**Gene names**

- SGR5
- RGA2
- GRG1
- RGA1
- GAI
- AXR4
- CTL1

**Phenotypes**

- Stems are 32% taller than that of wild type Ler.
- No increase of germination or restoration of male fertility compared to the single ga1-3
- No bolting.
- Early flowering.
- Reduced pollen levels than wild type Ler and filaments shorter than carpels.
- Reduced, but still significant, number of branched trichomes.
- Partial suppression of the strong sti-EMU phenotype resulting in sta-like trichomes.
- Long carpels than those of the ga1-3 single mutant.

**References**

- [7630933]
- [7264933]
- [7264933]
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- [7264933]
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**Key Terms**

- **SAB**: Partial suppression of the strong sti-EMU phenotype resulting in sta-like trichomes.
- **GRS**: Reduced pollen levels than wild type Ler and filaments shorter than carpels.
- **RGA2**: Partial suppression of the strong sti-EMU phenotype resulting in sta-like trichomes.

**Additional Notes**

- Several mutants show reduced male fertility, which is partially rescued by adding ethylene biosynthesis inhibitors.
- The responsiveness of the mutant to increasing fluence rates of Rc was essentially identical to the wild type.

**Other Mutants**

- AGO1
- GAI
- RGA2
In the homozygous progeny: During early stages of embryogenesis the development of mea-1 embryos is indistinguishable from wild-type siblings in cleared or sectioned specimens. Visible differences between wild-type and mea-1 embryos begin at the late globular stage. Globular mea-1 embryos show excess cell proliferation and enlarge abnormally, eventually becoming severely deviant. Wild-type embryos reach the mid to late heart stage, while mea-1 embryos are still globular and contain small ramified cells with curvilinear cell walls and sometimes irregular cell division planes. In the ground tissue and procambium, fasciplasia and hypophysis are normal, and cotyledons initiate synchronously as in the wild type. Thus, despite increased cell proliferation and occasional irregular cytokinesis, morphogenesis progresses normally. However, each stage is prolonged and delayed relative to the wild-type. Meiotic divisions, as well as meiotic and mitotic chromosome segregation, are delayed in mea-1. Although plant heart stage mea-1 embryos are present along with late torpedo or cotyledon stage wild-type embryos, mea-1 heart-stage embryos have experimentally cell layers. Mea-1 heart-stage embryos are fully differentiated, most mea-1 embryos have reached the late heart stage and remain up to 10 days longer than wild type, most mea-1 embryos degenerate during desiccation. These results suggest that mea controls cell proliferation during embryogenesis, allowing morphogenesis to progress normally, albeit slowly. Endosperm development in mea-1 seeds is indistinguishable from that of the wild-type at early stages. When cellularization begins normally in wild-type seeds the transition from the globular to the heart stage, no cellularization is observed in sibbing mea-1 seeds. Although nuclear divisions take place more slowly than in wild type, the distribution of endosperm nuclei is as in the wild type. Partial cellularization occurs at the apertures where mea-1 embryos reach the late heart stage in desiccating seeds, but fewer nuclei have been generated, mostly of the cotyledons.

In the homozygous progeny: siliques are large with reduced development conditions.

The mutant is defective specifically in the qE component of NPQ. However, it exhibits non-photochemical quenching, demonstrating that violaxanthin de-epoxidation is required for the bulk of rapidly reversible nonphotochemical quenching; altered regulation of photostatic energy conversion is associated with increased sensitivity to desiccation.

In the homozygous progeny, anthocyanin accumulation (purple coloration) in the cotyledons and darkness. The dark germinated seedlings of the mutant did not exhibit slight epinasty of their leaves and flowers, and display reduced apical dominance. Free amino acid levels in fresh tissues of the mutant plants at 30 DAI were similar to those in wild type, whereas the levels of glutamic acid and aspartic acid showed a significant reduction in wild type plants. Glutamic acid was the only amino acid which showed a significant reduction in wild-type plants during desiccation. Endogenous levels of 12 amino acids were at least 2-fold greater in wild-type than in the mutant plants after 30 DAI desiccation. Amino acids that exhibited marked increases were leucine (352-fold), isoleucine (350-fold), proline (99-fold) and valine (150-fold). Aspartic acid was the only amino acid which showed a significant reduction in wild-type plants during desiccation. In desiccated tissues of the mutant, 9 amino acids increased more than 2-fold during desiccation, however the increase in the mutant plants were less pronounced than those in wild-type plants. Glycine and alanine showed greater increases in comparison to wild type, whereas the levels of glutamic acid and aspartic acid showed a reduction in the mutant during desiccation.

The homozygous progeny, dark purple seeds. In the homozygous progeny, dark purple seeds. The homozygous progeny, dark purple seeds. In the homozygous progeny: During early stages of embryogenesis the development of mea-1 embryos is indistinguishable from wild-type siblings in cleared or sectioned specimens. Visible differences between wild-type and mea-1 embryos begin at the late globular stage. Globular mea-1 embryos show excess cell proliferation and enlarge abnormally, eventually becoming severely deviant. Wild-type embryos reach the mid to late heart stage, while mea-1 embryos are still globular and contain small ramified cells with curvilinear cell walls and sometimes irregular cell division planes. In the ground tissue and procambium, fasciplasia and hypophysis are normal, and cotyledons initiate synchronously as in the wild type. Thus, despite increased cell proliferation and occasional irregular cytokinesis, morphogenesis progresses normally. However, each stage is prolonged and delayed relative to the wild-type. Meiotic divisions, as well as meiotic and mitotic chromosome segregation, are delayed in mea-1. Although plant heart stage mea-1 embryos are present along with late torpedo or cotyledon stage wild-type embryos, mea-1 heart-stage embryos have experimentally cell layers. Mea-1 heart-stage embryos are fully differentiated, most mea-1 embryos have reached the late heart stage and remain up to 10 days longer than wild type, most mea-1 embryos degenerate during desiccation. These results suggest that mea controls cell proliferation during embryogenesis, allowing morphogenesis to progress normally, albeit slowly. Endosperm development in mea-1 seeds is indistinguishable from that of the wild-type at early stages. When cellularization begins normally in wild-type seeds the transition from the globular to the heart stage, no cellularization is observed in sibbing mea-1 seeds. Although nuclear divisions take place more slowly than in wild type, the distribution of endosperm nuclei is as in the wild type. Partial cellularization occurs at the apertures where mea-1 embryos reach the late heart stage in desiccating seeds, but fewer nuclei have been generated, mostly of the cotyledons.

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Glucose 3-phosphate level is below detection limits.

Relative decrease the effective quantum yield of PSII (ΦII).

Leaf shape slightly altered: longitudinal length of blade more affected than lateral
asymmetric and lobed rosette leaves, leaf edges curl under irregularly.

Leaves expand more slowly than those of wildtype controls.

Glucose 3-phosphate level is about one-fourth of that of wild type.

Altered vegetative morphology and response to hormones

Postembryonic growth of roots (primary and lateral) severely impaired.

Growth severely affected during reproductive growth phase: onset of flowering varies with
other sequences throughout the genome; also, clear reactivation of subgenomic expression.
cttosupression sequences; exons are a cytosome methyltransferase bonding.

Defective in acquired thermotolerance. Plant growth and development, seed set and
conversion of nearly all of the cells into sepal cells. Sepals replace stamens in the
second whorl.

Definitive in acquired thermotolerance. Plant growth and development, seed set and
conversion of nearly all of the cells into sepal cells. Sepals replace stamens in the
second whorl.

In short days (SD), flowering time is unaffected. rsf1 plants were indistinguishable from
wild-type plants in both FR and blue
Hypocotyl elongation is less inhibited than in wild-type plants in both FR and blue
However, unlike phyA null mutants (phyA-211), they clearly responded to increasing
fluctuations of FR light.

Mutant plants had pale-green cotyledons and leaves.

The homozygous progeny is self-sterile.

Defective in acquired thermotolerance. Plant growth and development, seed set and
conversion of nearly all of the cells into sepal cells. Sepals replace stamens in the
second whorl.

The RNA polymerase promoters in

...glucose and fructose must be less effective in...
Germination of mutant seeds was not affected and visual inspection did not reveal any drastic change in phenotype compared with WT plants, except for a slightly lighter pigmentation.

Germination of adult seeds was not affected and visual inspection did not reveal any drastic change in phenotype compared with WT plants, except for a slightly lighter pigmentation.

The level of the xanthophyll cycle pigments (VAZ-pool) was higher than in WT plants.

The 26S proteasome subunits were absent. Deregulation of AG and AP3 expression in floral meristem and floral organ primordia.

Enhanced flower phenotype compared with both single mutant plants, reduction in floral organ number and enhanced carpeloidy of whorl 1 organs. Whorl 2 organs are completely aborted. Demarcation of A and MP expression in floral meristem and floral organ primordia.

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Reduced SA accumulation in response to pathogens, reduced pathogenesis-related gene expression, and enhanced resistance to pathogens.

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Defective in floral organ identity and organ number; late-arising flowers exhibited more severe phenotypes than early-arising flowers; in the last-arising flowers, the organ number in whorl 2 and 3 is reduced; on average, only 3 organs are found in whorl 2, and 2 organs in whorl 2; 3% of whorl 1 organs develop partial homeotic transformation and assume petal/pedal or petal/calyx monstrosity; whorl 2 organs are often narrow petals, or endospermic petals that are occasionally observed; alternatively, petals can be replaced by filamentous or tubular structures; whorl 3 stamens are typically reduced slightly in size, the whorl 4 gynoecium is often slightly split at the top; sometimes, horn-like structures are seen at the gynoecium apex. Narrow floral organs; narrow leaves; reduced leaf blade (fused shoot); increased lateral branching; reduced number of seeds per silique.

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Under hourly R pulses, the pks mutation also had no effect in the phyA background.

Stomata are far less sensitive to ABA.

Dwarf (growth under long-day photoperiod).

In short day conditions, mutant formed a greater number of cauline leaves.

With respect to cotyledon unfolding and greening, the double mutant was

Decrease root length (54% of that of wildtype) when grown on D-galactose-free medium.

No emission of NO (nitric oxide) under condition in which wild-type does. Wounding-

Narrow leaf lamina phenotype.

Mutant plants contained chlorophyll amounts comparable to those of the wild-type

embryo lethal. Embryos sensitive to ABA have reduced hypocotyl, cotyledons that
remain green late in development; reduced protein and lipid bodies with starch being predominant storage product in mutant embryos. Trichome formation on cotyledon after germination; internal cells of cotyledons enlarge, vaculate and resemble leaf mesophyll cells; intercellular spaces are prominent in cotyledons; enlarged shoot apical meristem; cotyledons are found on surface of cotyledons of mutant embryos; mature seeds are dehiscence-resistant, however, immature seeds can be removed from dehiscent pods by physical means.

In long day conditions, no significant differences in flowering behavior between mutant and wildtype.

In short day conditions, mutant formed fewer rosette leaves before bolting.

Decrease root length (54% of that of wildtype) when grown on D-galactose-free medium.

