The protein kinase TOUSLED facilitates RNAi in Arabidopsis

Mohammad Nazim Uddin1,†, Patrice Dunoyer2,†, Gregory Schott2, Salina Akhter1, Chunlin Shi1, William J. Lucas1,3, Olivier Voinnet2,4,* and Jae-Yean Kim1,*

†Division of Applied Life Science (BK21+/WCU program), PMBBRC, Graduate School of Gyeongsang National University, Jinju 660-701, Korea, 2Institut de Biologie Moléculaire des Plantes du CNRS, UPR2357, Université de Strasbourg, Strasbourg Cedex, France, 3Department of Plant Biology, College of Biological Sciences, University of California, Davis, CA 95616, U.S.A. and 4Department of Biology, Swiss Federal Institute of Technology (ETH), 8092 Zurich, Switzerland

Received February 24, 2014; Revised April 26, 2014; Accepted May 1, 2014

ABSTRACT

RNA silencing is an evolutionarily conserved mechanism triggered by double-stranded RNA that is processed into 21- to 24-nt small interfering (si)RNA or micro (mi)RNA by RNaseIII-like enzymes called Dicers. Gene regulations by RNA silencing have fundamental implications in a large number of biological processes that include antiviral defense, maintenance of genome integrity and the orchestration of cell fates. Although most generic or core components of the various plant small RNA pathways have been likely identified over the past 15 years, factors involved in RNAi regulation through post-translational modifications are just starting to emerge, mostly through forward genetic studies. A genetic screen designed to identify factors required for RNAi in Arabidopsis identified the serine/threonine protein kinase, TOUSLED (TSL). Mutations in TSL affect exogenous and virus-derived siRNA activity in a manner dependent upon its kinase activity. By contrast, despite their pleiotropic developmental phenotype, tsi mutants show no defect in biogenesis or activity of miRNA or endogenous trans-acting siRNA. These data suggest a possible role for TSL phosphorylation in the specific regulation of exogenous and antiviral RNA silencing in Arabidopsis and identify TSL as an intrinsic regulator of RNA interference.

INTRODUCTION

Ribonucleic acid (RNA) silencing is triggered by double-stranded RNA (dsRNA), processed into 21- to 24-nt small interfering (si)RNA or micro (mi)RNA by RNaseIII-like enzymes called Dicers, or Dicer-like (DCL) in plants (1–3). Small RNAs guide ARGONAUTE (AGO)-containing RNA-induced silencing complexes (RISCs) to suppress target gene expression at the level of transcription, RNA stability or translation. In Arabidopsis, 21-nt siRNA and miRNA mainly incorporate into AGO1 to promote cleavage or translational inhibition of target transcripts (4,5), whereas 24-nt siRNAs guide heterochromatin formation by recruiting AGO4, AGO6 or AGO9 (6). In higher plants, the effect of RNAi can also extend beyond the sites of its initiation, owing to the movement of signal molecules with defensive and developmental roles (7,8). The mobile signal is at least composed of siRNAs because these are necessary and sufficient to convey the sequence specificity of cell-to-cell and long distance silencing spread (9–11). The spread of virus-derived siRNA (vsiRNA) most likely immunizes surrounding cells that are yet to be infected (12), whereas movement of endogenous trans-acting (ta)siRNA generates a gradient of target gene expression participating in organ polarization (13,14).

Several genetic screens have been conducted to uncover genes required for RNAi or its non-cell-autonomous aspects in plants. The identified factors include the DCLs that hierarchically generate the various small RNAs, the AGOs into which small RNAs are loaded, as well as several cofactors required for efficient and/or accurate processing, protection or activity of small RNAs as part of the AGO or DCL ribonucleoprotein complexes (15). Several mutations have also been shown to compromise silencing cell-to-cell and/or long-distance spread through still highly elusive mechanisms. These include the largest subunit of the plant-specific heterochromatic NUCLEAR RNA POLYMERASE-IVa (NRPD1a), the RNA-DEPENDENT RNA POLYMERASE 2 (RDR2) or...
the SNF2 domain-containing protein, CLASSY1 (CLSY1) (16–18).

