Imprinting of the MEDEA Polycomb Gene in the Arabidopsis Endosperm

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In flowering plants, two cells are fertilized in the haploid female gametophyte. Egg and sperm nuclei fuse to form the embryo. A second sperm nucleus fuses with the central cell nucleus that replicates to generate the endosperm, which is a tissue that supports embryo development. MEDEA (MEA) encodes an Arabidopsis SET domain Polycomb protein. Inheritance of a maternal loss-of-function mea allele results in embryo abortion and prolonged endosperm production, irrespective of the genotype of the paternal allele. Thus, only the maternal wild-type MEA allele is required for proper embryo and endosperm development. To understand the molecular mechanism responsible for the parent-of-origin effects of mea mutations on seed development, we compared the expression of maternal and paternal MEA alleles in the progeny of crosses between two Arabidopsis ecotypes. Only the maternal MEA mRNA was detected in the endosperm from seeds at the torpedo stage and later. By contrast, expression of both maternal and paternal MEA alleles was observed in the embryo from seeds at the torpedo stage and later, in seedling, leaf, stem, and root. Thus, MEA is an imprinted gene that displays parent-of-origin-dependent monoallelic expression specifically in the endosperm. These results suggest that the embryo abortion observed in mutant mea seeds is due, at least in part, to a defect in endosperm function. Silencing of the paternal MEA allele in the endosperm and the phenotype of mutant mea seeds supports the parental conflict theory for the evolution of imprinting in plants and mammals.

INTRODUCTION

Flowering plant reproduction is characterized by the fertilization of two cells (reviewed in van Went and Willemse, 1984). Within the Arabidopsis ovule, a single sporule replicates and generates the female gametophyte, which is composed of an egg cell and two synergids cells at the micropylar end, a central cell in the middle, and three antipodal cells at the chalazal end. All are haploid except for the central cell, which contains two polar nuclei that fuse to form a diploid nucleus. Reproduction begins when a pollen tube enters the micropylar opening of the ovule and discharges two haploid sperm cells. Fertilization of the egg generates the diploid embryo, whereas fertilization of the central cell generates the triploid endosperm. Surrounding and protecting the developing embryo and endosperm are maternal cell layers, namely, the seed coat. These cell layers are derived from the ovule integuments.

In Arabidopsis, the fertilized egg undergoes an asymmetric transverse cleavage to produce a small cytoplasmically dense apical cell and a large vacuolated basal cell. The apical cell divides many times and generates cells that comprise most of the embryonic structures found in the mature seed (Bowman and Mansfield, 1994). During embryo development, two primary organ systems (i.e., axis and cotyledon) and three tissue layers (i.e., protoderm, procambium, and ground meristem) are specified (Lindsey and Topping, 1993; Jürgens, 1994; Meinke, 1994). The embryo passes through a series of stages that have been defined morphologically as globular, heart, torpedo, walking stick, early maturation, and maturation (Goldberg et al., 1994). By contrast, the embryonic basal cell divides and forms a single file of cells that comprise the suspensor, which is an ephemeral organ that represents the physical connection between the embryo and maternal tissues during the early stages of embryogenesis (Yeung and Meinke, 1993).

Embryo and endosperm are genetically identical except for their ratio of maternal-to-paternal genomes, which are 1:1 and 2:1, respectively. However, the pattern of endosperm development is quite distinct from that of the embryo. The fertilized central cell nucleus undergoes a series of mitotic divisions to produce a syncytium of nuclei that surround the embryo and fill the expanding central cell (Mansfield and Briarty, 1990a; Webb and Gunning, 1991; Berger, 1999; Brown et al., 1999). At the heart stage, cellularization
begins, and endosperm cytoplasm and nuclei are sequestered into discrete cells (Mansfield and Briaty, 1990b; Berger, 1999; Brown et al., 1999). Endosperm cells produce high levels of storage proteins, starch, and lipids.

The endosperm is thought to interact with the embryo during seed development. The chalazal-oriented portion of the endosperm is located next to a pad of maternal proliferative tissue that is adjacent to the vascular tissue. The relative position of these tissues has led to the suggestion that the chalazal-oriented endosperm may be involved in nutrient transfer into the developing seed (Schulz and Jensen, 1971; Berger, 1999; Brown et al., 1999). Also, in many dicot plants, the nutrients produced and stored in the endosperm are ultimately absorbed by the embryo (Lopes and Larkins, 1993). Hence, the endosperm is thought to function to support the growth and development of the embryo.