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Mutants produce less than one petal per flower on average, although most basal flowers

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Blocking of greening was enhanced in the mutant exposed to hourly pulses of FR. No visible difference in leaf morphology and variegation when grown under normal light and temperature conditions compared to wild-type.

The rate of chlorophyll leaching from mutant plants was threefold higher than the rate of wild-type plants.

Reduced-growth phenotype.

In this line the wol-1 allele appears recessive compared to cre1-3.

Root elongation markedly reduced in the presence of kinetin.

No metaxylem and no phloem differentiation.

Cytokinin insensitivity.

Strong cytokinin insensitivity.

Deficient root elongation, dwarf, sterile, rapid senescence in mature leaves.

Mutant leaves were small and irregular in shape compared with the wild type. Both surfaces of mutant leaves differed from the wild type. Adaxial surface of the wild type showed the characteristic zigzag palisade shape of pavement cells. In the mutant, the cells contained fewer, larger holes. Epidermal cells on the abaxial surface of mutants were collapsed. This collapsed appearance was consistent in views of the abaxial leaf surface of mutant plants but was never observed on the adaxial surface of wild-type leaves or on the abaxial surface of either the wild-type or mutant plants.

Mutant roots were closer to flowers than wild-type plants (0.14 versus 0.24 under 0.8× phasephotograph). Plant roots produced smaller buds, but flower morphology and fertility were normal, and siliques were similar in size to those on wild-type plants. The smaller buds of the mutant yielded only 62 mg seed/plant compared with 177 mg seed/plant for wild-type plants. Harvested mutant seedlings appeared smaller and darker than wild-type plants that had been grown alongside the mutants. Examination by light microscopy revealed that 30% of mutant seeds contained green embryo that could be distinguished through the tests. When the green and normal brown seeds from a mutant plant were germinated separately, the green seeds showed 70% germination compared with 100% germination for the brown seeds.

The cotyledon layer on the abaxial surface of mutant leaves was not significantly different in cross-sectional thickness from that of control wild-type leaves. However, the adaxial cotyledon layer on mutant leaves was substantially thinner than the wild-type.

Seed set is greatly reduced in mutant plants, and most siliques either fail to develop or contain few (2–3) seeds.

The phenotype of the mutant in an ABI background is almost indistinguishable from that of wild-type plants when grown in vitro or in soil. When grown in soil, mutant siliques are distinguishable from wild-type siliques after about 3 weeks due to their slightly narrower, darker green leaves.

The roots of wild-type seedlings are as short, both when grown in the light or in darkness. In contrast to the root system, the shoot system morphology and flowering time of wild-type plants resembles the 35S:CHS system, which was used as the control. Cell elongation and cell proliferation rate in the root meristem and elongation zone were decreased in wild-type seedlings, contributing approximately one-third and one-third, respectively, to the total difference in root length as compared with 35S:CHS seedlings.

Wild-type roots.

Develops metaxytome as wild-type plants.

Jaundiced hypocotyl develop small and yellowish callus indicating a strong insensitivity to phototropin, which induce callus and greening around.

Root elongation is indistinguishable from that of wild-type.

Strong cytokinin insensitivity.

Cytokinins insensitivity.

No metaxytome and no phloem differentiation.

Root elongation markedly reduced in the presence of kinetin.

Same phenotype as wild-type.

Root cross-sections are identical to those of wild-type: observed re-appearance of a normal xylem and phloem tissue on each side. Root cross-sections are identical to those of wild-type: observed re-appearance of a normal xylem and phloem tissue on each side. Root elongation markedly reduced in the presence of kinetin. No metaxytome and no phloem differentiation. Root elongation markedly reduced in the presence of kinetin.
Lesion mimic mutant; exhibits light conditional appearance of propagative HR.

When grown in darkness, mutant seedlings exhibited mild photomorphogenic phenotypes, with inflorescences take 7-10 days longer than ap1 cal mutant to begin producing flowers.

The hypocotyl length of the double mutant is slightly decreased; this effect is largely

The leaves of the double mutant expand more slowly than those of wildtype. At 17 days

Strong cytokinin-insensitive phenotype.

The leaves of the triple mutant expand more slowly than those of wildtype. At 17 days

Dependence on ethylene perception.

Partial suppression of the dwarf phenotype.

The rate of leaf primordial formation is slightly decreased for the phylostoch is normal.

The rate of leaf primordial formation is slightly decreased for the phylostoch is normal.

Normal or slightly reduced sensitivity to cytokinin in shoot induction assay (exogenous application of cytokinins induces wildtype shoot formation).
Adaxial surface of first whorl organs are unaffected. Profound changes in early arising flowers. Both organ numbers and organ identity are changed in a highly variable manner.

All flower organs are converted to leaf-like organs, most strikingly on their adaxial surface. Abnormal epidermal cells are made up of a mixture of leaf- and seed-like characteristics. Leaf characteristics include an abundance of branched trichomes.

 cuddleflower-like early after bolting but now start producing cuttlefish-like flowers on their periphery.

Flower meristems behave like inflorescence meristems and continuously elaborate new meristems, resulting in the 'callousflower' phenotype. Eventually flowers resemble those of old single mutants eventually appear and set seeds.

Fresh germination defects in the inflorescence meristem and continually elaborate new meristems, resulting in the 'callousflower' phenotype. Eventually flowers resembling those of old single mutants eventually appear and set seeds.

Early flower mutant phenotypes are observed in later-arising flowers which appear more normal whilst still displaying significant abnormalities of organ development.

Profound changes in early arising flowers. Both organ numbers and organ identity are affected in a highly variable manner.

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Profound changes in early arising flowers. Both organ numbers and organ identity are affected in a highly variable manner.

Completion of flowers in the scale of first-whorl organs.

ARF19

Serrated petals and sepals. Fertility is 40% that of wildtype.

The endogenous levels of ABA are significantly lower than those of the aao3 single mutant.

When seedlings are grown vertically under dark conditions, the mutant has a small and epinastic rosette leaves; reduced auxin sensitivity. nph4-1 arf19 is disrupted. The primary root of the mutant is highly branched, as is the wild type.

Fewer lateral roots after IBA treatment. Not generally defective in auxin responses. Displays peroxisomal defects such as reduced sensitivity to exogenously applied IBA. Reduced numbers of seeds set.

The double mutant exhibits a phenotype stronger than those of the single mutants. Adult double mutant plants have thick and short inflorescence stems, and their leaves are smaller and epinastic. In addition, it has reduced numbers of flowers stems, suggesting enhanced auxin dominance. By contrast, its flowers appear to be normal, and they form normal.
The arp4-1 mutation causes partial sterility. Homozygous mutants had poorly developed siliques with a few or no seeds, compared with heterozygous mutant or wild type siliques that were fully filled with seeds. Flowers on the homozygous sterile plants were often slightly smaller and open for considerably longer periods than wild type, and a majority of over 80% to 90% remained unfertilized. Otherwise, mutant plants remained only very morphologically and developmental phenotypes. The authors from the sterile plants were average smaller, more heart shaped, and contained fewer pollen grains compared with wild type authors, which were somewhat oblong and fully filled with pollen. In addition, the mutant pollen grains were clearly larger than wild type. Because the mutant stamens had shorter filaments than the wild type self-pollination was seldom efficient. However, upon manual pollination, pollen from the homozygous mutant plants germinated on self or wild type stigmas and produced fertile seeds, indicating that the mutant pollen grains, although larger, were viable. When homozygous mutant plant was pollinated with wild type pollen, the cross-pollination resulted in near normal development of siliques and production of seeds suggesting that the female development was not affected by the arp4-1 mutation. Sterility in the homozygous mutant plants is the result of production of fewer pollen and inefficient self-pollination. Mutant plants had a 25 to 60% reduction in the amount of pollen protein compared with wild type.

Plants display decreased sensitivity to the inhibitory effect of radiobiologic acid (RA) on root elongation, while remaining sensitive to inhibition concentrations of single- and polyunsaturated fatty acids. They maintain their ability to initiate lateral roots in response to auxin and cytokinin through a CUL3-dependent repression of the WUSCHEL-RGL1-ESCRT pathway. Moreover, the CUL3-dependent repression of WUSCHEL-RGL1-ESCRT pathway is specifically required for lateral root initiation and for the maintenance of meristem identity in the lateral root initials, thereby facilitating lateral root initiation and maintenance of meristem identity in the lateral root initials. Moreover, the CUL3-dependent repression of WUSCHEL-RGL1-ESCRT pathway is specifically required for lateral root initiation and maintenance of meristem identity in the lateral root initials. Moreover, the CUL3-dependent repression of WUSCHEL-RGL1-ESCRT pathway is specifically required for lateral root initiation and maintenance of meristem identity in the lateral root initials.
temperature-sensitive mutant, seedlings grown at the permissive temperature (22°C) appeared almost normal. At 28°C, both hypotrochis and root explants of the srd2 mutant could not establish shoot apical meristems de novo. When primary root segments of srd2 were cultured in the induction medium (HEB) on 3% agar, abnormal lateral root primordia lacking functional apical meristems were frequently observed, except that they had fewer lateral roots than the wild-type counterparts. At the restrictive temperatures (28°C) however, the development of true leaves and primary roots in srd2 seedlings was severely retarded. Hypothetical root explants of the srd2 mutant formed calli on collagen-coating medium (CCM), at either 22°C or 28°C, callus formation from root hypotrochis explants was severely inhibited at 28°C.

**PMI1**

Semi-sterile, reduced fertility. Progress through prophase I, meiosis I is delayed. Short stamens, reduced fertility. Embryo lethal.

**FTSH1**

More variegated than ftsh2.

**PLL5**

Severely attenuated chloroplast movement, similar phenotype to pmi1-2.

**ISPF**

Reduced growth, 50% of the seeds are aborted at the embryo heart stage, the seed chloroplasts have reduced galactolipids, and reduced 18-bohyl fatty acids, lessen accumulate trigalactolipids/kgigylcercylic, trigalactolipid and trigalactolipids.

**RAN5**

Seed defects include smaller leaves, decreased cell number in leaves, mesophyll and vascular patterning disturbed, organ-shaped cotyledons, few small cells, small cells, columns of cells range from 2 to 4, deformed root cap.

**VND5**

Class III KNOX, during hypocotyl elongation, the shoot meristem is probably slightly delayed and the overall number of dividing cells is reduced. The delay in cell cycle activation is linked to delayed radicle emergence.

**VIS1**

Class II KNOX, reduced fertility, decreased shoot growth, elongation and weight, is reduced.

**VTE1**

Hypersensitive to methyl methanesulfonate (MMS), a DNA alkylating agent. Enhanced resistance to increasing concentrations of MMS as compared to wild type.

**ZYP1a**

No observable phenotype under normal (125 μmol photons/m²/s), high (450 μmol photons/m²/s) or low (15 or 50 μmol photons/m²/s) light.

**ZYP1b**

Mutant plants exhibit more severe autonomously cauliflorous mutations under repressed fluorescence of light. Leaf cross sections revealed that regardless of the light condition, chloroplasts are more evenly distributed in leaf mesophyll cells in mutants than in the wild-type.

