Synergistic interaction of three ERECTA-family receptor-like kinases controls Arabidopsis organ growth and flower development by promoting cell proliferation

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Summary
Growth of plant organs relies on coordinated cell proliferation followed by cell growth, but the nature of the cell-cell signal that specifies organ size remains elusive. The Arabidopsis receptor-like kinase (RLK) ERECTA regulates inflorescence architecture. Our previous study using a dominant-negative fragment of ERECTA revealed the presence of redundancy in the ERECTA-mediated signal transduction pathway. Here, we report that Arabidopsis ERL1 and ERL2, two functional paralogs of ERECTA, play redundant but unique roles in a part of the ERECTA signaling pathway, and that synergistic interaction of three ERECTA-family RLKs define aerial organ size. Although erl1 and erl2 mutations conferred no detectable phenotype, they enhanced erecta defects in a unique manner. Overlapping but distinct roles of ERL1 and ERL2 can be ascribed largely to their intricate expression patterns rather than their functions as receptor kinases. Loss of the entire ERECTA family genes led to striking dwarfism, reduced lateral organ size and abnormal flower development, including defects in petal polar expansion, carpel elongation, and anther and ovule differentiation. These defects are due to severely reduced cell proliferation. Our findings place ERECTA-family RLKs as redundant receptors that link cell proliferation to organ growth and patterning.

Supplemental data available online

Key words: Arabidopsis, Receptor-like kinase, Cell proliferation, Organ size, Flower development, Functional redundancy

Introduction
The control of body and organ size of multicellular organism remains one of the unresolved questions in developmental biology. In plants and animals, increasing evidence supports the view that, although cell proliferation and cellular growth are an instrumental process of organ growth, the final size and form of organs is governed by the intrinsic mechanisms that monitor and balance the number and size of cells within the context of developmental programs (Conlon and Raff, 1999; Day and Lawrence, 2000; Mizukami, 2001; Nijhout, 2003; Potter and Xu, 2001). Studies found that experimental manipulation of cell cycle regulators, for example, does not always lead to altered organ size, as defects in cell number are compensated by alteration of cell size (Hemerly et al., 1995; Neufeld et al., 1998). Similarly, alteration of cellular growth in Drosophila by manipulation of Myc expression, as well as promotion of cell expansion in tobacco by induced expression of the Arabidopsis auxin-binding protein 1 (ABP1), conferred limited impact on overall organ size because of cell number compensation (Johnston et al., 1999; Jones et al., 1998).

In higher plants, lateral organs are generated reiteratively by the continual activity of the shoot apical meristem (SAM). Because plant cells are encapsulated by cell walls, organogenesis occurs in the absence of cell migration or the removal of overproduced cells. As such, unraveling developmental programs that coordinate cell proliferation and expansion during organ growth is key for understanding plant organ size control. The molecular links that integrate regulation of cell proliferation and organ size/shape as a unit in plants have just begun to emerge. One such regulator is the Arabidopsis AINTEGUMENTA (ANT) gene, which encodes an AP2-domain transcription factor (Elliott et al., 1996; Klucher et al., 1996). ANT acts to prolong the duration of cell proliferation by sustaining the expression of D-type cyclins (Mizukami, 2001; Mizukami and Fischer, 2000). Consequently, overexpression of ANT confers hyperplasia. The recent finding that the auxin-inducible gene ARGOS acts upstream of ANT suggests a role for the phytohormone auxin in regulating inherent organ size (Hu et al., 2003).

We aim to uncover the molecular basis of cell-cell communication that fine tunes coordinated cell proliferation during plant organ growth. The Arabidopsis ERECTA gene is a candidate for this. ERECTA is highly expressed in the SAM and developing lateral organs, where cells are actively dividing (Yokoyama et al., 1998). Loss-of-function erecta mutations confer compact inflorescence with short lateral organs and internodes, and these phenotypes are largely attributable to reduced cell numbers in the cortex cell files (Shpak et al., 2003;
Torii et al., 2003; Torii et al., 1996). The shortened *erecta* pedicels (floral stems) are associated with an increase in 4C cells, suggesting a possible aberration in cell cycle progression (Shpak et al., 2003). **ERECTA** encodes a leucine-rich receptor-like serine/threonine kinase (LRR-RLK) (Torii et al., 1996), a prevalent subfamily of signaling receptors in plants (Shiu and Bleecker, 2001; Shiu and Bleecker, 2003). LRR-RLKs regulate a wide-variety of signaling processes, including development of the SAM and microspores, brassinosteroid perception, floral abscission, pathogen recognition and symbiosis (for reviews, see Becraft, 2002; Carles and Fletcher, 2003; Kistner and Parniske, 2002; Li, 2003; Torii et al., 2004). The structure, expression patterns, and cellular and developmental phenotypes all support the notion that **ERECTA** mediates cell-cell signals that sense and coordinate organ growth.

We have previously shown that expression of a dominant-negative form of **ERECTA** (a ΔKinase fragment) enhances the growth defects of the null *erecta* plants, suggesting redundancy in the **ERECTA** signaling pathway (Shpak et al., 2003). To reach a full understanding of how **ERECTA** controls inherent plant size, it is imperative to identify its redundant receptors.

