boiling for 2 min in 50 µl 2x SDS loading buffer. Anti-HA-peroxidase (Roche, 11 867 423 001) and anti-GFP- peroxidase (Miltenyi Biotec, 130-091-833) antibodies were used for immunodetection.

**Yeast two-hybrid assay**

Yeast two-hybrid assays were performed with the GAL4 Two-Hybrid System (Clontech). The complete ORFs of the TPL, BES1 and BES1-EARm proteins were introduced by LR clonase recombination into the pGADT7 and pGBK7 Gateway-compatible vectors (Clontech). The NINJA-pGBT9 plasmid was a kind gift from Dr Roberto Solano (CNB-CSIC). Appropriate plasmid combinations were transformed into the yeast strain AH109 by the lithium acetate method and reporter gene activation was assayed by selection on SD-LWHA plates.

**Luciferase activity assays**

*N. benthamiana* leaves were co-infiltrated with *A. tumefaciens* cultures bearing the pDWF4::LUC reporter construct, alone or in combination with 35S::BES1-GFP, 35S::BES1-EARm-GFP, 35S::bes1-D-GFP or the 35S::bes1-D-EARm-GFP effector constructs. Two days after inoculation, 0.5 cm diameter leaf discs were collected and transferred to 96-well microtiter
plates filled with 165 µl 0.5× MS liquid media and 35 µl 1× D-Luciferin substrate (20 µg/ml). At least 12 discs were measured per sample. Luciferase activity was measured with the LB 960 Microplate Luminometer Center using MikroWin software (Berthold).

**Quantitative RT-PCR analysis**

Total RNA was extracted from whole seedlings using the High Pure Isolation kit (Roche). 1 µg RNA was used for first-strand cDNA synthesis using SuperScript II Reverse Transcriptase (Invitrogen). 1 µl of the cDNA reaction was used for quantitative PCR using the FastStart Universal SYBR Green Master Mix (Roche) and a 7500 Real-Time PCR System (Applied Biosystems), following the manufacturer’s instructions. Expression levels were calculated relative to the 35S::GUS gene, using the ΔΔ threshold cycle (Ct) method (Applied Biosystems). Primers used are listed in Table S2. Results correspond to three biological replicates.

**GUS staining**

Freshly harvested plant material was placed in cold 90% acetone for 20 min, washed once with water and transferred to staining solution (50 mM NaHPO₄ buffer pH 7.2, 2 mM potassium ferricyanide, 2 mM potassium ferrocyanide, 2 mM X-glucuronide, 0.2% Triton X-100). After 5 min vacuum infiltration, samples were placed at 37°C overnight. Next day, they were incubated for 30 min in 20%, 30% and 50% ethanol, fixed in FAA (50% ethanol, 5% formaldehyde, 10% acetic acid) and kept in 70% ethanol until visualization with a stereomicroscope.

**Chromatin immunoprecipitation assays**

ChiP assays were performed as described previously (Lee et al., 2007). 3 g of 6-day-old Col-0, 35S::BES1-GFP and pTPL::TPL-HA:bes1-D-GFP seedlings were used for chromatin preparation. The chromatin pellet was sonicated at 4°C with a Diagenode Bioruptor to achieve an average DNA fragment size of ~0.3-0.9 kb. 1 µl anti-GFP (MBL, 598), 1 µl anti-HA (purified in house; 2.2 µg) and 10 µl protein G coupled to magnetic beads (EpiQ) were used for ChiP. DNA was purified using the MiniElute Reaction CleanUp Kit (Qiagen). An aliquot of untreated sonicated chromatin was reverse cross-linked and used as input DNA control for PCR amplification. Primers used are listed in Table S2.

**Confocal microscopy**

Analysis of QC cell division rates and visualization of columella cell starch granules were carried out by imaging fixed stained primary roots obtained through a modified pseudoSchiff-propidium iodide (mPS-PI) staining method (Bernardo-Garcia, S., de Lucas, M., Martinez, C., Espinoza-Ruiz, A., Daviere, J.-M. and Prat, S. (2014); BR-dependent phosphorylation modulates PIF4 transcriptional activity and shapes diurnal hypocotyl growth. Genes Dev. 28, 1681-1694).