To identify new factors required for intracellular and/or non-cell-autonomous RNAi, we designed a sensitive transgenic system whereby siRNA production is driven by the phloem-restricted and moderately expressed, AtSUC2 promoter. This system not only allows the identification of factors required for non-cell-autonomous RNAi but also of genes whose requirements in cell-autonomous RNAi may be bypassed when strong and constitutively expressed promoters, such as the Cauliflower mosaic virus 35S promoter, are used to express dsRNA inducers (16,19). Using this system in a forward genetic screen, we identified and characterized the serine/threonine protein kinase TOUSLED (TSL) (20). We show that TSL is required for RNAi in Arabidopsis, in a manner dependent upon its kinase activity. We further present evidence that TSL specifically affects exogenous and viral-derived siRNA activity without overt effect upon miRNA or endogenous tasiRNA biogenesis or activity.

MATERIALS AND METHODS

Plant materials

Mutant lines dcl1-16 (Salk_013118), dcl2-1 (Salk_064627), nrpd1a-4 (Salk_083051), nrpd1b-11 (Salk_029919), tsl-8 (Salk_152957) and tki1-1 (Salk_064187) were obtained from the Arabidopsis Biological Resource Center (ABRC). Mutant lines dcl4-2, dcl3-1, rdr2-1, rdr6-15, ago1-27, asf1ab and transgenic SUC::SUL (SS) line have been described previously (17,21). Genotyping of the Transfer DNA (T-DNA) insertion lines was performed by polymerase chain reaction (PCR), using allele-specific primers. PCR primers are listed in Supplementary Table S1. Seeds were surface-sterilized and sowed at a density of ∼500 seeds per plate for luminescence image screening.

DNA constructs and plant transformation

The T-DNA expression cassette for firefly luciferase (p35S::LUC-3′ Nos) was cut with EcoRV, and inserted into the PmeI site of the binary vector pC1300 containing the hygromycin resistance gene. We constructed double-banded luciferase (dsLU) by including the first 400 bp sequence from the start codon; a PCR amplification product was inserted into the XhoI/KpnI and XbaI/ClaI sites of pHannibal, respectively. The dsLU region containing the pyruvate dehydrogenase kinase (PDK) intron from pHannibal was transferred into the binary vector pC2300, containing the kanamycin resistance gene. The phloem-specific promoter, pSUC2, was amplified from Arabidopsis genomic DNA and inserted in front of the dsLU. For the pSUC2::dsLU-p35S::LUC, the p35S::LUC was inserted into the PmeI site of pSUC2::dsLU. Another construct (pSUC2::GUS-dsLU-p35S::LUC) was made with a β-glucuronidase (GUS) reporter fused downstream of the AtSUC2 promoter.

For generating the TSLK438E mutation, the complementary DNA (cDNA) sequence for the catalytic domain with the codon for Lys-438 changed to a codon for Glu was generated by a PCR-based method (22). TSL and TSLK438E were cloned into the gateway entry vector (pENTR/D-TOPO) (Invitrogen) and inserted by sequenc- ing. The entry clones were subsequently transformed into gateway binary vector pEG101 to produce p35S::TSL-YFP and p35S::TSLK438E-YFP, respectively. As tsl mutants have a defective floral developmental phenotype, we used heterozygote tsl/+ plants for all transformations. These constructs were transformed into Agrobacterium tumefaciens GV3101 and introduced by the floral dip method (23).

Luminescence imaging

Both 7-day-old seedlings and plants at the rosette stage were sprayed with 1 mM luciferin (in 0.01% (v/v) Triton X-100) and kept in darkness for 4 min to allow full penetration of luciferin into the tissues. Luminescence images were acquired over a 100-s period using a pre-chilled charge-coupled device camera (−60°C) (ANDOR iXon Technology) (24).