Here, we report the identification and functional characterization of **ERL1** and **ERL2**, two redundant, paralogous **ERECTA**-like receptors that play a role in a part of **ERECTA** signaling pathway. Although loss-of-function mutations in **ERL1** and **ERL2** loci gave no detectable phenotype, they each enhanced *erecta* defects in a unique manner. Strikingly, loss of the entire **ERECTA**-family LRR-RLKs conferred extreme dwarfism and abnormal flower development. Molecular and cellular analysis revealed that **ERECTA**-family RLKs link cell proliferation to organ growth and patterning via a novel mechanism.

**Materials and methods**

**Plant materials and growth conditions**

The *Arabidopsis* ecotype Columbia (Col) was used as a wild type. The T-DNA knockout seed population that contains *erl1-2* and *erl2-1* mutants was obtained from the Biological Resource Center. All mutant lines were backcrossed three times to Col wild-type plants prior to any phenotypic analysis. The conditions for plant growth were as described by Shpak et al. (2003).

**Oligo DNA sequences**

Lists of oligo DNA sequences used for all experiments are available as supplementary data at [http://dev.biologists.org](http://dev.biologists.org).

**Cloning of **ERL1** and **ERL2****

RT-PCR was performed using wild-type cDNA as a template, and using primer pairs: **ERL1**: 1.4coding and **ERL1**g6054rc for **ERL1**; and **ERL2**: 3coding and **ERL2**g3525rc for **ERL2**. The 5′ ends of mRNA were recovered by a rapid amplification of cDNA ends (RACE) using FirstChoice™ RLM RACE kit (Ambion, Austin, TX). Eik1-300rc or Eik2-300rc was used as the outer primer, and Eik1-185rc or Eik2-185rc was used as the nested primer for **ERL1** and **ERL2**, respectively. The amplified fragments were cloned into pCR2.1-TOPO (Invitrogen, Carlsbad, CA) and sequenced.

**Reverse transcriptase-mediated (RT) PCR**

RNA isolation, cDNA synthesis and RT-PCR were performed as described by Shpak et al. (Shpak et al., 2003) with various cycles. Primer pairs used are as follows: **ERECTA**, ERg4359 and ERg5757rc; **ERL1**, ERL1g2846 and ERL1g4411rc; **ERL2**, ERL2g3085 and ERL2g4254rc; **ANT**, 5′ant-1 and ANT1600rc; **STM**, STM781 and STM2354rc; **WUS**, U3WUS5 and U34WUS3rc; **KNAT1**, BP681 and BP3100rc; **CYCLIN D2**, CycD2.501 and CycD2.801rc; **CYCLIN D3**, CycD3.501 and CycD3.935rc; and **ACTIN**, ACT2-1 and ACT2-2.

**Complementation of **erecta** by **ERL1** and **ERL2****

Full-length genomic coding regions for **ERL1** and **ERL2** were cloned into the **ERECTA** promoter-terminator cassette by the following procedure. PCR was performed using the wild-type Col genomic template and primer pairs: **ERL1**: g3036 and **ERL1**-3endrc for **ERL1**; and **ERL2**: g2166 and **ERL2**-3endrc for **ERL2**. The amplified fragments were digested with SpeI and Xbal, and inserted into SpeI-digested pKUT522 to generate pESH208A and pESH209A for **ERL1** and **ERL2**, respectively. Subsequently, PCR was performed using primer pairs: **ERL1**: 5end and **ERL1**g4411rc for **ERL1**; and **ERL2**: 5end and **ERL2**ge3182rc for **ERL2**. The amplified fragments were digested with SpeI and Xbal, and inserted into SpeI-digested pESH208A and pESH209A, respectively, to generate pESH208 (**ER**: **ERL1**) and pESH209 (**ER**: **ERL2**). The plasmids were introduced into *Agrobacterium tumefaciens* strain GV3101/pMP90 by electroporation, and into *Arabidopsis erecta*-105 plants by vacuum infiltration.

**ERECTA::GUS, **ERL1::GUS** and **ERL2::GUS** transgenic plants**

For construction of **ERECTA::GUS**, the **GUS** gene was inserted as a SpeI fragment into pKUT522 between the **ERECTA** promoter and terminator. The plasmid was named pNI101. To make **ERL1::GUS** and **ERL2::GUS** constructs, the EcorI/PstI fragment of pKRT2-GUS was cloned into pZP222 (Hadjukiewicz et al., 1994). The plasmid was named pESH244. The **ERL1** promoter region was amplified with primers ERL1g3680link and ERL1g403linkrc, using the MMI1 BAC clone as a template. The **ERL2** promoter region was amplified with primers ERL2g4364link and ERL2g4linkrc, using the T28J14 BAC clone as a template. The amplified fragments were digested with EcoRI and inserted into pESH244. The plasmids were named pESH245 (**ERL1::GUS**) and pESH246 (**ERL2::GUS**). pNI101, pESH245 and pESH246 were introduced into *Arabidopsis* wild type as described above. **GUS** histochemical analysis was performed according to Sessions et al. (Sessions et al., 1999).