**AAA FTSH**

Leaves are rounder and paler than wild-type.

**EMB1738**

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**EMB529**

Hypersensitive to methyl methanesulfonate (MMS), a DNA alkylating agent. Enhanced resistance to increasing concentrations of MMS as compared to wild type.

**EMB142**

Development of true leaves and primary roots in srd2 seedlings was severely retarded. Hypothetical root explants of the srd2 mutant formed calli on collagen-coating medium (CCM), at either 22°C or 28°C, callus formation from root hypotrochis explants was severely inhibited at 28°C.

**EMB2284**

Reduced growth, 50% of the seeds are aborted at the embryo heart stage, the seed chloroplasts have reduced galactolipids, and reduced 18-bohyl fatty acids, lessen accumulate trigalactolipids/kgigylcercylic, trigalactolipid and trigalactolipids.

**EMB70**

Reduced growth, 50% of the seeds are aborted at the embryo heart stage, the seed chloroplasts have reduced galactolipids, and reduced 18-bohyl fatty acids, lessen accumulate trigalactolipids/kgigylcercylic, trigalactolipid and trigalactolipids.

**EMB529**

Hypersensitive to methyl methanesulfonate (MMS), a DNA alkylating agent. Enhanced resistance to increasing concentrations of MMS as compared to wild type.

**EMB142**

Development of true leaves and primary roots in srd2 seedlings was severely retarded. Hypothetical root explants of the srd2 mutant formed calli on collagen-coating medium (CCM), at either 22°C or 28°C, callus formation from root hypotrochis explants was severely inhibited at 28°C.
Aborted vascular system containing few protoxylem cells in the primary root. Normal responding reGulaTor 3 lengthens the period of the clock in all conditions.

In heterozygous plants, 39% of ovules are aborted compared to 6% for wild-type siblings. Similar to the phenotype of parental lines, mini3-1 and iku2-3. Seed size and weight of mini3-1 and iku2-3 are comparable to single mutants lines.

Mutant plants had biosynthetic mutants pollen grains, contrary to trichotomous pollen in the wild type, due to failure to undergo cytokinesis at pollen mitosis. Mutant pollen contained two free nuclei and remained uncellularized. Nuclei in mutant embryos showed various numbers (2 to 5) of nuclei located toward the micropylar pole without visible cellular boundaries. After fertilization, mutant embryos did not develop further and remained uncellularized. At early bicellular pollen stage, approximately 1/3 of dividing microspores had incomplete callose walls, which were correctly positioned at the generative cell pole but did not persist and are degraded before mid-bicellular pollen stage. Subsequently, at mid-bicellular pollen stage, when the generative cell nucleus is highly condensed in wild-type, in approximately 1/3 of mutant pollen, the smaller generative pols nucleus remains round and relatively uncondensed and does not divide further.

Downwards bending of cotyledons indicating differential growth in the adaxial and abaxial sides. Delay in rate of leaf formation. Longer plastochrone. Hypersensitive to exogenous and endogenous ABA during germination due to accumulation of high levels of ABA. The lengths of the main root, hypocotyl and stem of ahg2-1 were highly condensed in wild-type, in approximately 1/3 of mutant pollen, the smaller generative pollen nucleus remains round and relatively uncondensed and does not divide further.

Reduction in primary root length (about 5-fold compared to wildtype). The hypocotyl vascular system only contains xylem cells. Secondary vascular tissue develops in the upper part of the hypocotyl. The hypocotyl vascular system only contains xylem cells. Secondary vascular tissue develops in the upper part of the hypocotyl.
Shorter hypocotyls than wild-type when grown in white light but increase in length when grown in red- and far-red-light. No difference in chlorophyll content compared to wild-type.

Chlorophyll content reduced compared to single mutant ahk3-7.

Almost completely infertile but can be allowed to self-fertilize under favorable conditions.

Three- to tenfold higher cytokinin concentrations required to induce callus formation and shoot development.

Increased cytokinin resistance compared to double mutant ahk2-5 ahk3-7.

Increased copper accumulation in both roots and shoots of mutant when grown on medium containing 10 microM Cu.

Significantly impaired in NO biosynthesis in response to exogenous H2O2 compared to wild-type.

Reduced length and width of leaves but overall form and heteroblasty is not altered.

Increased susceptibility to T-DNA transformation.

Significantly impaired in NO biosynthesis in response to exogenous H2O2 compared to wild-type.

Reduced ability to respond to cytokinin by callus or shoot formation.

Significantly impaired in NO biosynthesis in response to exogenous H2O2 compared to wild-type.

Increased number of vascular cell files with intervening procambial and phloem cell files; protoxylem differentiation occurred sporadically along the root.

Stomatal aperture not affected by treatment with sodium nitroprusside (SNP).

Increased cytokinin resistance compared to wild-type.

Reduced response to ABA for induction of nitric acid (NO) production in the guard cells of this mutant (HMA5).

Increased response of shoots to cytokinin as compared to wild-type. No alteration of rate of leaf formation.

Increased number of vascular cell files with intervening procambial and phloem cell files; protoxylem differentiation occurred sporadically along the root.
No visible phenotypes were observed during vegetative stages. When grown on medium supplemented with 2,4-D, root development was more rapid than in the wild type or single mutants.

Mutants were grown on MS medium supplemented with 2,4-D, IAA, and sirtinol, and roots were stained with trypan blue. In the homozygous mutant progeny, embryo development was arrested at the early globular stage. Although the normal embryos continued to develop, the arrested embryos exhibited increased nuclear division and abnormal cell structure. Furthermore, asynchronous divisions of the embryo were observed in the homozygous mutant as compared with the wild type. The number of filaments and/or staminoid organs in the double mutant as compared with the wild type was increased.

In addition to the arrested embryo phenotype, aberrant cell divisions were also observed. These resulted in the formation of an elongated epidermal cell or stamen prope rather than the typical glandular epidermis in wild-type plants. A notable phenotype of the ufo-11 mutant was that 70% of the mutant embryos displayed aberrant positioning of the division planes and asymmetric divisions. Furthermore, asymmetric divisions of the embryo prope and meristem cells were observed.

The number of filaments and/or staminoid organs in the double mutant was increased. The petals are usually missing in ufo-11 flowers or are sometimes replaced by filaments or staminoid organs. Ufo-11 flowers have fewer anther trichomes and the third, and also produce monoecious plants and plants are isolated.

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SEX1 contains about 18% of wild-type phylloquinone content but 50-70% of wild-type PSI

LPA1

No increase in H2O2 content in light- or dark-adapted mutant plants. 

GI

The mutants have defects in energy transfer within PSII or a partial loss of PSII.
Significantly delayed leaf senescence.

Compared to wildtype, mutant cells gradually lose their ability to form calluses as they grow in dark for 3 weeks on soil. wak2-1 plants have lost hyponasty extension than wild-type, earlyly affects the rate of cell elongation in root, than the wild-type.

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Starch granules are slightly larger than those of wild type.

Significant reduction in cellulose.

Strong reduction in maltose accumulation compared to the be2-1 be3-2 double mutant.

Water-soluble glycans are composed of very short malto-oligosaccharides made of 80% smaller than wild type and develop fasciation.

The mutant siliques contained a percentage of shriveled seed remnants, which manifested as gaps in the developing line of green seeds.

Seed germination in the dark after far red light treatment was almost completely suppressed as in the case of wild type.

Increased starch phosphorylase activity compared to wild type.

Reduced stature, early flowering, and altered leaf morphology.

Mutant showed a similar sensitivity to 25 mM trehalose as wild type (inhibition of root elongation).
IPT1
Increased levels of auxin-binding protein (ABP) and auxin-binding protein (ABP) compared to wild type.

IPT1
Increased levels of cytokinin riboside (cZR) and cytokinin riboside methosulfate (cZRMP) compared to wild type.

IPT1
Double mutant roots were dramatically reduced compared with the wild-type roots. The aerial part normally in the double mutant plantsehomogeneously reduced to less than 20% of those of wild type.

IPT1
Slight increase in delay in flowering under LD conditions compared to soc1-2 single mutant.

IPT1
Increased delay in flowering time compared to both parental single mutants.

IPT1
Increased delay in flowering time compared to wild type; in the latter, the rapid rise to MRE was followed by a slower phase, whereas in the mutant, the slower phase was almost completely absent. The reduction in fP in the CTR; CTR mutant plants was observed at all light intensities, with a maximum reduction of ~60% in the mutant.

IPT1
Increased levels of cis-zeatin riboside (cZR) and cis-zeatin riboside monophosphate (cZRMP) compared to wild type.

IPT1
Some seeds are aborted but surviving ones are larger than those of wild type.

IPT1
Increased delay in flowering time compared to both parental single mutants.

IPT1
Increased levels of GRF, GRF, GRF, GRF, and GRF, compared to wild type, low in the mutants.

IPT6
suppressor of FRIGIDA4
Increased delay in flowering time compared to both parental single mutants.

IPT6
Reduced plant growth under sulfate starvation condition. Reduced sulfate uptake.

IPT6
Slight reduction (~30%) of glucose and fructose contents in leaves, whereas sucrose content is similar to that of wild type under normal growth conditions.

IPT6
Reduced levels of CTR1, CTR1, CTR1, CTR1, and CTR1, compared to wild type.

IPT6
Reduced stem growth under sulfate starvation condition. Reduced sulfate uptake.

IPT6
Slight increase in delay in flowering under LD conditions compared to co-1 single mutant.

IPT6
Some seeds are aborted but surviving ones are larger than those of wild type.

IPT6
Reduced stem growth under sulfate starvation condition. Reduced sulfate uptake.

IPT6
Reduced levels of CTR1, CTR1, CTR1, CTR1, and CTR1, compared to wild type.

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Reduced stem growth under sulfate starvation condition. Reduced sulfate uptake.

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Reduced levels of CTR1, CTR1, CTR1, CTR1, and CTR1, compared to wild type.
Exposure of seedlings to 50 μM Cd2+ for 2 days does not induce phytochelatin.

When grown in soil or hydroponically, the double mutant line was not obviously different from the wild type.

Retarded root growth, variegated and distorted leaves, distorted flowers, partial sterility of the double mutant,

Viscera, roots and shoots were lighter green than WT plants throughout the life cycle.

When grown on soil, the mutant showed less than 5% plants which germinated, compared to the equivalent wild type.

DNA methylation profile of the centromere. Centromere repeats in interphase nuclei are decondensed relative to those in metaphase. No centromere repeat hypomethylation phenotype.

Significant increase in the content of the aliphatic amino acid Val.

Susceptibility to the virulent powdery mildew *Golovinomyces orontii* remains.

Significant increase in the expression of the GFP-CAO transgene.

Partial suppression of the gid1a-1 gid1b-1 gid1c-1 triple mutant phenotype.

Under normal growth temperature conditions, the double mutant leaves' content in glucose and fructose is slightly reduced (~30%) in a similar fashion to that observed with the single mutant lines.

Whereas, as plants matured, WT rosette leaves curled down, mutant leaves remained flat.

Biosynthesis.