The Arabidopsis MEA gene encodes a SET domain Polycomb protein (Grossniklaus et al., 1998; Kiyosue et al., 1999; Luo et al., 1999). The SET acronym is derived from the names of three genes that share a common 130-amino acid motif. These genes are the Suppressor of position-effect variegation gene Su(var)3-9, the Enhancer of zeste polycomb group gene E(z), and the Trithorax gene trx-G (Jenuwein et al., 1998). In mammals, insects, and fungi, SET domain polycomb proteins have been shown to regulate gene transcription by participating in the formation of complexes at specific sites within the genome (Pirrotta, 1998). In Arabidopsis, MEA functions as a suppressor of endosperm development (Kiyosue et al., 1999). Loss-of-function mea-3 and mea-4 mutations cause precocious endosperm formation before fertilization and prolonged endosperm nuclear proliferation after fertilization (Kiyosue et al., 1999). Mutations in the MEA gene also cause embryo abortion (Chaudhury et al., 1997; Grossniklaus et al., 1998; Kiyosue et al., 1999). The relationship between the mutant endosperm and embryo phenotypes remains to be elucidated.

Genetic analysis has shown that only the maternal wild-type MEA allele, and not the paternal MEA allele, is required for proper embryo and endosperm development (Chaudhury et al., 1997; Grossniklaus et al., 1998; Kiyosue et al., 1999). For example, when a heterozygous plant is pollinated with wild-type pollen, only those seeds inheriting a maternal mutant mea allele are defective. When the reciprocal cross is performed, no defective seeds have been observed. One explanation for these parent-of-origin-specific effects is that MEA gene expression, which is essential for embryo development, occurs before fertilization in the female gametophyte. Another possibility is that MEA could be an imprinted gene whose expression in seeds is dependent on the parent of origin. In this model, the maternal MEA allele is expressed and the paternal MEA allele is silenced, perhaps due to transcriptional silencing (Martienssen, 1998).

To understand the molecular basis for the parent-of-origin effects of mea mutations on reproductive development, we monitored expression of the maternal and paternal wild-type MEA alleles in the F1 progeny of crosses between two Arabidopsis ecotypes. Here, we show that expression of the maternal MEA allele is predominant in the endosperm from seeds at the torpedo stage and later. By contrast, both maternal and paternal MEA mRNAs were detected in approximately equal concentrations in the embryo from seeds at the torpedo stage, and later, in seedling, leaf, stem, and root. Thus, the paternally derived MEA allele is silenced specifically within the endosperm. These results suggest that mea embryo abortion is due, at least in part, to a defect in endosperm function. Our results characterizing the phenotype of loss-of-function mea mutants (Kiyosue et al., 1999) and describing the silencing of the paternal mea allele support the parental conflict theory for the evolution of imprinting in plants and mammals (Haig and Westoby, 1989, 1991).

**RESULTS**

**Strategy for Measuring Maternal- and Paternal-Specific MEA mRNA Levels**

To test the hypothesis that paternal gene silencing is responsible for parent-of-origin-specific effects of mea mutations on seed and plant development, we measured maternal and paternal MEA mRNA levels in reproductive and vegetative tissues. As shown in Figure 1A, to distinguish maternal and paternal MEA RNAs, we identified a DNA sequence polymorphism (i.e., a T versus a G residue) in the MEA gene isolated from two Arabidopsis ecotypes, Landsberg erecta (Ler) and RLD (Hardtke et al., 1996). The polymorphism resides in the 17th exon that encodes 3' untranslated MEA mRNA (Figure 1B). A derived cleaved amplified polymorphic sequence primer (Neff et al., 1998), MEA-R2d (Figure 1A), was designed to convert this DNA sequence polymorphism to a BamHI restriction endonuclease site polymorphism (Figure 1C). Reverse transcription–polymerase chain reaction (RT-PCR) amplification of Ler MEA sequences followed by BamHI digestion was predicted to produce a 239-bp DNA sequence. For RLD, the same procedure was predicted to produce 207- and 32-bp DNA sequences (Figure 1C). To test this strategy, RNA from Ler and RLD floral buds was mixed, and MEA sequences were amplified and digested as described above. As shown in Figure 1D, the expected size and abundance of restriction fragments were detected, indicating that the assay is semiquantitative and that we can distinguish MEA RNAs transcribed from the Ler and RLD genomes.