**Screening and isolation of the **Arabidopsis** T-DNA insertion mutants**

Screening and isolation of T-DNA insertion lines were as described for the *Arabidopsis* KO Facility ([http://www.biotech.wisc.edu/Arabidopsis/](http://www.biotech.wisc.edu/Arabidopsis/)). The **erl1-2** was isolated from an α population (vector pD991, kanamycin resistance), and **erl2-1** was isolated from a β population (vector pROK2, basta resistance), using gene-specific primers and JL-202 T-DNA left border primer. The gene-specific PCR primers were: ERL1K765 and ERL1K6137rc for **ERL1**; and ERT1J70 and ERT1S855rc for **ERL2**. Precise locations of the insertions were determined by sequencing the PCR fragments. Both **erl1-2** and **erl2-1** were backcrossed three times. The B3F2 populations of **erl1-2** and **erl2-1** exhibited a 3:1 ratio of kanamycin resistance and Basta resistance, respectively (**erl1-2**, KanR:KanS=163:58, $\chi^2=0.183$, $P=0.669$; **erl2-1**, BastaR:BastaS=203:76, $\chi^2=0.747$, $P=0.388$), indicating a single T-DNA insertion. PCR-based genotyping confirmed that these single insertions disrupt the **ERL** loci.

**Generation of double- and triple-knockout plants**

To generate *erl1* and *erecta* double mutants, **erl1-2** and **erl2-1** plants were crossed with *erecta*-105 plants. To generate **erl1**
erl2 double mutants, erl1-2 plants were crossed with plants of the genotype erecta-105/erecta-105 erl1-2/erl1-2 erl2-1/+ . Plants of a correct genotype were isolated from the F2 populations. erecta-105/erecta-105 erl1-2/+ erl2-1/erl2-1 plants were self-fertilized to obtain the erecta erl1 erl2 triple mutants. The T-DNA insertion that disrupts the ERL1 locus in erl1-2, and the ERL2 locus in erl2-1, conferred resistance to kanamycin and Basta, respectively. Thus, progeny of each cross were first tested for resistance, then subsequently the genotype of individual plants, whether they were heterozygous or homozygous, was determined by PCR using gene-specific primer pairs, and a combination of T-DNA- (JL-202) and gene-specific primers. The presence of the erecta-105 mutation was determined by PCR using the primer pairs: ERGl2248 and er-105 (Torii et al., 2003).

**Light and scanning electron microscopy**

Fixation, and embedding and sectioning, of tissues for light microscopy using Olympus BX40, as well as preparation of samples for scanning electron microscopy using JOEL 840A, were performed as described by Shpak et al. (Shpak et al., 2003).

**Cell number measurement**

Light microscopy images of four regions of sectioned wild-type, erecta-105, erecta-105 erl1-2 and erecta-105 erl2-1 pedicels were taken, and the number of cells in a middle longitudinal cortex row was determined. This number was used to calculate the total number of cells in the cortex row of an average length pedicel. The number of cells was counted in three sectioned erecta-105 erl1-2 erl2-1 pedicels and the average was determined.

**Accession numbers**

The GenBank accession numbers for the ERL1 and ERL2 sequences reported in this paper are AY244745 and AY244746, respectively.

**Results**

**ERL1 and ERL2, two ERECTA-like LRR-RLKs in Arabidopsis**

To identify candidate RLKs that act in parallel pathways with ERECTA, we surveyed the Arabidopsis genome and found two ERECTA-LIKE genes, ERL1 (At5g62230.1) and ERL2 (At5g07180.1). We subsequently isolated full-length cDNA clones for ERL1 and ERL2 by a combination of RT-PCR and 5’ RACE-PCR (Fig. 1A). Among the 225 Arabidopsis genes encoding LRR-RLKs (Shiu and Bleecker, 2003), ERECTA possesses an unusual, characteristic exon-intron structure with 26 introns (Torii et al., 1996). A comparison of genomic and cDNA sequences reveals that ERL1 and ERL2 also contain 26 introns, all of which are located at identical positions to the introns of ERECTA. The predicted ERL1 and ERL2 proteins share high overall sequence identity to ERECTA (60% identity, 72% similarity), and even higher sequence identity between each other (78% identity and 83% similarity). The LRR region and the kinase domain possess the highest degree of sequence conservation (Fig. 1A). The juxtamembrane domain and the extracellular paired cysteine regions adjacent to the LRR region have relatively high sequence identity, whereas the N-terminal signal sequence and the C-terminal tail region are poorly conserved (Fig. 1A). The phylogenetic, parsimony analysis suggests that ERL1 and ERL2 have evolved by recent duplication, and that they are immediate paralogs of ERECTA (Fig. 1B). The result is consistent with the neighbor-joining analysis of the LRR-RLK phylogeny reported by Shiu and Bleecker (Shiu and Bleecker, 2001), as well as by Yin et al. (Yin et al., 2002). The finding that ERL1, ERL2 and ERECTA constitute a subfamily of LRR-RLKs opens the possibility that the two ERLs may have functions related to ERECTA.

**ERL1 and ERL2 rescue the erecta phenotype when expressed under the ERECTA promoter and terminator**

To investigate whether ERL1 and ERL2 genes are functional homologs of ERECTA, ERL1 and ERL2 were expressed in the null allele erecta-105 under the control of the native ERECTA promoter and terminator. Both constructs rescued the erecta defects. Transgenic erecta-105 plants expressing ERECTA::ERL1 or ERECTA::ERL2 displayed phenotypes, such as elongated inflorescence and pedicels, nearly identical to the wild-type plants (Fig. 1C). Therefore, both ERL1 and ERL2 can substitute for ERECTA function when expressed in the tissue and cell types that normally express ERECTA, suggesting that the two ERLs are capable of perceiving and transducing the same signal as ERECTA.