Both the size and number of the epidermal cells were found to be decreased in the mutant.

In darkness, the mutant is resistant to cytokinins (only small decrease in hypocotyl growth). The amount of hypocotyl were not significantly different from those of the equivalent wild-type.

Double mutants were indistinguishable from hbp1 single mutants.

Susceptibility to the virulent *Golovinomyces orontii*.

Intact root growth, undamaged and distorted leaves, distorted flowers, partial sterility of the double mutant.

Phenotype of the double mutant was not obviously different from wild type.

Despite the increase in hypocotyl cell length, the root meristem ceased to elongate.

The mutant had shorter, more slender inflorescence stems with fewer auxiliary branches and side branches. Mutant produced fewer flowers than WT and had fewer and shorter siliques, flower size per siliqua and a higher percentage of sterile siliques, resulting in lower seed production. More than half of the mutant flowers were sterile, and although they were smaller than WT flowers, they opened normally and had normal arrangements and numbers of floral organs. Some sterile flowers were open, while others remained closed. The reason for sterility is the failure of the stamens to emerge from the fruit as a result of cold or heat at several stages during floral development. In WT plants, stamens were longer than the pistil and bracketed against the stigma to allow pollination and fertilization.

The amounts of glucose, fructose, sucrose, cellulose (roots) and starch in the mutant were not statistically significantly different from those of the equivalent wild-type.

In contrast to wild type, blue light does not inhibit hypocotyl elongation in the double mutant.

The amounts of glucose, fructose, sucrose, cellulose (roots) and starch in the mutant were not statistically significantly different from those of the equivalent wild-type.

Significant increase in the content of the aliphatic amino acid Val.
During the first two to three DAG, the double homozygous mutant progeny displayed the histone mono-ubiquitination 2.

In the absence of ABA treatment, root elongation of ggt1-1 was reduced nearly 50%.

At the reproductive stage, the mutants exhibit severe developmental defects that result in dwarf stature and the loss of apical dominance (52 DAG).

In double homozygous progeny, anthocyanin accumulation (purple coloration) in the cotyledons was observed. The double mutant progeny display the typical phenotypes observed in the homozygous mutants.

In double homozygous progeny, significant reduction of CSN1, CSN6, CSN7, and CSN8 and in the cellular pools of the COP9 signalosome complex subunits: CSN3, CSN5, CSN6, CSN7, and CSN8, are observed. Expression of this phenotype is associated with high arsenic tolerance.

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Mutation is lethal in the homozygous state.

Same phenotype as ggt1-1.

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Light green cotyledons.

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Light green cotyledons.

Light green cotyledons.

Light green cotyledons.

Light green cotyledons.
The defect exhibited by the double mutant in ABA-induced stomatal closure was similar to the wild-type. In contrast to wild-type plants, the mutant seedlings did not develop fully differentiated chloroplasts.

The cauline leaves in the mutant plants started senescence at 28 DAG, at least 10 days earlier than those in the wild-type plants. Further, the developing mutant siliques were always fused due to lack of early STM activity. In the remaining 21 double mutant 23010 double mutant seedlings, leaves initiated from the base of the cotyledons, which were always fused due to lack of early STM activity. In the remaining 21 double mutant 23010 double mutant seedlings, leaves initiated from the base of the cotyledons, which were always fused due to lack of early STM activity.

About 51% of stm-5 trn2-23010 double mutant seedlings produced leaves by 8 days after germination and all double mutant progeny developed leaves by day 28. In 19 start trn2-23010 double mutant seedlings, leaves initiated from the base of the cotyledons, which were always fused due to lack of early STM activity. In the remaining 21 double mutant progeny single leaves or side shoots arose laterally, from the outside of the fused base of the cotyledons instead of being initiated from the shoot apex and thus resembled start-1 mutant side shoots which are initiated after a long delay.

The shoot apex and the very young emerging leaves of homozygous mutant grown in the absence of 33 mM nitrate were pale green and their leaves turned chlorotic while growing. After 6 weeks on sucrose-containing agar, surviving mutant plants were able to produce an inflorescence again; the young sepals of the flower were pale green and became white subsequently.

In the mutant's homozygous progeny, mature rosette leaves were retarded in growth. The cauline leaves of mutants showed a significantly higher rate of senescence than WT leaves in the presence of arsenate.

In the mutant's homozygous progeny, mature rosette leaves were retarded in growth. The cauline leaves of mutants showed a significantly higher rate of senescence than WT leaves in the presence of arsenate.

The occurrence (at 24 DAG) and progression (at 28 DAG) of senescence in mutant rosette leaves were not accompanied by a significant reduction in the amounts of nitrogen-containing compounds. Nitrate reductase activity was always lower in mutants compared to the wild-type plants, do not contain fully differentiated chloroplasts. The mutant's lack of developed chloroplasts."
A number of ester-bound monomers were reduced in the mutant. The double mutant suppresses leaf variegation due to var2 loss of function. First leaves are sterile. Defects in embryonic cell patterning in essentially all double mutants. Pleiotropic defects include reduced stature, reduced apical dominance, and reduced reproductive output. No embryo development defects. The root-meristem size of the double mutant was indistinguishable from that of the ahk3 mutant.

Increased cuticle permeability compared with WT. Increased abundance of miRNA precursors. The mutant showed severe damage at a lower concentration of BASTA compared with WT Col-0.

The distinct osmium-dense cuticular membrane representing insoluble lipid-derived extracellular matrix sometimes had a distinct laminated structure. The remaining outer epidermal cells usually had normal shape and size, and salt stress was tested. Salt treatment stimulated the activity of the enzyme in the mutant leaves. The amount was reduced to 15-20% of WT amount. The total amount of omega-hydroxylated fatty acids and their derivatives was reduced 4-5-fold in the mutant compared with Col-0. The impact of mutation on the amount of dicarboxylic acids, characteristic of Arabidopsis cutin, was particularly strong, and the accumulation of these increased more than 5-fold in the mutant compared with Col-0. The impact of mutation on the amount of dicarboxylic acids, characteristic of Arabidopsis cutin, was particularly strong, and the accumulation of these increased more than 5-fold in the mutant compared with Col-0.

Mutant plants were indistinguishable from WT, except for a delay in time to flowering, a delay of about 10 days in the number of flowers and the total leaf number at flowering. On average, the mutant plants flower 10 days and 64 days later than WT plants under long and short day growth conditions, respectively. Mutant plants resembled with 64 days flowering earlier that the wild-type plants. The mutant plants resembled with 64 days flowering earlier that the null-suppressor plants. Thirty percent was removed for 2,6-DNT at the same rate as wild-type plants whereas 30% was removed by the plants after 1 d. Necrotic leaf lesions in short day conditions at low light. Light-induced accumulation of H(2)O(2) and constitutive expression of genes for copper/zinc superoxide dismutase 2 and ascorbate peroxidase 1.

Defective cotyledon development phenotypes at incomplete penetrance, including meiosporogenous seedlings, seedlings with partially fused cotyledons, tricots or various type fusion combinations. The inappropriate cotyledon development leads to developmental defects including reduced stature, reduced apical dominance, and reduced reproductive output. Defective cotyledon development phenotypes at incomplete penetrance, including meiosporogenous seedlings, seedlings with partially fused cotyledons, tricots or various type fusion combinations. Defective cotyledon development phenotypes at incomplete penetrance, including meiosporogenous seedlings, seedlings with partially fused cotyledons, tricots or various type fusion combinations. Defective cotyledon development phenotypes at incomplete penetrance, including meiosporogenous seedlings, seedlings with partially fused cotyledons, tricots or various type fusion combinations.

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The homozygous progeny does not form flower buds. Short, darkgrown hypocotyls, reduced cell adhesion and a dwarfed mature plant. 50% of the double mutant germinated much better in response to increasing red light fluences. At a red light fluence of 60 μmol.m⁻².s⁻¹, the double mutant germinated 17%, whereas the wildtype and the single mutants germinated only 7%. At a higher red light fluence (300 μmol.m⁻².s⁻¹), all seeds germinated.

The double mutant germinated much better in response to increasing red light fluences. At 0 μmol.m⁻².s⁻¹ red light fluence, the double mutant germinated 15%, whereas the wildtype and the single mutants did not germinate under this light condition. At 5 μmol.m⁻².s⁻¹, the double mutant germinated 60%, whereas the wild type and the two single mutants germinated only 7%. At a higher red light fluence (80 μmol.m⁻².s⁻¹), all seeds germinated.

Long primary root when grown on low Pi. Reduced root growth at pH 4.7. Hypersensitive to proton (H⁺) and aluminum (Al₃⁺) cations, both the uptake at long times and the accumulation of K⁺ were directly correlated with Pi stress. Whereas the initial rate of uptake (less than 20 min) was not significantly affected by Pi stress, the uptake at longer times was dramatically reduced. The uptake of both Pi species was higher in the mutant than in wild-type. More lanceolate cauline leaves. Less fertile. Under short day conditions, plants stopped growing. Once they were transferred to the long day conditions (after being grown in constant light until they reached the rosette leaf stage and were ready to bolt), the mutant grew similarly to wild type except that their growth was slightly reduced. After flowering, plants developed a flower stalk (or inflorescence) including cotyledon expansion, development of vascular networks, root elongation, and shoot development. The greenhouse-grown mutant was slightly dwarfed. Following *Pythium irregulare* infection, the increase in JA levels was comparable to the ein2-5 single mutant. There is no noticeable effect on hypocotyl length compared to wild-type.

Vegetative growth of the mutant appears to be comparable with wild-type. More lanceolate cauline leaves. Accumulated less chlorophyll than wild-type. Smaller and more compact rosettes than wild-type. Fewer but enlarged plastids. Contain short FtsZ filaments within a single oversized plastid. Reduced root growth at pH 4.7. Hypersensitive to proton (H⁺) and aluminum (Al₃⁺) cations, both the uptake at long times and the accumulation of K⁺ were directly correlated with Pi stress. Whereas the initial rate of uptake (less than 20 min) was not significantly affected by Pi stress, the uptake at longer times was dramatically reduced. The uptake of both Pi species was higher in the mutant than in wild-type. More lanceolate cauline leaves. Less fertile. Under short day conditions, plants stopped growing. Once they were transferred to the long day conditions (after being grown in constant light until they reached the rosette leaf stage and were ready to bolt), the mutant grew similarly to wild type except that their growth was slightly reduced. After flowering, plants developed a flower stalk (or inflorescence) including cotyledon expansion, development of vascular networks, root elongation, and shoot development. The greenhouse-grown mutant was slightly dwarfed. Following *Pythium irregulare* infection, the increase in JA levels was comparable to the ein2-5 single mutant. There is no noticeable effect on hypocotyl length compared to wild-type.

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ARABIDOPSIS THALIANA KN 1 ATK1
1

The mutants failed to elongate their telomeres, and exhibited a heterogeneous profile of telomere lengths in wild-type siblings. Telomeres in the double mutants shortened at the same rate as in either single mutant.

Homozygous embryos grown on MS medium at 25°C for 7 days. Homozygous seedlings grown on MS medium at 25°C for 7 days.