**Western blot analysis**

Seedlings were roots were homogenized in extraction buffer: 1× PBS, 0.1% SDS, 0.1% Triton X-100, 100 µM PMSF, 5 µM β-mercaptoethanol and protease inhibitors (Roche). Extracts were cleared by centrifugation at 13,000 rpm (17,900 g) for 15 min, and the protein concentration determined by Bradford assay (Bio-Rad). Protein samples were boiled in 2× SDS loading buffer and loaded on 8% SDS-PAGE gels. Blots were probed with anti-GFP antibody (Roche) and peroxidase-conjugated secondary antibody (Amersham, NA931V). Anti-RPT5 was used as a loading control.

**Acknowledgements**

We thank Dr David Sommers (Ohio State University) for tpi-1 OX and pTPL::TPL seeds, Dr Patrick Laufs (INRA Versailles) for pCUC3::GUS seeds, and Dr Genji Qin (Peking University) for pTPL::GUS seeds.

**Competition interests**

The authors declare no competing or financial interests.

**Author contributions**

S.P., A.E.-R. and C.M. designed the experiments. M.d.L. performed initial studies. A.E.-R. obtained the double mutants and performed their phenotypic and molecular characterization. A.E.-R. and C.M. analyzed TPL and BES1 interaction and carried out the GUS expression studies. A.E.-R. and S.P. performed the LUC transactivation studies. C.M. performed the ChiP experiments and analyzed expression of BRAVO repression. N.F., N.B. and A.I.C.-D. studied QC cell division. A.E.-R. and S.P. wrote the manuscript. All authors revised the manuscript.

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**Supplementary information**

Supplementary information available online at http://dev.biologists.org/lookup/doi/10.1242/dev.143214.supplemental


Fig. S1. BES1 interacts with TPL through the EAR domain. (A) Yeast two-hybrid assay showing TPL and BES1 interaction. TPL interacts with the intact BES1 protein but not with BES1-EARm (EARm), where core Leucine residues in the EAR motif (LXLXL) were substituted by Alanine. TPL interaction with NINJA is included as a positive control. Yeast cells were grown on the synthetic dropout minimal medium lacking Leu and Trp (-LW), or synthetic dropout without Leu, Trp, His and Ade (-LWAH). (B) BiFC showing BES1 and TPL interaction. Nuclear YFP fluorescence is observed in *N. benthamiana* leaves infiltrated with the BES1-eYFP<sup>N</sup> and TPL- eYFP<sup>C</sup> constructs. PIF4-eYFP<sup>N</sup> and TPL-eYFP<sup>C</sup> are included as a negative control. Red fluorescence corresponds to chlorophyll. Scale bars represent 14 µm in the BES1-TPL panel and 50 µm in the PIF4-TPL panel. (C) Co-IP assay. TPL-HA is pulled-down by immunoprecipitation of GFP-tagged BES1, but not by BES1-EARm (EARm-GFP). *N. benthamiana* leaves were agroinfiltrated with BES1-GFP, BES1-EARm-GFP and TPL-HA. Two days after agroinfiltration, total protein extracts were immunoprecipitated with an anti-GFP antibody. TPL-HA was detected in these fractions with an anti-HA antibody.
Fig. S2. The EAR domain is required for the repressor activity of the BES1 factor. (A) The DWF4 promoter containing two BRRE elements was fused to the LUC reporter gene and co-transfected with the 35S::BES1, 35S::bes1-D, 35S::BES1-EARm or 35S::bes1-D-EARm effector constructs into N. benthamiana leaves. (B) TPL regulation of DWF4 expression. Leaves were co-infiltrated with the DWF4 reporter and combinations of Agrobacteria expressing the pTPL::TPL, 35S::BES1, 35S::BES1+pTPL::TPL, 35S::BES1+tpl-1 OX, 35S::BES1-EARm, 35S::BES1-EARm+ pTPL::TPL or 35S::BES1-EARm+ tpl-1 OX, as indicated. Leaf discs were collected 48 hours after infiltration and luciferase activity was measured. Error bars represent SD (n=20). Schematic representation of the reporter construct shows the position of the BRRE elements. Asterisks indicate significant difference compared to the DWF4 reporter (p<0.05, Student’s t-test).
Fig. S3