**ERECTA, ERL1 and ERL2 display overlapping, but unique expression patterns**

The inability of ERL1 and ERL2 to complement erecta mutants when expressed under their endogenous promoter (Fig. 1C) suggests differences in expression patterns. At the same time, if ERL1 and ERL2 are the RLKs whose function is inhibited when expressed under their endogenous promoter, we should expect them to be expressed, at least in part, in an overlapping manner with ERECTA. To clarify these points, we next analyzed the developmental expression of ERL1 and ERL2.

RT-PCR analysis showed that, similar to ERECTA, expression levels of the two ERLs were higher in developing organs, including bud clusters, flowers, siliques and young rosettes, lower in mature aboveground organs, such as leaves, stems and pedicels, and barely detectable in roots (Fig. 2). The expression levels of ERL1 and ERL2 in mature organs were much lower than those of ERECTA.

To examine the organ- and tissue-specific expression patterns of ERL1 and ERL2 in detail, promoter fragments of ERL1 (4.1 kb) and ERL2 (4.4 kb) were fused transcriptionally to the GUS gene and introduced in Arabidopsis wild-type plants. The expression patterns of ERECTA::GUS, ERL1::GUS and ERL2::GUS mark the actively-proliferating organs (Fig. 3). At the vegetative stage, both ERL1::GUS and ERL2::GUS were strongly expressed in the shoot meristem, leaf primordia and juvenile leaves (Fig. 3A-C). At the reproductive stage, GUS expression was detected in the young developing flowers up to stage 12 for ERECTA and ERL2, and up to stage 14 for ERL1 (Fig. 3D-I). ERECTA::GUS and ERL1::GUS were detected in inflorescence meristem and were visibly upregulated during flower initiation and formation of flower organs (Fig. 3J-L). GUS expression was also detected in cells that will differentiate into pedicels (Fig. 3J-L). In developing flowers, the expression of ERECTA, ERL1 and ERL2 was in the actively growing region of the floral organs, and thus altered dynamically as the developmental stages of the floral organs progressed (Fig. 3G-I). At the early stages, all three genes were expressed in an overlapping manner in all flower organs (Fig. 3D-L, and data not shown). Later, their expression became confined to different subsets of proliferating tissues.
For example, at flower stage 11, \texttt{ERECTA::GUS} was expressed largely in the mesocarp, and to a lesser degree in ovules, whereas \texttt{ERL1::GUS} was expressed predominantly in ovules, and \texttt{ERL2::GUS} in style and ovules (Fig. 3M-O). The finding that \texttt{ERL1} and \texttt{ERL2} display overlapping but unique expression patterns suggests their roles to be parallel to, or a part of, the \texttt{ERECTA} signaling pathway.

**Isolation of the null alleles of \texttt{ERL1} and \texttt{ERL2}**

To investigate the roles of the two \texttt{ERLs} in \textit{Arabidopsis} growth and development, we next identified T-DNA-tagged, loss-of-function alleles of \texttt{ERL1} and \texttt{ERL2}. Locations of the insertions are shown in Fig. 4. \textit{erl1-2} has a T-DNA insertion at nucleotide +3410 from the translation initiation codon, within exon 18, which encodes the sixteenth LRR (Fig. 4A). \textit{erl2-1} has a T-DNA insertion at nucleotide +2454 from the translation initiation codon, within exon 14, which encodes the twelfth LRR (Fig. 4B). The T-DNA insertions in \textit{erl1-2} and \textit{erl2-1} are associated with a deletion of 59 and 76 nucleotides, respectively, suggesting that they represent the knockout (null) alleles. Indeed, no detectable \texttt{ERL1} transcripts were observed in \textit{erl1-2} and no \texttt{ERL2} transcripts were observed in \textit{erl2-1} by RT-PCR (Fig. 4C,D).

The absence of either \texttt{ERL1} or \texttt{ERL2} transcripts had no

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**Fig. 1.** \texttt{ERECTA-LIKE} genes \texttt{ERL1} and \texttt{ERL2} are immediate, functional paralogs of \texttt{ERECTA}.