Homozygous embryos observed frequently showed hypoplastic and smaller cotyledons. However, the general organization of the tissues in the embryonic axis, such as procambial strands, ground tissue, and pericarp, was indistinguishable from that of wild-type embryos described in the literature.

Homozygous mutant seedlings were reduced in size compared with wild-type embryos, and their cotyledons were smaller, with irregular borders, pointed tips, and more veins.

Homozygous embryos matured into normal-looking seedlings. In the late stages of development, morphological changes start to occur only after the first stage.

Homozygous mutant seedlings were reduced in size compared with wild-type embryos during the later stages of development. Morphological changes start to occur only after the first stage.

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Double homozygous mutant seedlings are completely deficient in RUB-modified CUL1.

The first meiotic division of pollen mother cells because the homologs neither pair nor sporulate. The mutants failed to elongate their telomeres, and exhibited a heterogeneous profile of CROWD NUCLEI 2 CRWN2 LITTLE KAKU2 LINC1 ASYNAPTIC 1; ATASY1; F1N21.19 anaphase-promoTinG complex 13 APC13. The chromosome fragmentation phenotype of the asy1/ Atrad51 double mutant is delayed leaf senescence, slightly shorter petioles, round and enlarged leaves, an increased number of inflorescences, a late flowering phenotype and increased biomass. Reduced RUB modification of CUL1.

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ARABIDOPSIS THALIANA  KN 1  ATK1  AGL23  AT1G05207

SIS8  18310462  1
4  ATXIB  MYOSIN XI B  myosin XI B  MYOSIN
pny phenotype

Resembles seu-1 single mutant with reduced stamen number.

Similar to knat6;bp;pny except that it shows greater suppression on bp pny silique retarded growth, reduced NPQ amplitude, limited electron transport rate

Increased number of lateral roots. Reduced acropetal auxin transport.

arrest in embryo sac development; albino due to absence of chloroplast

Increased tolerance of salt stress. Seedlings germinate in the presence of high

Dwarf phenotype, early flowers are sterile while late flowers are fertile. Reduced

NAD-ME1  Similar to knat6;bp;pny except that it shows greater suppression on bp pny silique

SEU  18310462  1
retarded growth, reduced NPQ amplitude, limited electron transport rate

KNAT6  18390591  1
MYA1  LURP1  ALAAT2

Increased number of lateral roots. Reduced acropetal auxin transport.

arrest in embryo sac development; albino due to absence of chloroplast

Increased tolerance of salt stress. Seedlings germinate in the presence of high

Neurons of XI-8  XI-8  XI-B

compromised in RPP4-mediated resistance. Mutants allow increased growth of

Arabidopsis ER-TYPE CA2+-transporting PPM1  T8F5_14

a higher propensity to develop a single cotyledon than wild-type embryos. Hypocotyl, and they lack discernible vasculature in their cotyledons. These mutants have

These triple mutants do not make a primary root, they have an extremely reduced hypocotyl. These mutants have

These mutants have shorter hypocotyls than wild-type plants when grown in low R:FR ratio light. They mutants have 60% of the free auxin

These mutants have shorter hypocotyls, shorter petioles, and more leaf area than wild-

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The root of this mutant show almost no sensitivity to the ethylene precursor ACC, but sensitivity is largely restored by the addition of the levels of IAA that do not (tryptophan). ACC-ripened dark-green apical hook formation is also compromised in this mutant. Root cell shape of the mutant is altered, and it is not corrected by the addition of IAA. Root growth is also severely impaired in this double mutant than in either single mutant. The plant mutants are shorter than wild type, have reduced venation in their leaves, exhibit reduced apical hook formation, and produce abnormal flowers. BOX1-EXPRESSION is also diminished in these double mutants, consistent with a 30% reduction in levels in these mutants. Most meristematic cells differentiate in this mutant, leading to a loss of the stem cell niche and the cessation of root growth. This mutant also lacks root rhizobia in the genotypes.

The hypocotyl of this mutant responds normally to ACC when grown in the dark, but its roots are moderately less sensitive to ACC than wild type roots under the same conditions. This difference in sensitivity can be eliminated when the mutants are treated with ACC and low levels of IAA, indicating that both hypocotyl and root tips respond similarly to IAA in the absence of ACC. The removal of hypocotyl and root elongation mutants was studied in experiments with the acetate-acetaldehyde mixture.

Although ectopic overexpression of HDG11 causes increased drought tolerance, the HDG11-2 double mutant has altered gene expression levels and dehydration tolerance. In double mutants, there are no obvious morphological defects related to leaf, root, flower, stem, and siliques development. Notably, cotyledons are narrow and sericidal. In examination of development, hair cell layers formed in the mutant, and the cessation of root growth. This mutant also lacks valves in the gynoecia. Mutant plants show constitutively higher levels of Pro. Superoxide dismutase activity is also higher in seedlings. Mutant seedlings accumulate higher levels of ABA following PEG treatment, and mutant seedlings are not able to activate Pro-resistant mutants under stress conditions. This difference in sensitivity can be eliminated when the mutants are treated with ACC and low levels of IAA, indicating that both hypocotyl and root tips respond similarly to IAA in the absence of ACC. The removal of hypocotyl and root elongation mutants was studied in experiments with the acetate-acetaldehyde mixture.

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Reduced transmission through pollen. Pollen grains are viable, but pollen germination is impaired.

Increased sensitivity to salt stress. Increased leaf chlorosis in response to Pseudomonas syringae pv tomato DC3000 inoculation. Dwarf plants with reduced vigor, dies before expansion of the true leaves, and appears disorganized. Primordia are irregular and lateral organs produced include tubular and finger-like structures. Also affects the development of roots. Primary root growth is inhibited. The root apical meristems are enlarged and lack distinct columella cells on starch grana.

Homozygotes are susceptible to infection by E. coli and act invasion of A. brassicicola in the periphery. Histones and chloroplast proteins are lost in leaves of seedlings treated with 0.1% NPA.

Increased resistance to Pseudomonas syringae pv tomato DC3000 colonization. This putative papain-like cysteine protease is highly expressed in the flowers of ecotype Landsberg erecta (Ler) plants. FLC expression is repressed. There are gene-specific changes in the patterns of histone modification and nucleosome positioning in this mutant.

In both conditions, the chloroplast size and number per cell in the drp5A mutants is decreased. The flowering of ubc1/2 double mutants is accelerated compared to wild type plants under long days and short days. Histone2B ubiquitination is lost in drp5A mutants and FLC expression is repressed. There are gene-specific changes in the patterns of histone modification and nucleosome positioning in this mutant.

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Under conditions of low boron, nilp6-1 mutants have smaller, darker green, and more irregularly shaped young rosette leaves than wild type plants. These leaves have smaller cells and lack intercellular air spaces. Lower boron levels accumulate in these young rosette leaves to come in about 2 weeks after germination when these young rosette leaves are grown under nilp6-1 conditions, but, wild type levels of boron accumulate when these plants are grown with sufficient boron. These low boron conditions, there are no significant differences in boron levels between wild type and mutant plants in mature leaves. In addition, under normal boron conditions, the leaves of nilp6-1 mutants grow normally and accumulate wild type levels of boron.

21560780

19037657

Abnormal leaf venation. Reduced number of leaf veins.

2

RPA1A

2

FEZ

ARABIDOPSIS THALIANA RING 1B

1

Reduced levels of cytokinin inducible gene expression, specifically AAR5-7. Lower biomass than WT. Delayed bolting. Reduced copper accumulation.

3

GLIP2

2

19153602

2

19135368

BT3

2

2

19043666

19054356

0

RPA1A

19000166

Delayed growth during later stages of development.

3

GTG1

0

AGC1.7

0

GTG1

1

plasTocyanin 1

CIB5

1

has increased number of lateral roots, hypocotyls have impaired gravitropic curvature.

2

SKIP33

4

0

PETE1

1

RPA1A

19000166

Embryo lethal - not recovered.

19054356

3

2

DRT112

3

gtg1-1 mutant plants do not show any obvious phenotypic abnormalities and are indistinguishable from wild-type plants.

2

XIB

19054356

19048287

19000166

XI-1

1

IBR5

0

ORE12

1

BREVIS RADIX NIP3;1 NLM9

2

19064932

0

19084994

19135895

3

prefoldin 6

PFD6

4

Reduced cambial activity and reduced secondary growth in both shoots and roots.

5

ATXIB MYOSIN XI B myosin XI B MYOSIN

0

0

0

0

0

AT2G06510

AT1G53940

AT1G79250

AT1G64990

AT1G03770

AT1G20340

AT1G76100

AT1G26870

AT1G48050

AT1G07128

AT1G04160

AT1G17580

AT1G05690

AT1G31880

AT2G04550

AT1G14000

AT1G07530

AT1G80760

AT1G48520

AT1G21270

AT1G78820

AT1G35470

AT1G21610

AT1G24720

AT1G20360

AT1G76500

AT2G03180

AT1G01440

AT1G08240

AT1G60450

AT1G34290

AT1G61400

AT2G04280

AT1G25850

AT1G54610

AT2G11620

AT1G03850

AT1G58770

AT1G70800

AT1G45870

AT1G12970

AT1G45630

AT1G51540

AT1G43280

AT2G14610

AT2G08870

AT1G64750

AT1G63800

AT2G06640

AT2G02300

AT2G11830

AT2G01790

AT1G01790

AT1G13040

AT1G07000

AT1G65500

AT1G15320

AT1G40850

AT1G44600

AT1G44270

AT1G44550

AT2G18040

AT1G35290

AT1G74640

AT2G03590

AT1G36670

AT2G14105

AT1G27330

AT1G67220

AT1G76630

AT1G05950

AT1G05450

AT1G26140

AT1G37800

AT2G03360

AT2G07860

AT2G06980

AT2G11130

AT1G07510

AT1G07520

AT1G51100

AT1G50460

AT1G64270

AT1G54430

AT1G18700

AT1G52470

AT1G32810

AT1G29870

AT2G05680

AT1G52310

AT1G67150

AT1G53400

AT1G63610

AT1G74470

AT1G73420

AT1G53280

AT1G59120

AT1G60660

AT1G18920

AT2G09740

AT2G12930

AT2G08690

AT2G11710

AT1G65390

AT1G06640

AT1G54310

AT1G31920

AT1G63430

AT1G01540

AT1G46480

AT1G33450

AT1G77570

AT1G31340

AT1G64910

AT1G21380

AT1G73130

AT1G34760

AT2G12850

AT1G54240

AT1G32790

AT1G65380

AT1G05770

AT1G73310

AT1G63590

AT1G57760

AT1G21650

AT1G67550

AT1G65620

AT1G67010

AT1G68410

AT2G11550

AT1G05940

AT1G53080

AT1G67660

AT1G41360

AT1G67380

AT1G51050

AT1G58780

AT2G08710
The rpa1a mutant has normal vegetative growth, but lower levels of fertility. Siliques are shorter in rpa1a mutants than in wild type plants, and their mean seed set per silique is reduced by ~50%. Pollen viability is also reduced in the mutants. Mutations in pollen mother cells proceed normally from early prophase I to the pachytene stage where synapsis is observed, in the mutants. However, a reduced number of chiasmata are detected in the mutants during chromosome condensation at meiosis I and therefore, aneuploid tetrads are observed following meiosis II. There is no evidence of chromosome fragmentation in these mutants, suggesting that PRL1 is not required for the repair of double strand breaks during meiosis. There are no major defects in anther formation or meiotic complex formation in these mutants, nor are the number of MMR and MLH1 foci, suggesting that more recombination intermediates are repaired as non-cross-overs.