Ethyl methanesulfonate (EMS) mutagenesis

Surface-sterilized seeds (~4000) from the homozygous transgenic plants carrying pSUC2::dsLU-p35S::LUC construct (PL) were exposed to 30 mM EMS for 12 h. Seeds were then rinsed five times with double distilled water, sowed uniformly on soil and cold-treated at 4°C for 3 days. M2 seeds were harvested as pools, with each pool containing 50 plants. Seeds (~5000) from a single pool were surface-sterilized and sowed at a density of ∼500 seeds per plate for luminescence image screening.

Genetic mapping

F2 mapping populations were obtained by crossing impaired luciferase silencing 1 (ils1) plants (in the ecotype Col-0) to Landsberg erecta. Genomic DNA was isolated from F2 seedlings pre-screened for mutant phenotype and kanamycin resistance. An initial mapping population of 60 F2 plants, a series of simple sequence length polymorphism (SSLP) and cleaved amplified polymorphic sequence (CAPS) markers were used to determine the linkage of the ils1 mutation within the short interval between the markers nga106 and nga139, on chromosome 5. Using the Mon- santo Arabidopsis Polymorphism Database, we generated additional SSLP and CAPS markers between 6897 kb and 7369 kb. With an increased mapping population of 720 F2 plants, the ils1 mutation was positioned to a 32-kb region (BAC f22d1), which contained several predicted genes. Genomic DNA sequencing of the candidate genes in the ils1 mutant identified the mutation in TSL.

Virus induced gene silencing (VIGS)

VIGS was carried out as previously described (25,26) with a Tobacco mosaic virus (TMV) carrying a 500-bp insert corre- sponding to the A. thaliana PHYTOEONE DESATURASE
RT-PCR and qRT-PCR
Total cDNA was synthesized using the SuperScript III first-strand synthesis system for RT-PCR (Invitrogen), according to the manufacturer’s instructions. For RT-PCR, PCR was performed on diluted cDNA using Taq polymerase (Solgent, South Korea). For qRT-PCR, we quantified the cDNA using the QuantiMix SYBR Kit (Philekorea Technology, South Korea) and gene-specific primers using the EcoTM Real-Time PCR system (Illumina), according to the manufacturer’s protocol. Cycling conditions were as follows: 95°C for 10 min, followed by 40 cycles of 95°C for 10 s, 55°C for 40 s and 72°C for 15 s. For each cDNA synthesis, quantification was performed in triplicate. The ACTIN2 was used as a reference as it is stably expressed across a wide range of conditions.

GUS staining
GUS staining was performed on the T2 generations of transgenic lines, as previously described (27).

Northern analysis
Total RNA was extracted from Arabidopsis rosette leaves with Trizol reagent (Sigma), according to the manufacturer’s instructions. RNA gel blot analysis of high and low molecular weight RNA was performed with 10 and 30 μg of total RNA, respectively, and was as described previously (28). Ethidium bromide staining of total RNA, before transfer and U6 were used to confirm equal loading. RNA hybridizations were performed using the ULTRA-Hyb Oligo solution, according to the manufacturer’s instructions (Ambion). Radiolabeled probes for detection of the LUC, SUL or PDS siRNAs were made by random priming reactions in the presence of [α-32P]-dCTP (Amer sham). The template used was a 400 bp PCR product amplified from LUC cDNA. The 400 bp (for SUL) and 500 bp (for PDS) PCR products were amplified from Arabidopsis cDNA. DNA oligonucleotides complementary to miRNAs, tasiRNAs or ha-acting siRNAs were end-labeled with [γ-32P]-ATP using T4 polynucleotide kinase (New England Biolabs). All hybridization signals were detected by phosphor-imaging (Cyclone Plus Storage Phosphor System; PerkinElmer).