(A) Amino-acid sequence alignment of \texttt{ERECTA} and its paralogs. The alignment was generated by the CLUSTAL X program. Identical amino acids and similar amino acids are highlighted by black and gray backgrounds, respectively. Arrows indicate the positions of introns. Respective domains are highlighted with colored underlines: N-terminal signal sequence, blue; extracellular paired cysteine regions, red; the LRR-domain, green; the transmembrane domain, black; the juxtamembrane domain, purple; the kinase domain, pink; and a C-terminal tail region, cyan. (B) A phylogenetic tree of \texttt{ERECTA}, \texttt{ERL1} and \texttt{ERL2}. The single most parsimonious tree generated using heuristic searches (PAUP*) based on the kinase domain sequence is shown. BR1 and CLV1 were used as outgroups. Branch lengths are proportional to the number of amino-acid substitutions, and the numbers at the branch points indicate bootstrap values of 500 replications. (C) \texttt{ERL1} and \texttt{ERL2} genes rescue the \texttt{erecta} phenotype when expressed under the \texttt{ERECTA} promoter and terminator. Shown are the inflorescences apices from wild type, \texttt{erecta-105}, \texttt{erecta-105} plants expressing \texttt{ERECTA::ERL1} and \texttt{erecta-105} plants expressing \texttt{ERECTA::ERL2}. Scale bar: 5 mm.
effect on ERECTA expression levels (Fig. 4C,D). Similarly, the expression levels of ERL1 and ERL2 were not altered in erecta-105 plants, which do not express any ERECTA transcripts (Fig. 4E). The lack of up- or downregulation among the three ERECTA-family LRR-RLKs implies that their signaling pathways do not constitute an interconnected feedback loop.

Both ERL1 and ERL2 are redundant

erl1-2 and erl2-1 were subjected to further phenotypic characterization. erl1-2 and erl2-1 single mutant plants were indistinguishable from wild-type plants (Fig. 5A-D). Their inflorescence undergoes elongation of the internodes between individual flowers, and they all displayed normal length petioles, stems (Fig. 5A), pedicels (Fig. 5B,D) and siliques (Fig. 5C,D). The lack of any visible phenotype suggests that ERL1 and ERL2 are redundant.

As ERL1 and ERL2 appear to have undergone recent gene duplication (Fig. 1B), it may be necessary to remove both gene products in order to reveal their biological functions. To test this hypothesis, we generated an erl1-2 erl2-1 double mutant. erl1-2 erl2-1 plants did not exhibit any visible phenotype (Fig. 5A-D). Although ERL1 and ERL2 are capable of rescuing the growth defects of erecta-105 (Fig. 1C), erl1 and erl2 single mutants, as well as the erl1 erl2 double mutant failed to confer any developmental phenotype. This finding suggests that loss-of-function of ERL1 and ERL2 is masked by the presence of the functional ERECTA gene.

erl1 and erl2 enhance a subset of erecta defects in a unique manner

To uncover the developmental role of ERL1 and ERL2 in the absence of functional ERECTA, erl1 and erl2 mutations were introduced into erecta-105 plants (Torii et al., 1996; Torii et al., 2003). Both erl1 and erl2 enhanced the erecta defects in a unique manner. The erl1-2 mutation notably exaggerated the silique and pedicel elongation defects of erecta-105. erecta-105 erl1-2 double mutant plants developed very short, blunt siliques and short pedicels (Fig. 5B-D), both of which are reminiscent of part of the phenotype conferred by the dominant-negative ΔKinase (Shpak et al., 2003). The presence of the erl1-2 mutation did not significantly affect the height of erecta-105 plants (Fig. 5A).

By contrast, the erl2-1 mutation primarily enhanced the internodal elongation defects of erecta. erecta-105 erl2-1 double mutant plants were much shorter than erecta-105, and developed very compact inflorescence with tightly clustered flowers and flower buds at the tip (Fig. 5A,E). The architecture of erecta-105 erl2-1 inflorescence resembles that of the transgenic erecta-105 expressing ΔKinase (Shpak et al., 2003).

Fig. 2. Semi-quantitative RT-PCR analysis of ERECTA, ERL1 and ERL2 transcripts in different tissues. The actin fragment was amplified simultaneously as a control. ERECTA, ERL1 and ERL2 were amplified for 32 cycles; the control actin was amplified for 30 cycles.

Fig. 3. ERECTA, ERL1 and ERL2 are expressed in young proliferating tissues in an overlapping but unique manner. Expression of ERECTA::GUS (A,D,G,J,M), ERL1::GUS (B,E,H,K,N) and ERL2::GUS (C,F,I,L,O) reporter genes in: a 14-day-old seedling (A-C); inflorescence apices at lower (D-F) and higher (G-I) magnifications; inflorescence meristem (J-L); and a stage 11 flower (M-O). Scale bars: 3 mm for A-C; 2 mm for D-F; 0.5 mm for G-I; 50 μm for J-L; 0.2 mm for M-O.
al., 2003). In addition, the *erecta-105 erl2-1* siliques were slightly shorter than those of *erecta-105* (Fig. 5C,D).

The morphology of the silique tip was analyzed in detail. The *erecta-105* silique tip has a blunt appearance due to a wide style that protrudes less from the valves than does the wild type. Both *erl1* and *erl2* mutations exaggerated this characteristic *erecta* silique phenotype, with even wider valves and shorter, broader styles (Fig. 5F). This indicates that the enhancement of the silique phenotype by *erl1-2* and *erl2-1* is not due to general elongation defects unrelated to the ERECTA pathway. From this, we conclude that *ERL1* and *ERL2* act in an overlapping but distinct part of the ERECTA signaling pathway in regulating inflorescence architecture and organ shape.