When exposed to MMS, mutants grew consistently more vigorously than wild-type. Reduced fertility. Increased root length (longer roots). Hypersensitive to salt stress. Fewer chiasmata formed per cell.

The aco mutant appears to have only ~85% of the ethylene of wild type plants.

Reduced seed set. Pollen tubes are delayed in germination/growth.

The paq1 mutant enhances the SAM phenotype. 50% of double mutants show slight after-growth and production of the first two sets of leaves. Shoots regenerate at a 1:1 frequency.

The lacs1-1 lacs2-3 double mutants had a synergistic phenotype, compared to either of the single mutants, with drastically reduced stem wax and cutin contents, increased cuticle permeability, and severe male sterile in low humidity.

The tpst-1 has an abnormally shaped root apical meristem due to disorganized cell division and early boundary formation
Columella root cap cells fail to detach.

Same as smb-3 single mutant

Related to AP2

20197506

20460499

Homozygote has a WT phenotype, even under conditions of Mg\(+\) stress.

Nonphotochemical quenching measurements were lower than either of the single mutants.

WT phenotype

20087601

TMM

4

20215588

20473553

Mutants have reduced seed 18:1 delta nine fatty acids. An analogous change in fatty acids is seen in the leaf, but it is more subtle than in seed.

Increased sensitivity to drought stress.

20197506

PNSL2

20197506

BRN1

Wider lamina in the third cauline leaf than the respective single mutants.

Delayed growth, short roots, multiply branched root hairs. Radially expanded root and meristem in the triple mutant, giving it a messy appearance. Remains of complete LRC layers, and the appearance of the cells in those layers closely resembles that in smb-3. However, partial remains of older LRC layers remain attached to the meristem in the triple mutant, giving it a mossy appearance. Remains of old LRC cup layers can be found still attached to the root along its whole length.

Increased sensitivity to drought stress.

20197506

PNSL2

20197506

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Wider lamina in the third cauline leaf than the respective single mutants.

Decreased organ size and fertility.

20197506

TAM

20551347

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Increased sensitivity to drought stress.
Short-root phenotype, characterized by short primary root and more branched root system.  

Endoplasmic reticulum (ER)-associated degradation process is blocked in hrd1a hrd1b emb2004 AThrd1B homolog of yeasT Hrd1 mutants exhibit hypersensitive growth response to UV-B irradiation. Reduced microspore formation is defective; microtubule arrays displayed abnormalities during the meiosis-associated process of microspore formation.

Vegetative and reproductive growth are greatly reduced with respect to wild type. Pale cotyledon leaf phenotype. Double mutants are self-sterile, producing non-viable pollen grains.

Treatment with low concentrations of ABA reduces ROS levels in both whole leaves (10 μM ABA application) and in guard cells (5 μM ABA application). Low concentrations ABA does not reduce ROS levels in both whole leaves and in guard cells. Treatment with ABA increases ROS levels in both whole leaves and in guard cells. Drought stress in comparison with wild-type plants. The ROS levels increase in the mutant in comparison with wild-type plants in both the whole leaves and in guard cells. Treatment with low concentrations of ABA reduces ROS levels in both whole leaves (10 μM ABA application) and in guard cells (5 μM ABA application) in the mutant plants.

The mutant shows ABA insensitivity in stomatal movement, including promotion of stomatal closure and inhibition of stomatal opening. The detached leaves of the mutant lose more water than those of wild-type plants under dehydration condition, both young seedlings and mature plants of the mutant have lower capacity to conserve water during drought stress in comparison with wild-type plants. The ROS levels increase in the double mutants in comparison with wild-type plants in both the whole leaves and in guard cells. Treatment with low concentrations of ABA reduces ROS levels in both whole leaves and in guard cells. Low concentrations ABA reduces ROS levels in both whole leaves (10 μM ABA application) and in guard cells (5 μM ABA application) in the mutant plants.

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WOL

Reduced sensitivity to cytokinin in root growth assay (exogenous application of cytokinin inhibits wildtype root elongation).

Occasionally produce inflorescences stems with abnormal and non-functional flowers which did not produce seeds.

Shoot and root growth is very slow and leaf number is decreased compared to wildtype.

Reduced cytokinin-induced inhibition of adventitious root formation compared to wildtype.

No significant response in the cytokinin-induced assay for stimulation of cell division and greening of hypocotyl-derived calli.

Shoot and root growth is very slow and leaf number is decreased compared to wildtype.

This mutant has delayed flowering compared to wild type plants when grown under long day conditions.

Reduced cytokinin-induced inhibition of adventitious root formation compared to wildtype.

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Reduced sensitivity to cytokinin in root growth assay (exogenous application of cytokinin inhibits wildtype root elongation).

No inhibition of stimulation of cell division and greening of hypocotyl-derived calli.

Enhancement of the inhibition of cytokinin-induced stimulation of cell division and greening of hypocotyl-derived calli compared to the responded observed with CRE1 single mutants (e.g. cre1-10).

No cytokinin-induced inhibition of adventitious root formation.

Reduced sensitivity to cytokinin in root growth assay (exogenous application of cytokinin inhibits wildtype root elongation).

This mutant has delayed flowering compared to wild type plants when grown under long day conditions.

Shoot and root growth is very slow and leaf number is decreased compared to wildtype.

Reduced cytokinin-induced inhibition of adventitious root formation.
| Gene names | phenotype                                                                 | pubmed id |
|------------|---------------------------------------------------------------------------|-----------|
| pom2       | This flower had reduced filament elongation as well as thickening of the style | 7743935   |
| pom2       | low fertility                                                               | 7743935   |
| CORE       | shoot cell expansion                                                        | 7743935   |
| CORE       | severe defects in cell elongation, root growth (as defined by length increase) was severely reduced | 7743935   |
| KNAT1      | overexpression of genes active in the shoot apical meristem can lead to abnormal leaf development | 9427751   |
| AGO1       | fewer flower                                                                | 9427751   |
| ACL        | defective in general cell expansion and may also be affected in basic processes of cell wall biosynthesis | 9427751   |
| MEA        | regulating gene expression through modulation of higher-order chromatin structure | 9545225   |
| ABA1       | abscisic acid–deficient                                                     | 9668132   |
| NPQ1       | synthesizes sufficient abscisic acid                                        | 9668132   |
| AWCB       | initiates both proplastid and chloroplast division                          | 10117176  |
| ARC6       | Chloroplast size                                                            | 10117176  |
| ARC1       | ARC1 acts independently of the other four ARC genes                        | 10117176  |
| LER        | early flowering under short days                                           | 10469647  |
| GI         | GI mutants have elongated hypocotyls and are resistant to the herbicide paraquat | 10469647  |
| ABC        | produce the four organ types of the typical eudicot flower                 | 10821278  |
| ABC        | specify the fate of flower organ primordia                                 | 10821278  |
| MADS-box   | diverse aspects of plant development and their functional roles correlate closely with their domains of RNA accumulation | 10821278  |
| ERECTA     | internode elongation between internal flowers                              | 10821278  |
| SEP1/2/3   | overlapping functions required for petal, stamen and carpel development    | 10821278  |
| RFP1       | hypocotyl elongation was less inhibited in both FR and blue light          | 10992420  |
| RFP1       | cryptochrome-mediated blue-light signaling                                  | 10992420  |
| EGO1       | mutants show meiosis defects and sterility                                  | 11019554  |
| CRE1       | CRE1 expression conferred a cytokinin-dependent growth phenotype on a yeast mutant that lacked the endogenous histidine kinase SLN1 | 11234017  |
| UROD       | responsible for the accumulation of uroporphyrin III and lesion-mimic phenotype | 11499187  |
| P4        | encodes a protein with similarity to phosphatidylethanolamine binding protein; | 10852905  |
| FWA       | controls floral meristem identity genes redundantly with LFY              | 10852905  |
| LFY        | LFY may activate other floral meristem identity genes, which could be repressed by the combination of FWA | 10852905  |
| AN         | regulate the polarity of cell growth by controlling the arrangement of cortical MTSs; regulates polar elongation in the leaf-width direction | 11889033  |
| BOT3       | regulates polar elongation in the leaf-length direction                     | 11889033  |
| MER15      | play a role at the early stages of leaf morphogenesis                      | 11889033  |
| shvA       | plays an essential role in coordinating plant growth, especially in response to environmental factors | 17217468  |
| PIP5K      | have nonredundant roles in hydrolyzing inositol second-messenger substrates and that regulation of Ins(1,4,5)P3 levels is important during germination and early seedling development | 17237190  |
| At5PTase1  | have nonredundant roles in hydrolyzing inositol second-messenger substrates and that regulation of Ins(1,4,5)P3 levels is important during germination and early seedling development | 17237190  |
| At5PTase2  | key regulators of the formation of secondary walls in woody tissues of Arabidopsis thaliana | 17237351  |
| NST1       | key regulators of the formation of secondary walls in woody tissues of Arabidopsis thaliana | 17237351  |
| NST3       | controls the identity of the adaxial side of various organs, including xylem (Talbert et al., 1995; Zhong and Ye, 1999; Emery et al., 2003), is perhaps involved in regulating the identity of xylem because ifl1 mutant plants fail to form interfascicular fibers in inflorescence stems but differentiate ectopic xylem-like sclerified cells in upper regions of inflorescence stems as a result of a reduction in basipetal transport of auxin | 17237351  |
| IFI1/REV   | has been reported to play roles in various aspects of plant development      | 17237351  |
| TEOSINTE   | induce abnormal development in various organs, regardless of their identity | 17237351  |
| BRANCHED1, CYCLOIDEA, and PCF (TCP) | cotyledons and lateral organ primordia, preventing organ development | 17237351  |
| cp52s1a    | cotyledon and lateral organ primordia, preventing organ development          | 17307931  |
| BRE1       | cell size                                                                   | 17309365  |
| LFY        | transcriptionally activated upon the floral transition                      | 17351828  |
| SAG12      | expressed early in embryonic development, in regions associated with cell division and in vascular cells, is localized to the nucleus | 17355433  |
| PARL1      | control embryo development in specific and early embryo expression domains  | 17369435  |
| AP2        | control embryo development in specific and early embryo expression domains  | 17378809  |
SnRK2 is activated by hyperosmotic stress and is also involved in abscisic acid (ABA) signaling in response to water stress. 

APX1 is a key hydrogen peroxide (H2O2) removal enzyme (Pauwels et al., 2003), the expression of which is known to be induced by wounding and other oxidative stresses. 