Western analysis
Total proteins were isolated from either seedlings, rosette leaves of 1-month-old plants or flowers. Protein aliquots (20 μg) were resolved on an 8% SDS-PAGE gel, followed by electrophoretic transfer to Immobilon-P membranes (Millipore). Membranes were blocked in Tris-buffered saline (TBS) buffer (25 mM Tris-HCl, pH 8.0, 125 mM NaCl) containing 5% skimmed milk for 1 h. Membranes were incubated with the respective antibodies diluted in TBS buffer (1:1000) containing 5% skimmed milk for 1 h. Blots were washed in TBS buffer containing 0.1% (v/v) Tween-20 and were then exposed to X-ray film.

Microscopy imaging
For confocal microscopy, plant leaf samples were stained with propidium iodide (10 μg/ml) for 1.5 min and subsequently 4’,6-diamidino-2-phenylindole (DAPI; 4 μg/ml) for 20 min. Leaf was imaged using an Olympus Fluoview1000 confocal microscope, with the following laser and filter combinations: 488-nm laser line with a 500–545 nm band-pass emission for YFP; the 559-nm laser line with a 575–675 nm band-pass emission for propidium iodide and 405-nm laser excitation and a 425–475 nm emission for DAPI. When more than two fluorochromes were imaged at the same time, the sequential laser scanning method was used to prevent cross-bleeding between different fluorophores.

RESULTS AND DISCUSSION
Establishment and characterization of transgenic RNAi lines
To identify new factors required for RNAi, we established an inverted repeat (IR) construct corresponding to the 5’ region (‘LU’) of the firefly LUCIFERASE (LUC) gene driven by the phloem specific AtSUC2 promoter. Processing of the LU dsRNA in companion cells triggers extensive RNAi of a p35S:LUC transgene carried by the same T-DNA, resulting in an almost complete loss-of-luminescent signal in transgenic Arabidopsis (referred to hereafter as Parental Line (PL); Supplementary Figure S1A–E). Phloem-specific expression of the dsLU was confirmed by introducing the GUS open reading frame downstream of the pSUC2. The resulting pSUC2:GUS-dsLU-p35S:LUC construct recapitulated the extensive LUC silencing phenotype observed in the PL and revealed a vein-restricted GUS staining pattern (Supplementary Figure S1F–I). Moreover, 35S promoter-driven expression of the Tomato bushy stunt virus P19 silencing suppressor led to a strong luminescence recovery in the PL, supporting post-transcriptional silencing mediated by LU-derived 21-nt siRNAs, for which P19 displays high and selective affinity (Supplementary Figure S1J–L).

In order to determine the basic genetic requirements for LUC silencing, we crossed the PL to several mutants previously implicated in either biogenesis, movement/perception or activity of IR-derived siRNAs (16,30). We found that LUC silencing was relieved in the dcl4 mutant background, but remained unaffected in the dcl2, dcl3 or the double dcl2/dcl3 mutant backgrounds, further supporting post-transcriptional silencing of LUC (Figure 1A–G). Moreover, luminescence was also recovered in a dcl1 hypomorphic mutant background, agreeing with the documented role for DCL1 in optimizing the primary processing of IRs, which presumably facilitates their access and processing by other DCLs (16,31). Extensive silencing of transgenes, as opposed to endogenous, usually entails the amplification of siRNA production through RDR6 and downstream DCL activities. These amplified secondary siRNAs can also spread from their...
sites of biogenesis to the neighboring cells, resulting in amplified silencing movement (32,33). As expected from the transgenic nature of the target transcript in the PL, extensive LUC silencing was fully dependent on RDR6 activity (Figure 1H). In agreement with previous findings, luminescence in the PL was also recovered, although to a slightly lower extent, in nrpd1a and rrd2 mutant backgrounds, but not in the nrpd1b mutant background (Figure 1I–K) (16,17). Surprisingly, LUC silencing was only moderately impaired by the ago1-27 mutation (Figure 1L, see legend), possibly because the ago1-27 allele is still partially competent for endonucleolytic cleavage of target mRNAs (5). Alternatively, other AGOs might contribute cooperatively with AGO1 to silence the LUC mRNA in the PL. Collectively, these results suggest that the LUC silencing system has similar genetic requirements to those of previous IR-based systems designed to study both cell- and non-cell-autonomous RNAi in Arabidopsis (16,17,30,32).