A  

WT  bes1-D  EARm13  EARm33

BES1-P  BES1

BES1-P  BES1

B  

WT  bes1-D  EARm13  EARm33

C  

Mock  BRZ

WT  bes1-D  EARm13  EARm33

D  

Light  Dark

Mock  BRZ

E  

Relative expression

WT  bes1-d  EARm13  EARm33
**Fig. S3.** The EAR domain is essential for BES1 function. (A) Western blot of 2-weeks old WT, 35S::bes1-D-GFP (bes1-D) and 35S::bes1-D-EARm transgenic seedlings (EARm13 and EARm33). (B) Phenotype of adult WT, 35S::bes1-D-GFP and 35S::bes1-D-EARm-GFP plants. Plants were grown for 4-weeks under long day conditions (16h light/8h dark). (C) Phenotype of WT, 35S::bes1-D-GFP and 35S::bes1-D-EARm-GFP seedlings grown on BRZ. Seedlings were grown for 6 days under short day conditions (Light) or in continuous dark (Dark) in MS growth media (Mock) or MS media supplemented with 0.5 µM brassinazole (BRZ). (D) Hypocotyl length measurements of plants grown in (C). Bars represent s. d. (n=20). Similar results were obtained in three independent experiments. Asterisks indicate significant difference compared to the WT genotype (p<0.05, Student’s t-test). (E) Expression levels of the CPD, DWF4, ROT3, IAA19 and PRE5 genes in plants grown in short day conditions as in (D). Samples were taken at ZT0. Bars represent the standard deviation of three independent biological replicates. Asterisks indicate significant difference compared to the WT genotype (p<0.05, Student’s t-test).
Fig. S4. Phenotypic characterization of the inflorescences. Significant differences by the Tukey’s multiple comparison test are indicated by letters above bars (P < 0.05). (A) A representative flower of the indicated genotypes. (B) Measurement of the pedicel, bud, sepal and petal length of flowers in the primary inflorescences (n=10 plants and 20 flowers of each genotype). F: first open flower; 1, 2 and 3: three oldest buds.
Fig. S5. Boundary-enriched BES1/BZR1-repressed targets include several boundary and patterning regulators. (A) Venn diagram showing the overlap of BR differentially expressed genes (Goda et al., 2004; Vert et al., 2005; Sun et al., 2010; Oh et al., 2012) and boundary enriched transcripts (Tian et al., 2014). BR-induced genes are not significantly enriched (44 found, 33 expected, hypergeometric test, p-value >0.01), while BR-repressed genes are strongly enriched in boundary-specific transcripts (94 found, 26 expected, hypergeometric test, p-value = 1.5 x 10^-25). (B) Heat-map representation of the expression profiles of the BR-repressed, boundary expressed transcription factors: bzr1-1D (Sun et al., 2010), bzr1-1D BRZ (Oh et al., 2012) and bes1-D (our own data). 8 out of 11 transcription factors were identified as direct BES1- or BZR1- targets (Sun et al., 2010; Yu et al., 2011). (C) Gene ontology analysis of the 94 boundary enriched, BR-repressed genes visualized with ReviGO.
Fig. S6. TPL is expressed in the shoot and root meristems. GUS staining of 6-day old pTPL::GUS seedlings. In the root, GUS staining was strong in the cell division and elongation zones. In aerial tissues, strong GUS staining was observed in the SAM and young, actively growing tissues.
**Supplemental Table 1.** Percentage of flowers that contain altered petal number.

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Supplemental Table 2. List of primers used in this study.

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