**Synergistic interaction of ERECTA, ERL1 and ERL2 in promoting organ growth and flower development**

To understand the biological function of the ERECTA-family LRR-RLK as a whole, we next generated an *erecta-105 erl1-2 erl2-1* triple mutant. For this purpose, F2 plants that were homozygous for *erecta* and *erl2*, but heterozygous for *erl1*, were self-fertilized. A subsequent F3 population segregated extremely dwarf, sterile plants at a ~25% ratio (dwarf plants:total=74/315, $\chi^2=0.382$, $P=0.537$), suggesting that they may be the triple mutant. To test this hypothesis, genotypes of 86 F3 plants were analyzed. Among 63 compact, fertile plants, 40 were heterozygous for *erl1*, 23 were wild type for *ERL1* and none were homozygous for *erl1*, consistent with the expected 2:1 ratio ($\chi^2=0.286$, $P=0.593$). By contrast, all 23 extremely dwarf, sterile plants were homozygous for *erl1* and thus carried *erecta-105 erl1-2 erl2-1* triple mutations. Furthermore, progeny of the F3 siblings with a genotype *erecta-105 ERL1 erl2-1* failed to segregate extremely dwarf plants (0/227 scored). These results provide statistical evidence that the triple mutations confer severe growth defects (Fisher’s exact test, $P<0.00000001$).

We subsequently analyzed a phenotype of *erecta-105 erl1-2 erl2-1* triple mutant plants during postembryonic development. The striking effects of *erecta-105 erl1-2 erl2-1* mutations on organ growth can be seen in all aboveground organs (Fig. 6A-E) and are evident soon after germination, at a time when cells start to divide. Decreased cotyledon growth is notable in 4-day-old *erecta-105 erl1-2 erl2-1* seedlings, and it is more striking in 12-day-old seedlings, which have small, misshaped cotyledons with very short petioles (Fig. 6A). Growth of primary leaves is strongly diminished in the triple mutant seedlings (Fig. 6A), whereas leaf primordia are forming on a flank of the SAM (data not shown). Interestingly, the triple mutations do not affect hypocotyl elongation, which occurs solely because of cell elongation (Gendreau et al., 1997). At a later stage of vegetative development, *erecta-105 erl1-2 erl2-1* plants form a small rosette with small, round leaves that lack petiole elongation (Fig. 6B). Transition to flowering occurs approximately at the same time in wild-type, *erecta-105* and *erecta-105 erl1-2 erl2-1* plants, suggesting that mutations in the three ERECTA-family genes do not affect phase transition (Fig. 6B, and data not shown).

The phenotypes of triple mutant plants at the reproductive stage are variable. Although the main inflorescence stem always exhibits severe elongation defects, axillary branches occasionally show various degrees of phenotypic rescue (Fig. 6C). A variable level of phenotypic rescue was also noticeable in flowers and pedicels at a later stage of axillary inflorescence development. Flowers with stronger phenotypes have a reduced number of organs with an occasional fusion of organs, and their pedicels are either absent or too short to be detected (Fig. 6C). Those with weaker phenotypes have all
four organs formed, but they are smaller in size and are incompletely developed (Fig. 6E). Such flowers have extremely short, but recognizable pedicels (Fig. 6E). Unlike *erecta-105*, the triple mutant flowers develop cylindrical, needle-like petals that lack polar expansion, very short gynoecium, and small anthers that are incompletely differentiated, all of which are visible in stage 9 flowers as well as in mature flowers (Fig. 6D,E,H). Ovule development is either absent or aborted at a very early stage (Fig. 6H), and this is consistent with the overlapping expression of *ERECTA*, *ERL1* and *ERL2* in developing ovules (Fig. 3M-O). These phenotypes are much more severe than *erecta-105* plants expressing *D* Kinase (Shpak et al., 2003) were incomplete. The results demonstrate that the *ERECTA*, *ERL1* and *ERL2* genes interact synergistically, and that these three *ERECTA*-family LRR-RLKs, as a whole, specify the proper growth and differentiation of all aboveground organs.

### Molecular analysis of *erecta erl1 erl2* inflorescence suggests a novel mechanism for organ growth regulation

To understand the molecular basis of organ growth/cell number regulation, we examined cellular morphology in petals and pedicels. *Arabidopsis* petals have a simple cell layer structure with epidermal cells that are uniform in size and shape (Bowman, 1993). Although petals of *erecta-105 erl1-2 erl2-1* plants are very small and filamentous in shape (Fig. 6E), their abaxial epidermis cells are slightly larger than in *erecta-105* petals (Fig. 6F).

As reported previously, *erecta-105* pedicels have a reduced number of expanded cortex cells (Shpak et al., 2003). Similar to *erecta-105*, *erecta-105 erl1-2 erl2-1* double mutants, and *erecta-105 erl1-2 erl2-1* triple mutations, confer reduced cell numbers associated with enlarged and irregular cell shape in the cortex (Fig. 6G). Interestingly, *erecta-105 erl1-2* and *erecta-105 erl2-1* mutations lead to disorganized cell growth in the cortex. Cells are irregular in size and shape, and have gaps in between. This phenotype is similar to transgenic *erecta-105* plants expressing *D* Kinase (Shpak et al., 2003). Cell numbers in a longitudinal cortex file are severely reduced in the mutants, with a concomitant decrease in the final pedicel length (Fig. 5B, Fig. 6I).