TSL contributes to LUC RNAi

To identify new components involved in plant RNAi, an EMS mutagenesis was conducted on the PL and four recessive mutants exhibiting luminescence recovery were identified and defined as impaired luciferase silencing mutants (ils1-ils4). The ils2, ils3 and ils4 mutations were rough-mapped to chromosomes 3, 4 and 4, respectively, and a genetic complementation assay indicated that ils2 is allelic to rdd6, confirming the results obtained by reverse genetics (Figure 1H). We report here the detailed characterization of the ils1 mutant.

Significant luminescence recovery associated with higher LUC mRNA levels was observed in ils1 compared to the silenced PL, at both the seedling and young rosette leaf stages (Figure 2A–C). However, this increase in LUC transcript levels was not accompanied by decrease in the level of 21-nt or 24-nt LUC siRNAs (Figure 2D), indicating that ILS1 is not required for LUC siRNA biogenesis or stability. Positional cloning and sequencing (Figure 2E; details in ‘Materials and Methods’ section) revealed that ils1 carries a C→T transition mutation in the 13th exon of TSL (At5g20930; Figure 2F). Homozygous introgression of the tsl-8 T-DNA insertion allele (Salk_152957) into the PL also reactivated luminescence (Figure 2G). Moreover, all individuals of an F1 progeny from a cross between ils1 and tsl-8 showed the LUC silencing-deficient phenotype (Figure 2H–I). Therefore, ILS1 is allelic to TSL.

TSL contributes to SULPHUR (SUL) silencing

The impact of TSL on RNAi was also assessed in the SUC:SUL (SS) system in which an IR construct, driven by the AtSUC2 promoter, directs silencing of the endogenous SUL mRNA (16,30). Processing of the phloem-specific SUL dsRNA generates 21- and 24-nt siRNAs and causes RNAi spread manifested by a chlorotic phenotype expanding 10–15 cells beyond the vasculature. Of the two siRNA species, only 21-nt siRNAs are involved in SUL RNAi, which, unlike in the LUC system, is not amplified by RDR6 owing to the endogenous nature of the silencing target (16,32). Introducing the homozygous tsl-8 mutation in the SS plants led to a marked reduction in the appearance of the SUL silencing phenotype without affecting SUL siRNA accumulation (Supplementary Figure S2A–H). This observation confirmed the results obtained with the PL and supports the notion that TSL acts downstream of DCL4 activity in the RNAi pathway, in a process that either affects siRNA movement or siRNA activity.

Impaired movement should translate into strongly reduced siRNA levels in the PL where the bulk of these molecules is mainly contributed by secondary siRNA generated in an RDR6-dependent manner from the ubiquitously expressed LUC transgene mRNA. These move extensively throughout the entire leaf lamina, unlike the limited amount of primary siRNAs generated in the SS system. Therefore, the unchanged LUC siRNA accumulation in tsl-8 compared to the PL (Figure 2D) and the fact that SUL siRNA levels also remain unaltered in the tsl-8 background (Supplementary Figure S2H) favor the hypothesis that TSL is required for IR-derived siRNA activity.

TSL acts downstream of small RNA biogenesis and is neither required for miRNA- nor endogenous siRNA-guided RISC activity