**Pattern of Maternal and Paternal MEA Allele Expression during Plant Development**

Previously, it was shown that the MEA gene is expressed in silicles with developing seeds (Grossniklaus et al., 1998;
Kiyosue et al., 1999). To examine the expression of paternal and maternal MEA alleles in seeds, we performed reciprocal crosses between Ler and RLD Arabidopsis plants. RNA was isolated from F1 seeds harvested at 4, 6, 7, and 8 days after pollination, and MEA sequences were amplified by using RT-PCR. These time points correspond to the heart, torpedo, walking stick, and early maturation stages of embryo development (Goldberg et al., 1994). To distinguish expression from maternal and paternal MEA alleles, we digested RT-PCR products with BamHI and subjected them to agarose gel electrophoresis. As shown in Figure 2, both maternal and paternal MEA RNAs were detected at all stages of seed development tested, although the level of maternal MEA mRNA appeared to be higher than the level of paternal MEA mRNA. These results show that both paternal and maternal MEA mRNAs accumulate during seed development.

During double fertilization, the embryo inherits one paternal MEA allele and the endosperm inherits another paternal MEA allele. To determine whether one or both paternal MEA alleles are expressed during seed development, we harvested F1 seeds from reciprocal crosses between Ler and RLD plants at 6, 7, and 8 days after pollination. Seeds (Figure 3A) were dissected, and RNA was isolated from the embryo (Figure 3C) and endosperm plus seed coat (Figure 3B) components. Using the procedures described above, we measured the level of maternal and paternal MEA mRNA.

As shown in Figure 3D, both maternal and paternal MEA gene expression was detected in embryos at all stages tested. Thus, the paternal MEA allele from the sperm that fused with the egg is expressed during seed development. However, a very different pattern of expression was observed for the paternal MEA allele inherited by the endosperm. As shown in Figure 3E, when the female parent was of the Ler ecotype, only the 239-bp product associated with the maternal Ler MEA allele was detected at all stages tested. Moreover, when the female parent was of the RLD ecotype, the 207-bp product associated with the maternal RLD MEA allele was detected at 6 and 7 days after pollination. Only at 8 days after pollination was a low level of paternal Ler MEA mRNA observed. Finally, in a control experiment, both maternal Ler and paternal RLD αVACUOLAR PROCESSING ENZYME gene (Kinoshita et al., 1999) expression were detected in endosperm plus seed coat.

Figure 1. Strategy for Distinguishing Maternal and Paternal MEA mRNA.

(A) DNA sequences. Asterisks show the DNA sequence polymorphism between the Ler and RLD MEA genes. The vertical line shows the mismatch position in the derived cleaved amplified polymorphic sequence primer MEA-R2d relative to the Ler and RLD MEA genes. Dots represent a translation stop signal. The arrow points to the 3′ end of the MEA-R2d primer.

(B) Position of primers. MEA-L1, MEA-R2d, and MEA-R1 represent primers used for RT-PCR amplification of MEA sequences. The asterisk shows the location of DNA sequence polymorphism. Positions of exons and introns are indicated.

(C) Predicted sizes of restriction fragments after RT-PCR amplification and digestion with BamHI restriction endonuclease.

(D) Amplification of MEA sequences from Ler and RLD floral RNA. RNA was isolated from Ler and RLD floral buds at stages 0 to 13 (Smyth et al., 1990), mixed in the indicated proportions, and subjected to RT-PCR amplification, BamHI restriction endonuclease digestion, and agarose gel electrophoresis. The lengths of the restriction fragments in base pairs are indicated at right.

Figure 2. Pattern of Paternal and Maternal MEA mRNA Accumulation in Seeds.

Reciprocal crosses between Ler and RLD plants were performed, and F1 seeds were harvested at 4, 6, 7, and 8 days after pollination, corresponding to the heart (H), torpedo (T), walking stick (Ws), and early maturation (Em) embryo stages, respectively. RNA was isolated from seeds and subjected to RT-PCR amplification with MEA primers, BamHI restriction endonuclease digestion, and agarose gel electrophoresis.
dissected from seeds 7 days after pollination (data not shown). Taken together, these results show that expression of the paternal MEA allele is greatly reduced in the endosperm.

To conclude that the paternal MEA allele is specifically silenced in the endosperm, we had to show that maternal MEA mRNA accumulates in the endosperm and not merely in the seed coat, which is maternal tissue. To address this issue, we crossed female RLD plants to male Ler plants and harvested F1 seeds 7 days after pollination. Beginning with 1948 The Plant Cell

Figure 3. Pattern of Paternal and Maternal MEA mRNA Accumulation in Dissected Seeds.