**erecta-105 erl1-2 erl2-1** triple mutants are defective in cell proliferation

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**Fig. 5.** *ERL1* and *ERL2* genes are partially redundant and show synergistic interaction with *ERECTA*. (A-C) Morphometric analysis of fully-grown eight-week-old wild-type, *erl1-2*, *erl2-1*, *erl1-2 erl2-1*, *erecta-105*, *erecta-105 erl1-2*, and *erecta-105 erl2-1* plants. (A) Plant (inflorescence) height (*n*=20). (B,C) Lengths of mature pedicels (B) and siliques (C) on the main stem (*n*=40; eight measurements per stem). Bars represent the average; error bars represent s.d. (D) Mature siliques and attached pedicels of wild-type, *erl1-2*, *erl2-1*, *erl1-2 erl2-1*, *erecta-105*, *erecta-105 erl1-2* and *erecta-105 erl2-1*. Scale bars: 5 mm. (E) Six-week-old plants of *erecta-105*, *erecta-105 erl1-2*, *erecta-105 erl2-1* and *erecta-105 erl1-2 erl2-1*. Scale bars: 3 cm. The top right insert is an image of an *erecta-105 erl1-2 erl2-1* plant at higher magnification (scale bar: 5 mm). (F) Scanning electron micrographs of silique tips from wild type, *erecta-105*, *erecta-105 erl1-2* and *erecta-105 erl2-1*, and a silique from *erecta-105 erl1-2 erl2-1*. Scale bar: 100 μm
defects conferred by the triple mutations, we analyzed the expression levels of four transcription factor genes that regulate shoot and floral organ size (Fig. 6J). \(\text{ANT}\) acts to prolong duration of cell proliferation during lateral organ development, and its loss of function confers reduced organ size (Elliott et al., 1996; Mizukami and Fischer, 2000). Loss-of-function mutations in \(\text{SHOOTMERISTEMLESS (STM)}\) and \(\text{WUSCHEL (WUS)}\) homeobox genes cause a decrease in the number of meristem cells and growth defects of lateral organs (Laux et al., 1996; Long et al., 1996). The \(\text{BREVIPEDICELLUS (BP)}\) locus encoded by the \(\text{KNAT1}\) homeobox gene interacts synergistically with \(\text{ERECTA}\) in promoting internodal elongation and floral organ size (Douglas et al., 2002). Semi-quantitative RT-PCR analysis of flower and bud clusters reveals that \(\text{erecta-105 erl1-2 erl2-1}\) triple mutations do not affect expression levels of \(\text{ANT}\), \(\text{STM}\), or \(\text{KNAT1}\) (Fig. 6J). \(\text{WUS}\) expression was slightly reduced in the triple mutant background (Fig. 6J). However, such a slight reduction is not likely to account for severe defects in shoot and floral organ growth, and internodal elongation in the triple mutants. It is known that \(\text{ANT}\) leads to prolonged expression of \(\text{D-type cyclins}\), which control the entry to cell cycle progression at the G1 stage (Cockcroft et al., 2000; Dewitte and Murray, 2003; Mizukami and Fischer, 2000). Transcript levels of two
D-type cyclins, CYCD2;1 and CYCD3;1, were not significantly altered by the triple mutations (Fig. 6J). This is consistent with the notion that the control of organ size by ERECTA-family RLKs involves mechanisms other than the pathway mediated by ANT. Taken together, the results suggest that the three ERECTA-family LRR-RLKs promote cell proliferation via a novel mechanism.

**Discussion**

Our previous study of a dominant-negative ERECTA action led us to predict that the ERECTA signaling pathway is redundant and shared by multiple receptors (Shpak et al., 2003). Here, we present direct evidence that two paralogous ERECTA-LIKE LRR-RLKs play a role in a subset of the ERECTA signaling pathway and that synergistic interaction of these three family members as a whole specifies aerial organ size by promoting cell proliferation.

**Functional redundancy and synergistic interaction among three ERECTA-family LRR-RLKs**

Duplications of developmental regulatory genes followed by subsequent mutation and selection are thought to have driven morphological diversity in multicellular organisms. Acquisition of novel gene functions occurs by alteration of protein function or of gene expression patterns. The fact that ERL1 and ERL2 are capable of substituting for ERECTA activity when driven by the ERECTA promoter and terminator (Fig. 1C) indicates that specificity among ERECTA, ERL1 and ERL2 lies largely in their cis-regulatory elements rather than in their protein-coding regions. Consistently, specific sites of enhancement of the erecta phenotype by either erl1 or erl2 mutation appear to correspond to the expression domains of these two LRR-RLKs, which are weaker and confined to a subset of ERECTA expression domains (Figs 2, 3). The dominance of cis-regulatory sequences over protein-coding regions in functional specification among closely-related multigene families has been documented for transcription factors regulating development, such as: Hox genes in mouse development; the Myb genes WER and GL1 in Arabidopsis epidermal patterning; and AGAMOUS-family MADS-box genes in Arabidopsis ovule development (Greer et al., 2000; Lee and Schiefelbein, 2001; Pinyopich et al., 2003).