TSL was previously implicated in leaf and floral development (20). Accordingly, the ils1 mutant (referred to hereafter as tls-9) exhibited pleiotropic developmental phenotypes, such as serrated rosette leaf margins, short primary root length, reduced fertility (or complete sterility in tls-8) associated with shorter siliques, as well as split and deformed gynoecia (Figure 3A–F). Given that such developmental defects are reminiscent of those exhibited by miRNA-deficient Arabidopsis mutants, we assessed the accumulation of various endogenous small RNAs in the tls mutant background. Northern analysis showed that the levels of DCL1-dependent miRNAs in tls-8 and tls-9 mutants were comparable to those of wild-type (WT) plants, as
Figure 2. Identification and characterization of the ils1 locus. (A) Luminescence image of ils1 in 8-day-old seedlings along with PL and transgenic plants expressing the p35S:LUC transgene (overexpressor, OX). (B) Luminescence images of 3-week-old plants. (C) Expression of LUC (LU- and C-specific probes) in leaves of PL, ils1, OX and different RNAi mutant (dc1-2, rdr6-15, ago1-27) plants in the PL background determined by qRT-PCR analysis. Expression levels were normalized to ACTIN2 (At3g18780). Error bars indicate standard deviation for three independent experiments. (D) Northern-blot analysis of different small RNA accumulation in leaves from PL, ils1, WT and tsl-8 plants. Upper panel, 21- and 24-nt LU siRNA; middle panel, 21-nt tasiRNA255; lower panel, 21-nt miR159; rRNA served as the loading control. (E) Map-based cloning of ils1. The ils1 locus was mapped between the SSLP marker nga106 and nga139 on chromosome 5. Number of recombinant plants is shown for each marker. The ils1 mutation was located on BAC f22d1, encoding several predicted genes indicated by different colored arrowheads. (F) Diagram of the TSL genomic locus. Dark red boxes indicate exons, black lines introns, blue boxes UTRs and triangle a T-DNA insertion in the tsl-8 mutant. A missense point mutation (C to T transition) in ils1 resulted in the amino acid substitution L575F in the 13th exon of TSL. (G) Reactivation of luminescence phenotype by tsl-8 in the PL background. (H–I) Luminescence and light images of ils1, tsl-8 and the F1 progeny from a cross between ils1 and tsl-8 in seedling (H) and rosette stage (I).

was the accumulation of several DCL1-/DCL4-dependent tasiRNAs (Figure 3G; Supplementary Figure S3A and B). In addition, representative passenger strand of miRNA (miRNAs*) such as miR390*, miR396* and miR173* showed similar level between WT and tsl mutants (Supplementary Figure S3C). In contrast to guide strand miR173 (Figure 3G), RNA blot signals of miR173* were barely detectable in both the WT and tsl mutants, suggesting a degradation of passenger strand miRNAs*. These data indicated that unwinding of the duplex miRNA/miRNA* and their loading onto the AGO1-RISC were unaffected in tsl mutants. Moreover, accumulation of known miRNA and tasiRNA targets remained unchanged in these tsl mutants, suggesting that neither pathway requires TSL function (Figure 3I; Supplementary Figure S4).

Several transcriptional gene silencing (TGS) factors were previously implicated in cell-to-cell movement or perception of RNAi signals in recipient cells, through still elusive mechanisms (16–18). These factors include RDR2, NRPD1a and CLSY1, which are all required for production, by DCL3, of 24-nt heterochromatic (hc)-siRNA and, ultimately, for DNA methylation at the hc-siRNA producing loci (6). TSL has also been implicated in maintenance of TGS by promoting heterochromatin formation at specific loci in a DNA methylation-independent manner (34), although a role for TSL in hc-siRNA accumulation was not investigated. Therefore, we decided to monitor the levels of a set of 24-nt siRNAs produced either from polIV-dependent (siRNA02) or polIV/polV-dependent loci (siRNA1003, AtREP2, SIMPLEHAT2 and 45S rDNA). Northern analysis revealed that none of these hc-siRNAs was affected in the tsl-8 or tsl-9 mutant backgrounds (Figure 3H), indicating that TSL is not required for hc-siRNA biogenesis.