Reciprocal crosses between Ler and RLD plants were performed, and F1 seeds were harvested at 6, 7, and 8 days after pollination, corresponding to the torpedo (T), walking stick (Ws), and early maturation (Em) embryo stages, respectively. Seeds were dissected into embryo and endosperm plus seed coat components. RNA was isolated and subjected to RT-PCR amplification, BamHI restriction endonuclease digestion, and agarose gel electrophoresis. (A) Intact RLD seed 7 days after pollination. (B) Endosperm plus seed coat from an RLD seed harvested 7 days after pollination. (C) Embryo from an RLD seed harvested 7 days after pollination. (D) Accumulation of allele-specific MEA mRNA in embryos. (E) Accumulation of allele-specific MEA mRNA in the endosperm plus seed coat. E, embryo; N, endosperm; SC, seed coat. Bars in (A) to (C) = 0.2 mm.

dosperm tissue that was visibly free from contaminating seed coat could be isolated (Figure 4A). However, because the endosperm is cellularized, a portion tended to adhere to the seed coat, resulting in a fraction comprised of the seed coat and some contaminating endosperm (Figure 4B). As shown in Figure 4C, only maternal MEA mRNA was detected in the endosperm as well as in the seed coat-endosperm fractions. By contrast, both paternal and maternal MEA mRNAs were detected in the embryo. These results strongly suggest that the maternal MEA allele, and not the paternal MEA allele, is expressed in the endosperm. From these results, we conclude that the paternal MEA allele is specifically silenced in the endosperm.

Both maternal and paternal MEA alleles are expressed during embryogenesis (Figures 3D and 4C). To determine

Figure 4. Pattern of Paternal and Maternal MEA mRNA Accumulation in Dissected Endosperm and Seed Coat. (A) Endosperm (N) from an RLD seed harvested 7 days after pollination. Bar = 0.15 mm. (B) Seed coat (SC) plus endosperm isolated from an RLD seed harvested 7 days after pollination. C, polygonal cell with central elevation, namely, the columella, that is associated with the Arabidopsis seed coat (Leon-Kloosterziel et al., 1994); asterisk, endosperm that adhered to the seed coat. Bar = 0.15 mm. (C) Accumulation of allele-specific MEA mRNA in dissected tissues. RLD females were crossed with Ler males. Seeds were harvested 7 days after pollination, corresponding to the walking stick embryo stage (Goldberg et al., 1994). Seeds were dissected into embryo (lane 1), endosperm (lane 2), and seed coat plus endosperm (lane 3) components. RNA was isolated and subjected to RT-PCR amplification, BamHI restriction endonuclease digestion, and agarose gel electrophoresis.
the predominate in the endosperm. These results suggest that leaf, stem, and root. By contrast, maternal allele expression specifically in the endosperm.

MEA allele in the endosperm can be activated and expressed after germination in vegetative tissues, we performed reciprocal crosses between Ler and RLD plants, and RNA was isolated from F1 seedling, rosette leaf, stem, and root tissue. As shown in Figure 5, we detected maternal and paternal MEA mRNAs in all vegetative tissues tested. Thus, silencing of the paternal MEA allele was only observed in the endosperm and not in the embryo or in postembryonic vegetative tissues.

**DISCUSSION**

**The Role of the Endosperm in Parent-of-Origin Effects on Seed Development**

Loss-of-function mutations in the MEA gene display parent-of-origin effects on seed development (Chaudhury et al., 1997; Grossniklaus et al., 1998; Kiyosue et al., 1999). A seed that inherits a wild-type maternal MEA allele develops normally, regardless of the genotype of the paternal MEA allele. Conversely, a seed that inherits a mutant maternal mea allele, regardless of the genotype of the paternal MEA allele, develops abnormally. To understand the molecular basis for these parent-of-origin effects, we compared the level of expression of maternal and paternal MEA alleles during seed and plant development. We found that both maternal and paternal MEA alleles are expressed in the embryo, seedling, leaf, stem, and root. By contrast, maternal allele expression predominated in the endosperm. These results suggest that the mea parent-of-origin effects on seed development are the result, at least in part, of silencing of the paternal allele specifically in the endosperm.