Because ERECTA-family genes encode putative receptor kinases, their functional equivalence indicates that ERECTA, ERL1 and ERL2 are capable of receiving the same ligand(s) and eliciting the same downstream response(s). This raises a novel view on how the extent of organ growth is monitored by cell-cell signaling in Arabidopsis. The prevalent model based upon *Drosophila* wing development is that final organ size is determined by the steepness of morphogen gradients (Day and Lawrence, 2000). According to this model, concentration gradients of ligands, such as Dpp or Wg, dictate where and when cells proliferate. By contrast, we hypothesize that tissue-specific and redundant expression of functionally equivalent receptors plays a regulatory-role in coordinating *Arabidopsis* aerial organ growth. In the organ primordium, where cells are proliferating ubiquitously, uniform expression of all three ERECTA-family LRR-RLKs maximizes the organ growth. As the organ matures, localized and non-redundant expression of each RLK fine-tunes local, subtle growth for elaboration of final form and size. Transient, non-overlapping expression of ERECTA, ERL1 and ERL2 in a developing gynoecium (Fig. 3M-O) reflects such intricate local growth patterns, as growth and differentiation of distinct tissues, such as stigma, style valves and ovules, must occur concomitantly during carpel development (Ferrandiz et al., 1999). This view is in accordance with previous findings that strength of the ERECTA pathway specifies final organ size in a quantitative manner (Lease et al., 2001; Torii et al., 2003; Torii et al., 1996). Future identification of the ligands shared by these three receptors will address this hypothesis.

A recent molecular evolutionary study implies that the RLK superfamily underwent radical expansion within the plant lineage. The existence of more than 600 RLK-coding genes in the *Arabidopsis* genome is in sharp contrast with the small numbers of their counterparts (Pelle/IRAK family) in animals: three in mice and four in humans (Shiu and Bleecker, 2003). Consistently, gene duplication events among RLK sub-families have been documented (Baudino et al., 2001; Nishimura et al., 2002; Searle et al., 2003; Shiu and Bleecker, 2003; Yamamoto and Knap, 2001; Yin et al., 2002), but their biological significance is not fully understood. Our finding confirms the effectiveness of the dominant-negative approach, and further provides a framework for understanding functional redundancy among recently duplicated plant RLK gene families.

**ERECTA family genes control plant organ size through coordination of cell proliferation**

The most prominent feature of *erecta* single and *erecta erl* double and triple mutations is a reduction in aerial organ size due to reduced cell numbers. In theory, cell numbers in lateral organs can be regulated by affecting the number of SAM cells available for recruitment to organ primordia, by promotion of cell proliferation, or by prolonging the duration (window) of cell proliferation during organ growth. Our results suggest that ERECTA-family genes are most likely to function in the promotion of cell proliferation. The triple mutations are not likely to disturb SAM function; even a strikingly tiny leaf of the triple mutant initiates and increases in size with the same timing as wild type. Consistently, *WUS* and *STM* expression levels are not significantly altered by the mutation (Fig. 6J).

Furthermore, expression of *CYCLIN D2*, whose overexpression confers an increase in growth rate by accelerating primordia initiation in the SAM (Cockcroft et al., 2000), is not affected in the triple mutant background. It is also unlikely that ERECTA-family genes prolong duration of cell proliferation, as *erecta erl1 erl2* mutations do not lead to early cessation of organ growth. Consistently, expression of ANT, which promotes the meristematic competency of developing organs through prolonged expression of *CYCLIN D* (Mizukami and Fischer, 2000), is not downregulated by the triple mutations.

In addition to growth defects, *erecta erl1 erl2* plants exhibit aberrant floral organ differentiation, notably in anthers and ovules. This may be due to inhibited primordia growth, which results in a diminished supply of progenitor cells for tissues that differentiate at later stages of flower development. Alternatively, ERECTA-family genes as a whole may play some specific roles in flower organ differentiation. In this regard, it is interesting that ANT, which also specifies organ size but via a distinct mechanism, is known to be required for
proper ovule differentiation and floral organ identity (Elliott et al., 1996; Klucher et al., 1996; Krizek et al., 2000).

In contrast to the main inflorescence, axillary branches of *erecta erl1 erl2* plants displayed various degrees of phenotypic rescue (Fig. 6C). One possibility that explains such rescue could be that the indirect effects caused by premature termination of the SAM (the main inflorescence) relieves the growth of axillary branches via ERECTA-independent mechanisms (Leyser, 2003). Alternatively, control of axillary branch development may involve factors that possess partially redundant function with ERECTA-family receptor-like kinases. Such factors might be more distantly related receptor-like kinases and/or gene products with no primary sequence similarity to ERECTA. It is noteworthy that ERECTA, ERL1 and ERL2 belong to the LRR-XIII family with four additional, distantly-related members (Shiu and Bleecker, 2001). The biological functions of these four members are not understood.

The increase in cell size in *erecta* single and *erecta erl* double and triple mutants is likely to be secondary to reduction in cell number. When cell proliferation is decreased, the total mass checkpoint often leads to decreased inhibition of cell growth, resulting in increased cell size (Conlon and Raff, 1999; Day and Lawrence, 2000; Mizukami, 2001; Nijbout, 2003; Potter and Xu, 2001). The expression of *ERECTA, ERL1* and *ERL2* in actively dividing tissues correlates well with their proposed function in cell proliferations. Interestingly, a striking decrease in cortex cell numbers occurs only at the vertical cell files, whereas compensatory cell expansion is much more prominent function in cell proliferations. Interestingly, a striking ERL2 in actively dividing tissues correlates well with their

**References**