TSL is required for optimal antiviral RISC function

The observations made with the PL and the SS transgenic systems (Figure 2A–C; Supplementary Figure S2A–H) and the finding that neither miRNA nor tasiRNA targets are affected in tsl mutants suggested that TSL might be specif-
Figure 3. Developmental defects and analysis of endogenous small RNA accumulation or activity in tsl mutants. (A) Developmental phenotype of 18-day-old PL (left) and tsl-9 mutant (right) plants. (B) Third rosette leaf of PL and tsl-9 plants. Note the serration present at the leaf margin of the tsl-9 mutant. (C) Primary root of PL and tsl-9 plants. (D) Mature inflorescence having significantly reduced seed set in tsl-9 compared to PL plants. (E) Siliques of tsl-9 mutant are smaller in size than those of the PL plants. (F) Flowers of PL and tsl-9; tsl-9 flowers lack various floral organs, such as sepals, petals, stamens and also have unfused gynoecia. (G) RNA blot analysis showing the accumulation of different miRNAs (miR159, miR173) and tasiRNAs (tasiR255, tasiR1511, tasiR2142) in WT, PL, tsl-9 and tsl-8 plants. U6 was used as a loading control. (H) RNA blot analysis showing the accumulation of different hc-siRNAs (siR02, siR1003, AtREP2, SIMPLISHAT2, 45S) in WT, PL, tsl-9 and tsl-8 plants. miR159 and U6 were used as loading controls. (I) qRT-PCR analyses to detect mRNA accumulation for different miRNA and tasiRNA target genes in WT, PL, tsl-9, tsl-8, hyl1-2, ago1-27 and rdr6-15 plants. Total RNA was extracted from rosette leaves for cDNA synthesis. The small RNAs that target each of these endogenous mRNAs are indicated in parenthesis. Quantification levels were normalized to ACTIN2, with the value from WT plants arbitrarily set to 1.0. Error bars represent standard deviation from two independent experiments in which triplicate PCRs were performed.
The TSL kinase activity is required for LUC RNAi

A single point mutation that converts the conserved Lys-438 into Glu (K438E) abolishes the kinase activity of TSL without impairing its stability (22,40). To test if this activity is required for LUC silencing, we transformed the tsl-9 mutant with a transgene constitutively expressing either the WT or the mutated (K438E) version of TSL (TSLK438E); two independent lines for each transgene were selected for further analysis. The WT TSL transgene successfully rescued the LUC silencing-deficient phenotype of tsl-9 (Figure 5A–E), whereas transgenic lines expressing the TSLK438E allele at comparable levels still exhibited luminescence (Figure 5F and G). We confirmed that the inability of TSLK438E to restore LUC silencing was not due to an impaired nuclear localization of the protein (Figure 5H) (22). Collectively, these results indicate that extensive silencing of the LUC mRNA in the PL requires an intact TSL kinase activity.

Our findings strongly suggest that catalytic, as opposed to structural features of TSL are required for its RNAi-related functions (Figure 5). Two studies have identified several phosphorylation sites on human AGO proteins that are implicated in protein localization or regulation of small RNA binding (41,42). Therefore, one attractive hypothesis is that TSL might modulate the activity of specific RISCs through phosphorylation of particular AGO1 residue(s) that may alter its subcellular localization and/or the recruitment of specific AGO1-interacting cofactors. The nuclear localization of TSL is not at odds with this hypothesis, given than AGO1 localizes in both the cytoplasm and the nucleus of WT Arabidopsis cells (43,44). Alternatively, AGO1-interacting cofactor(s) may require TSL-mediated phosphorylation in order to interact with the exogenous siRNA-loaded RISC and promote its activity. For instance, in animal systems, RISC components such as the VASA INTRONIC GENE (VIG) or the FRAGILE X MENTAL RETARDATION PROTEIN (FRMP) were reported to be phosphorylated (45,46).

TSL was previously shown to interact with ANTI-SILENCING FUNCTION 1B (ASF1B) and the SANT/myb-domain protein, TSL-KINASE INTER-ACTING PROTEIN 1 (TKI1) and phosphorylate them (40). LUC silencing remained unaffected in the homozygous double mutant, asf1ab (the two Arabidopsis homologues of the yeast and animal ASFI genes) (47) or the tkil−1 mutant background (Supplementary Figure S5B–E), suggesting that neither of these TSL substrates plays a role in the silencing deficient phenotype observed in tsl. In Caenorhabditis elegans and yeast, TOUSLED-
LIKE KINASE-1 (TLK-1) is a substrate activator of the AURORA B KINASE (48), but in a manner independent of the TLK-1 kinase activity (48,49), making it unlikely that a putative plant Aurora B homolog contributes to the RNAi defects of tsl mutants. A final possibility is that TSL signaling indirectly regulates the expression of one or several AGO1-interacting proteins as was shown in the control of human AGO2 expression through MAP kinase signaling (50).