TRANSPORT INHIBITOR RESPONSE1 (TIR1) mediates the degradation of AUXIN/INDOLE-3-ACETIC ACID (AUX/IAA) repressors in response to auxin. 

PIL5 increases abscisic acid (ABA) levels by activating ABA biosynthetic genes and repressing an ABA catabolic gene. 

UGE2 and UGE4 genetically influenced cell wall galactose content, which was correlated with shoot growth. 

NAA acts as a docking site at the inner nuclear pore for activities required for desumoylation and mRNA export and that disruption of this docking affects the expression of key regulators of plant development. 

EER4 regulates a previously unknown resetting or dampening mechanism for the ethylene signaling pathway. 

AIN2 necessary to induce developmental arrest during seed germination, and seedling establishment, as well as subsequent vegetative growth, thereby allowing the survival and growth of plants under the adverse environmental conditions. 

DUB promotes growth in lateral organs. 

FUL encodes a single-repeat MYB protein that acts as a negative regulator of trichome eye development, stress, and oncogenesis. 

SHP encodes a putative transcription factor with a single C2H2 zinc-finger domain. 

JAGGED encodes a putative transcription factor with a single C2H2 zinc-finger domain and promotes growth in lateral organs. 

BOP1 and BOP2 are largely restricted to the base of developing lateral organs. 

PULCHI encodes a putative APETALA2/ethylene-responsive element binding protein transcription factor, is required for the coordinated pattern of cell division during lateral root formation in Arabidopsis thaliana. 

XEROICO promotes accumulation of abscisic acid (ABA) that antagonizes GA effects. 

GAMYB modulates GA-regulated floral development. 

ATHB-1 encodes a homeodomain Leu zipper protein involved in leaf development. 

IAA13 is a repressor of auxin signaling involved in embryonic root development. 

SPATULA inhibit seed germination by repressing GA3ox transcription and inducing expression of GA2ox. 

PIL5 inhibit seed germination by repressing GA3ox transcription and inducing expression of GA2ox. 

MONOPTEROS encodes a transcription factor mediating embryo axis formation and vascular development. 

ORE7 encodes an AT-hook motif protein. 

PDLP1 damaging effect of reduced cell-to-cell communication. 

LOF1 has a role in meristem initiation and maintenance. 

CUC function in organ separation during reproductive development. 

LAS function in organ separation during reproductive development. 

A15g23940 encodes an acyl-transferase, also led to altered trichome phenotype. 

MOS4 suppress the autoimmune phenotypes of snc1, and that MOS4 is part of a nuclear complex called the MOS4-Associated Complex (MAC) along with the transcription factor AtCDC5 and the WD-40 protein PRL1. 

GL3 is known to activate the expression of downstream target genes, including an HD-Zip transcription factor GL2 and a WRKY transcription factor TTG2. 

TTG1 is known to activate the expression of downstream target genes, including an HD-Zip transcription factor GL2 and a WRKY transcription factor TTG2. 

GL1 is known to activate the expression of downstream target genes, including an HD-Zip transcription factor GL2 and a WRKY transcription factor TTG2. 

TRIPTYCHON (TRY) encodes a single-repeat MYB protein that acts as a negative regulator of trichome initiation. 

SBR-box control shoot maturation not only in the vegetative phase but also in the reproductive phase, and that SBR-box genes have divided roles in shoot maturation. 

FUL controls fruit and leaf development as well as inflorescence architecture. 

AtVP16 responsible for vacuoleless (vcI), which is defective in vacuole formation, and the homozygous mutant showed the embryonic lethal phenotype. 

PcG early flowering, that is also caused by mutations in genes encoding other proteins related to chromatin remodelling such as LIKE-HETEROCHROMATIN PROTEIN 1/TERMINAL FLOWER 2 (LHP1/TFL2), EARLY BOLTING IN SHORT DAYS (EBS) and INCURVATA 2 (IN7). 

STIMPY plays a unique role in maintaining pluripotency and proliferation in meristematic tissue in Arabidopsis. 

STIP acts downstream of cytokinin-sensing in the establishment of the SAM during this period. 

ABC40 transport diterpenoids associated with plant defense based on three findings (18 i) it is up-regulated by pathogen infection, (ii) its amino acid sequence is similar to those of other diterpenoid transporters such as NpABC1 and SpTUR2, and (iii) the atabc40 mutant plant is altered in tolerance to the toxicity of diterpenoid sciarol. 

BBRE1 regulates and enhances plant freezing tolerance. 

BRC prevents the rosette branch outgrowth downstream of the MAX pathway, and the pathway including BRC component required auxin induced apical dominance.
| Gene  | Function                                                                                   | Reference |
|-------|-------------------------------------------------------------------------------------------|-----------|
| HXK   | regulates ROS levels and perhaps also the signalling pathways leading to antioxidant defence responses | 21441406  |
| AtMan1-1 | Debranching enzyme activity is absent                                                         | 15743447  |
| ISA3  | fulfills the same role as ISA1/ISA2                                                           | 15743447  |
| ACX1  | root elongation                                                                            | 15743450  |
| NPR1  | plant immunity                                                                              | 15799997  |
| PR    | cell death                                                                                 | 15799997  |
| FRA3 mutant | displays an aberrant organization of F-actin cables and a dramatic reduction in secondary wall thickness in fiber cells | 15805481  |
| CalS1 | pathogen infection                                                                         | 15842618  |
| CalS12 | Pathogen infection                                                                         | 15842618  |
| Atpu1-1 mutant | No significant modification of the starch accumulation phenotype was observed in the Atpu1-1 mutant. | 15849301  |
| BMY8  | low temperature                                                                            | 15894744  |
| DE1   | shorter hypocotyls                                                                         | 15773850  |
| SWP   | defining the duration of the cell proliferation phase in the leaf primordium                | 15907226  |
| CDC2A | reduces cell proliferation in leaves while increasing cell size                             | 15907226  |
| SIM   | Shoot organogenesis induced on SIM medium in seedling-root explants of W1 and loc mutants. | 16034595  |
| SMT2  | growth and development                                                                     | 16040657  |
| BR    | hypocotyl elongation                                                                       | 16040657  |
| ADC2  | Overexpression of ADC2 in Arabidopsis induces dwarfism                                      | 16045478  |
| RDR1  | cell division                                                                              | 16055636  |
| AGO2  | embryo development                                                                         | 16091530  |
| OsERP3 | OsERP3 protein is homologous to C2-type Ca2+ binding motifs                                 | 16113226  |
| TAN   | functions both in the early and late phases of embryo development                           | 16113228  |
| PIN1  | auxin transport                                                                            | 16210544  |
| IKU2  | encodes a leucine-rich repeat receptor kinase, a large family of genes with roles in signal transduction pathways in plant development and metabolism | 16290693  |
| BMY8  | exhibit a more sensitive phenotype for photosynthetic apparatus functionality               | 16290706  |
| TWN2  | The first is ValRS, where the seed phenotype exhibited by twn2 (Zhang and Somerville, 1997) is indicative of a weak allele with an insertion in the 5′ untranslated region (UTR) of a gene thought to encode a protein localized to the cytosol and mitochondria. | 16290706  |
| WOL   | WOL is not essential for phloem development                                                 | 11114832  |
| STM   | redundant in embryo and vegetative development in the absence of AS1                       | 11934861  |
| STM   | they form fewer lateral shoots and more flowers, most of which remain incomplete            | 11934861  |
| SIM   | SM may have additional roles in meristem maintenance that are assumed by other factors redundant with STM that are only revealed in as1 stm-1 double mutants. | 11934861  |
| sm1-11 knat2 | double mutants have a stm phenotype and have no GUS expression                           | 11934961  |
| atgpat1-1 | To ascribe the impaired male fertility of the atgpat1-1 mutant to the disruption of AtGPAT1 | 12897259  |
| AtGPAT1 | The absence of AtGPAT1 may enhance or activate the expression of other GPAT isoforms to compensate for the loss of function normally exerted by AtGPAT1 during cell synthesis. | 12897259  |
| KU70  | Two types of experiments were performed to verify that the telomere elongation phenotype was associated with the T-DNA insertion in KU70. | 12032094  |
| aba2-11 | aba2-11 seeds were relatively insensitive to such osmotic stress, germinated well, and were able to green and expand cotyledons. | 12172025  |
| aba2-11 | aba2-11 plants were more sensitive to salt or water stress at later stages of development. | 12172025  |
| CRE1  | result in reduced cytokinin sensitivity in callus proliferation, greening, and shoot formation, and in inhibition of root growth, whereas hyperexpression of ARR1 results in the opposite phenotype. | 12410813  |
| AARR1 | result in reduced cytokinin sensitivity in callus proliferation, greening, and shoot formation, and in inhibition of root growth, whereas hyperexpression of ARR1 results in the opposite phenotype. | 12410813  |
| POLAR | two transcriptional corepressors have been identified that regulate lateral growth in leaves: AN, which promotes polar cell expansion | 12619538  |
| DRL1  | The relationship between DRL1 gene function and cell cycle regulation could explain the reduction in leaf cell number upon recessive mutation. | 12619538  |
| ant1  | The ANT gene promotes cell proliferation, and in the ant1 mutant, the reduced cell number in organs also is compensated for by an increase in cell size. | 12619538  |
| SLY1  | Mutations in SLY1 prevent the degradation of RGA in both the presence and absence of GA, leading to RGA inhibition of stem elongation and a dwarf phenotype. | 12724538  |
| rga-24 | The rga-24 mutation clearly resulted in a partial rescue of sly1-10 dwarf phenotype but did not significantly suppress the germination or fertility defects of sly1-10. | 12724538  |
| SLY1  | Loss of SLY1 function results in all of the phenotypes expected of a GA response mutant, including increased seed dormancy, growth as a dark green dwarf, delayed flowering, and reduced fertility. | 12724538  |
| sly1-2 | The first screen recovered the ethyl methanesulfonate-induced sly1-2 allele that suppressed the ability of abil-1 (abscisic acid insensitive) to germinate on 3 μM abscisic acid. | 12724538  |
Hypocotyl elongation is regulated by both PHYA and PHYB whereas PHYB translocates into the nucleus only under red light in FIS class genes all mutations lead to maternal-effect seed abortion.

HSP101 The expression of the chalcone synthase gene (CHS), which encodes the first enzyme in the anthocyanin biosynthesis pathway, is modulated by light.

AG is the class C gene of Arabidopsis and is expressed in the inner part of the development, weak expression is observed in stamens and carpels. AGL24 is also expressed in the floral meristem, and in later stages of flower meristems but was absent in the primary inflorescence meristem. These experiments showed that SVP is expressed in the secondary inflorescence is a repressor of the floral transition that AGL24 is a promoter of the floral transition.

Mutations in AGL24 confer a dosage-dependent late-flowering phenotype, indicating that AGL24 is a promoter of the floral transition. Other YABBY genes, such as FILAMENTOUS FLOWER (FIL) and YABBY3 (YAB3), are involved in organ polarity and inhibition of HMGR reduces cytokinin content and cell proliferation activity.