In certain situations, it appears that the silenced paternal MEA allele in the endosperm can be activated and expressed. For example, genetic background may have an effect on silencing. Eight days after RLD plants were pollinated with Ler pollen, paternal MEA allele expression was detected in the endosperm of F1 seeds (Figure 3E). No paternal MEA expression was detected in the F1 progeny of the reciprocal cross. In this regard, it is interesting that we have observed effects on the transmission of the mutant maternal mea allele in the progeny of crosses between different ecotypes (data not shown). We are currently determining whether there is a correlation between specific ecotypes, transmission of the maternal mutant mea allele, and the level and timing of paternal MEA allele expression in the endosperm.

Although our experiments suggest that paternal silencing in the endosperm is important, other mechanisms may also contribute to the parent-of-origin effects of mea mutations on seed development. First, it is possible that essential maternal MEA expression takes place before fertilization within the female gametophyte. Second, the paternal MEA allele may be silenced at an important period within the embryo before the torpedo stage, which is the earliest stage we were able to investigate (Figure 3). Further experiments are required to determine the status of these latter two mechanisms.

**Support of Embryo Development by the Endosperm**

Within the Arabidopsis seed, the endosperm and maternal seed coat serve to support the growth and development of the embryo. Early in embryogenesis, the suspensor is thought to play a critical role, perhaps by acting as a conduit for nutrients moving from maternal tissues to the embryo (Yeung and Meinke, 1993). Later, it is thought that chalazal-oriented endosperm might facilitate transfer of nutrients from maternal vascular tissue to the embryo (Schulz and Jensen, 1971; Berger, 1999; Brown et al., 1999). Finally, in as many other dicot seeds, the Arabidopsis endosperm is ephemeral, and most of its stored nutrients are absorbed by the embryo as the seed matures (Berger, 1999; Brown et al., 1999). Hence, it is thought that embryo development is dependent on support provided by endosperm and maternal tissues.

Verification of the idea that embryo development requires a functional endosperm has come from the analysis of the phenotype of mutant mea seeds and parent-of-origin MEA gene expression. Previously, it was shown that when a seed inherits a maternal mutant mea allele, the embryo aborts even when the paternal MEA allele is wild type (Chaudhury et al., 1997; Grossniklaus et al., 1998; Kiyosue et al., 1999). Here, we show that within the seed, the paternal MEA allele is expressed in the embryo (Figures 3D and 4C) and is silenced in the endosperm (Figures 3E and 4C). Thus, the compartment in the defective seed that most likely lacks MEA activity is the endosperm, and as a result, development of the embryo aborts. Hence, the parent-of-origin effects of mea mutations on embryo development are likely to be indirect and result from defects in endosperm function. These results demonstrate that proper endosperm development is a prerequisite for embryogenesis in dicot seeds.
Endosperm Imprinting and the Parental Conflict Theory

The parental conflict theory attempts to explain the existence of genomic imprinting in flowering plants and mammals (Haig and Westoby, 1989, 1991; Moore and Haig, 1991). During reproduction in these organisms, a mother sometimes has offspring by more than one father. Moreover, in both flowering plants and mammals, the embryo acquires a significant amount of resources from maternal tissues. As a result, fathers strive to extract the maximal amount of resources for their own offspring, whereas the mother endeavors to allocate resources equally among all offspring. According to the parental conflict theory, imprinting arose from this conflict between the maternal and paternal genomes in relation to the transfer of nutrients from the mother to the embryo via specialized acquisitive tissues—the endosperm in plants and the placenta in mammals. According to this theory in plants, a gene that tends to suppress endosperm development (e.g., MEA; Kiyosue et al., 1999) and restricts nutrient flow to the embryo would be preferentially expressed by the maternal allele, whereas the paternal allele would be silenced (Figure 6). By contrast, a gene that tends to promote endosperm development and therefore increases nutrient flow to the embryo would be preferentially expressed by the paternal allele, and the maternal allele would be silenced (Figure 6).

Results from both genetic and molecular analyses of the MEA gene support the parental conflict theory. Loss-of-function mutations in the maternal mea allele result in precocious endosperm development before fertilization and endosperm overproduction after fertilization, suggesting that the wild-type maternal MEA gene suppresses endosperm development (Kiyosue et al., 1999). As predicted by the parental conflict model for genes that suppress endosperm development, the maternal MEA allele is expressed, whereas the paternal MEA allele is silenced in the endosperm (Figures 3E and 4C).