CONCLUSION

It is likely that most generic or core components of the various plant small RNA pathways have been identified over the past 15 years of investigations. Consequently, new and more elaborated genetic screens are now required to isolate regulators of RNAi. Here, we have identified a plant factor required for RNAi, the protein kinase TSL that seems to act, directly or indirectly, on specific AGO1-containing RISC complexes. Indeed, although TSL seems to be required for exogenous siRNA activity (IR- and vsiRNA; Figures 2 and 4), it is apparently not necessary for endogenous small RNA-mediated regulation (miRNA, tasiRNA and hc-siRNA; Figure 3; Supplementary Figure S4). This specific effect is in line with recent findings that AGO1 might be partitioned into distinct pools, each binding preferentially to one specific small RNA class (51) and suggests that TSL may be defined, at least partly, as another layer of specificity between endo- and exo-siRNA loaded RISC. The observations that VIGS of the PDS mRNA was reduced but still functional in tsl mutants (Figure 4), and that faint SUL silencing remained visible in leaves of SS x tsl-8 plants (Supplementary Figure S2) suggest that TSL mediates a phosphorylation event that facilitates, but is not mandatory for exogenous siRNA-loaded RISC activity. Most likely, this facilitating effect would have gone unnoticed in transgenic systems using strong inducers of RNAi, as previously reported in studies of HUA ENHANCER 1 (16,19,21).

It is becoming increasingly apparent that post-translational modifications that are embedded into signaling cascades to reprogram gene expression regulate RNAi components. In animals, prolyl-4-hydroxylation, symmetric arginine dimethylation and polyADP-ribosylation have been shown to alter stability or activity of AGO or PIWI proteins, under both normal or stress conditions (52).

In plants, ubiquitination of AGO1 leads to its selective degradation through autophagy (53), whereas the CPL1 phosphatase might dephosphorylate HYPONASTIC LEAVES 1 (HYL1), the dsRNA binding partner of DCL1, to promote accurate and optimal processing of miRNA duplexes (54). Although it is still unknown whether TSL affects directly or indirectly AGO1 activity, our findings suggest that this kinase is an integral part of the signaling cascade that regulates exogenous small RNA-loaded AGO1 in Arabidopsis. The challenge ahead is now to identify the substrate(s) phosphorylated by TSL and to elucidate the precise regulatory function(s) of such protein(s) in the RNAi pathway.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

ACKNOWLEDGMENTS

We thank M. Feng for confocal imaging, D. Baulcombe for the P19 construct, Z. Gong for TSL cDNA, S. Macfarlane for a TRV-PDS construct, J.C. Carrington for rdr6-15, H. Vaucheret for ago1-27, A. Dong for asf1ab and ABRC for T-DNA mutant seeds.

FUNDING

Basic Science Research Program through the National Research Foundation of Korea funded by the Ministry of Education [NRF-2013R1A1A2007230]; the Next-Generation BioGreen 21 Program [SSAC, PJ009495]; Rural Development Administration, Korea, the U.S. National Science Foundation [IOS-0918433]; the Agence Nationale
pour la Recherche [ANR-10-LABX-0036_NETRNA]; the Bettencourt-Schuler foundation and core funding from the ETH-Z. Funding for open access charge; the Next-Generation BioGreen 21 Program [SSAC, PJ009495], Rural Development Administration, Korea.

Conflict of interest statement. None declared.

REFERENCES


Downloaded from https://academic.oup.com/nar/article-abstract/42/12/7971/1100472 by guest on 12 April 2019