In support of the parental conflict model in plants, analysis of progeny from interploidy crosses in many plant species (Haig and Westoby, 1991), including Arabidopsis (Scott et al., 1998), reveals that paternal genomic excess is associated with overproduction of endosperm, whereas maternal genomic excess is associated with endosperm reduction. Our results suggest that the effects on seed development of changing the ratio of maternal to paternal genomes may be due to changes in the ratio of maternal to paternal alleles of specific genes, such as MEA. Ultimately, successful reproduction in many plant species (Haig and Westoby, 1991), including Arabidopsis (Scott et al., 1998), may require the proper balance of expression of maternal and paternal alleles of multiple genes within the endosperm.

Differential Imprinting in the Embryo and Endosperm

Because of double fertilization, reproduction in flowering plants involves inheritance of two paternal gametes, one by the embryo and one by the endosperm. The question remains as to why the embryo-inherited paternal MEA allele is expressed, whereas the endosperm-inherited paternal MEA allele is silenced. One possibility is that analogous to mammalian gene imprinting in the germ line (Pagel, 1999; Tilghman, 1999), silencing of paternal MEA alleles occurs during pollen development, perhaps by methylation of specific MEA sequences. However, after fertilization of the egg, the silenced state of the paternal MEA allele may not be sustained during embryogenesis. This could be the result of failing to maintain the methylated state of the paternal MEA allele as embryonic cells replicate their DNA and divide. By contrast, the silenced state of the paternal MEA allele may be sustained in the endosperm. This could be accomplished by maintaining the methylation pattern of the paternal MEA allele as endosperm cells proliferate.

It is interesting that plant embryos tend not to be susceptible to the effects of parental imprinting (Martienssen, 1998). By contrast, among the parentally imprinted genes studied to date in plants, such as MEA, the paternal allele tends to be silenced in the endosperm (Kermicle and Alleman, 1990; Chaudhuri and Messing, 1994). Thus, a fundamental difference between the egg and central cells may be their capacity to maintain the silenced state of parentally imprinted genes after fertilization. Alternatively, it is possible that silencing of the MEA gene is only established in the endosperm after fertilization. Experiments designed to elucidate when paternal imprinting occurs will make it possible to distinguish between these models.

METHODS

Plant Material

The two Arabidopsis thaliana ecotypes used in these experiments are Landsberg erecta (Ler) and RLD (Hardtke et al., 1996). The amino
acid sequences predicted from the Ler and RLD MEA genes are 99.9% identical (data not shown), and parent-of-origin effects on seed development of the mea-3 mutation were observed in both the Ler (Kiyosue et al., 1999) and RLD (data not shown) genetic backgrounds.

Plants were grown in greenhouses under 16-hr-light and 8-hr-dark photoperiods generated by supplemental lighting. Plants were selected for reciprocal crosses 1 week after bolting. Flowers were pollinated 2 days after removal of anthers. F1 seeds were harvested from siliques at 4, 6, 7, or 8 days after pollination, as described in the text. Seeds were dissected into embryo, endosperm, and seed coat components by using a stereomicroscope. To confirm seed stage, we cleared seeds and visualized them with a Zeiss Axioskop microscope (Carl Zeiss, Inc., Thornwood, NY) with Nomarski optics (Ohad et al., 1999).

RNA Preparation and Reverse Transcription-Polymerase Chain Reaction Amplification

Tissue samples were ground in Trizol (Life Technologies, Inc., Gaithersburg, MD) reagent with a microglass homogenizer, and total RNA was isolated as described by the manufacturer. Total RNA was further purified by LiCl precipitation and resuspended in 25 μL of RNase-free water (Sambrook et al., 1989). All reverse transcription-polymerase chain reactions (RT-PCRs) were performed with 5 μL of RNA as starting material, using a RETROscript kit (Ambion, Inc., Austin, TX). Primers to amplify MEA sequences were MEA-R1 (5′-GGTTTAGTAAACACAAATAGCATTAC-3′) and MEA-L1 (5′-GACCTAACCTGCTACGGCCAAAG-3′), which span the 16th intron of the MEA gene. All PCR reactions were performed as follows: 1 min at 94°C; 40 cycles (94°C for 30 sec, 55°C for 30 sec, and 72°C for 30 sec) followed by 72°C for 7 min. To determine the ratio of RLD to Ler MEA sequences, we performed a second PCR amplification by using the conditions described above with the MEA-L1 primer and the MEA-R2d (5′-AAGGACGTGCTTGAGTTGCTGTCTCTCGGATC-3′) derived cleaved amplified polymorphic sequence primer (Neff et al., 1998). PCR products were digested with BamHI restriction endonuclease and subjected to electrophoresis on a 3% Metaphor (FMC BioProducts, Rockland, ME) gel.

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