HMGR is essential for cytokinin biosynthesis in tobacco Bright Yellow-2 cultured cells, and inhibition of HMGR reduces cytokinin content and cell proliferation activity.

YABBY expressed in primary lateral organs where they play roles in organ polarity and growth. KAN genes have roles in ovule development, as indicated by the reduced growth of the outer integument observed in some kan mutant combinations.

Roles of the NAC family genes include embryo and shoot meristem development, lateral root formation, auxin signaling, defense and abiotic stress response. These data strongly suggest that AtNAP and its homologs play an important role in leaf senescence in Arabidopsis and possibly in other plant species.

AtNAP The overexpression of either CCA1 or LHY caused longer hypocotyl and induction of CAB by light, whereas ELF3 overexpression caused shorter hypocotyls.

CCA1 Plants that constitutively express PRR5 or PRR9 exhibit a hypersensitive seedling deetiolation phenotype in Rc and flower early, indicating that the aberrant expression of these genes interferes with normal phytochrome responses.

PRR9 The reduced sensitivity of prr7 to Rc also was evident in the expansion of the cotyledons.

PRR7 prr7 also had a defect in its responsiveness to FRc, apparent as reduced inhibition of hypocotyl elongation.

PSI Both organisms are impaired in PSI activity, but differ substantially in that Ycf37-deficient Synechocystis cells can grow photoautotrophically and accumulate a functional PSI complex, whereas the higher plant mutant is lethal and lacks PSI activity.

HOT2 In previous work, we identified single recessive alleles of four loci required for thermotolerance of hypocotyl elongation. hot1-1, hot2-1, hot3-1, and hot4-1. Despite this decrease, 10-d-old hot3-1 plants showed normal acquired thermotolerance (Fig. 3), indicating that the level of Hsp101 must still be sufficient for thermotolerance at this growth stage.

PHYB whereas PHYB translocates into the nucleus only under red light.

CHS The characterization of phy mutants demonstrates that these photoreceptors have crucial functions during seed germination, seedling deetiolation, shade avoidance, and the transition from vegetative to reproductive growth.
Furthermore, in the axil of the first-whorl organs, a new ap1 flower develops. Expression of SEN1 is indicative of senescence.

Therefore, BPEp presumably acts downstream of the PI/AP3 heterodimer during petal senescence (o), rosette leaves (Lr), cauline leaves (Lc) and inflorescence stem (s) development.

Very recently, an E3 ubiquitin ligase-encoding gene, BIG BROTHER (BB), has been shown to limit plant organ size by controlling cell proliferation. The excess branching phenotype of the trichome in hdg1-1 is enhanced by hdg12-2, suggesting that both HDG11 and HDG12 act in repressing the outgrowth of trichomes. We have reported that amyloplasts in endodermal cells did not sediment in the Landsberg etr1 allele.

Our results suggest that the axr4 phenotype, including auxin-resistant root growth and reduced gravitropism, is caused by defective AUX1 trafficking in epidermal cells.

Analysis of GUS expression under the control of the SGR5 promoter revealed that SGR5 is mainly expressed in the endodermis, the gravity-sensing tissue in inflorescence stems.

Expression data and single and double mutant phenotypes of cia5 and At tic20-I suggested that CIA5 and Tic20 may perform similar functions and that CIA5 is more important for later stages of leaf development.

We renamed CIA5 as Arabidopsis Tic21 (At Tic21) and propose that it functions as part of the inner membrane protein-conducting channel and may be more important for later stages of leaf development. We renamed CIA5 as Arabidopsis Tic21 (At Tic21) and propose that it functions as part of the inner membrane protein-conducting channel and may be more important for later stages of leaf development.

Al-activated root exudation of malate and citrate was profiled in the root exudate solutions from WT and AtALMT1 MT plants grown in hydroponic culture. Al-activated root exudation of malate and citrate was profiled in the root exudate solutions from WT and AtALMT1 MT plants grown in hydroponic culture.
AP1: As the tissues used in this experiment were mostly from flower buds older than stages 5 and 6, BPEp accumulation is most likely to be controlled by the protein complex formed by AP1, PI, SEP, and API during petal organogenesis.

BPEp: Therefore, BPEp is the first protein that specifically limits petal organ size by controlling the postmitotic rate of cell growth and expansion.

AS1: demonstrating that AS1 and PIN1 function redundantly to promote leaf development.

esp3: One class of mutants represented by esp3 had reduced stature, early flowering (see below), and altered leaf morphology.

MS11: Development of ms11 as plants was delayed, and plants had a reduced rosette size, a delayed flowering time and reduced growth of primary shoots, although more severe symptoms of fasciation, such as stem bifurcation, were not observed.

WSGs: The absence of starch was coupled with the accumulation of very high levels of WSGs (whatever extraction method was used) that were not observed in other lines (Tables 3 and 4). Moreover, this double mutant displayed a lower growth rate, a reduced size of the mature plant, a pale color, and a general wilting of the inflorescence.

AtIPT3: Mutants lacking AtIPT3, 5, and 7 were severely inhibited in shoot growth, whereas lateral roots elongated more.

ELCis: The multinuclear phenotype found in elc mutants indicates that ELCis involved in the regulation of cell division.

SL1M1: Both slim-1 and slim-2 alleles showed 30% reduction of root growth compared with the parental line.

CP24: However, the photosynthetic rate in limiting light was slightly depressed in the plants lacking CP24, and there was a reduction in growth rate of the kochcb6 plants compared with the wild type: the rate of increase in rosette diameter was slower, the average time for flowering increased by several days, and the fresh weight was lower.

erpl-1: In the erpl-1 erpl-2 double mutant, arrest of cell cycle progression at G2/M and disordered cellular organization occurred in root tips.

FLC: vernalization represses FLC expression, thus causing rapid flowering.

mtk/eto3: When Met cycle knockout and ethylene overproduction were combined in the mtk/eto3 double mutant, a reduced capacity for ethylene synthesis was observed in seedlings.

mtk/eto3: The mtk/eto3 double mutant displayed a metabolic plant phenotype that was similar to mtk with reduced AdoMet levels at sulfur-limiting conditions.

AtEBP: AtEBP is an ethylene-induced gene that served as a positive control for ethylene treatment.

hac1: Consistent with the flowering phenotypes, the FLC mRNA levels in the hac1 hac5 and hac1 hac12 double mutants were considerably increased compared to those in the hac1 single mutants.

tmt1: In wild-type plants and 0.39 and 0.41 μmol/g fresh weight, respectively, in the two tmt1 mutant lines (Figure 8A representing slightly 30%) reduced glucose contents.

OMR1: Visual analysis of tha2-1/tha2-1 P3SS-cmr1-5 homozygotes showed some chlorosis, leaf curling, and misshapen flowers (see Supplemental Figure 10 online) but otherwise viable plants with normal seed set.

gid1a: Although single mutants developed normally, gid1a gid1c and gid1a gid1d displayed reduced stem height and lower male fertility, respectively, indicating some functional specificity.

DELLA: Deletions or specific missense mutations of the conserved motifs (DELLA and/or VHYNP) within the DELLA domain render the mutant proteins resistant to GA-induced degradation, leading to a GA-insensitive dwarf phenotype.

gal-3: This is clearly illustrated in the severely GA-deficient mutant gal-3, which displays dramatically reduced leaf expansion and stem and root elongation.

PAC: It is interesting to note that PAC can inhibit root growth further in the gid1a gid1b gid1c-1 mutant.

gid1a: The gid1a single mutant and both double mutants lacking functional GID1a display phenotypic defects in reproductive development, including stem length, silique length, and fertility.

cdka: In accordance, the overexpression of a mutant cdka1 allele in which the putative phosphorylated Tyr residue is mutated also did not result in an obvious cell division phenotype.

MADS-box: This suggests that while the MIKC factors are important for controlling flower development, type I MADS-box genes might control specific processes during ovule and seed development.

AGL80: In contrast, mutations that block ethylene responses, etr1-3 and ein2-5, enhance root formation and render it insensitive to the effect of ACC, even though these mutants have reduced root elongation at high ACC doses.

oyv: The oyn mutant also exhibits defects in fruit development as the oyn fruit shows a narrower replum, an abnormal pattern of lignification, and septum fusion defects.

bam3: Representative plants were selected to show the reduced growth rate of bam3 and bam4 mutants.

LUG: Second, we identified a relatively minor role of LUG compared with LUG in flower development, as the luh-1 single mutation does not affect flower development but luh-1/+ can enhance the floral phenotype of lug.
| Gene | Description |
|------|-------------|
| ARF2 | ARF2 has also been shown to mediate auxin-responsive gene expression and negatively regulates cell expansion |
| AP2 | Loss-of-function mutations in AP2, encoding a transcription factor, lead to a range of floral defects that correlate with increased seed mass |
| BIG | The E3 ligase BIG BROTHER (BB) negatively regulates the duration of cell proliferation in leaves and petals, possibly by targeting growth stimulators for degradation, and is proposed as a bona fide organ size regulator |
| PI3K | The broad and significant role of PI3K was first suggested by the results of Wolters et al. (1994) showing that plants containing an antisense construct for VPS4 are severely inhibited in growth and development |
| K-uk | The turnover rates of K-3 and K-uk might be different from those of other kaempferol glycosides, leading to abnormal levels of free aglycone kaempferol, which in turn affect plant development |
| STT3a | Mutations in STT3a, a subunit of the oligosaccharyltransferase complex responsible for protein N-glycosylation, may also affect the cell wall, particularly under salt stress |
| DC3000 | Transgenic Arabidopsis plants with constitutively suppressed AtEF5A-2 exhibited marked resistance to programmed cell death induced by virulent Pst DC3000, and there was a corresponding reduction in pathogen growth and development of disease symptoms in the plant tissue |
| AtEF5A-2 | The results indicate that AtEF5A-2 is a key element of the signal transduction pathway resulting in plant programmed cell death |
| DHS | For example, constitutive suppression of DHS in Arabidopsis results in several phenotypes, including delayed natural leaf senescence, delayed bolting, increased rosette leaf and root biomass, and enhanced seed yield |
| GL2 | Root hair-like cell expansion in the hypocotyl epidermis was previously observed in transgenic plants expressing recombinant GLABRA2 (GL2), which was modified to activate the expression of genes involved in root hair cell differentiation |
| ibr | Indeed, these ibr mutants display additional phenotypes associated with peroxisome defects, such as sucrose dependence during seedling development due to slowed oxidation of seed storage fatty acids |
| ibr1 | ibr1 and ibr10 mutants display IBA- and 2,4-DB-resistant root elongation |
| PAD4 | A reasonable hypothesis is the so-called amplification loop model, in which SA induces the expression of the PAD4 gene and then the PAD4 protein activates SA synthesis after pathogen infection |
| BAH1 | These results suggest that BAH1 regulates pathogen-induced localized cell death and age-related cell death in SA-dependent and SA-independent manners, respectively |
| LEC1 | a cellular environment that promotes embryo development and that this environment coordinates the morphogenesis and maturation phases |
| LEC2 | somatic embryo formation |
| FUS3 | encodes a regulatory protein |
| ABI3 | a transcription factor that operates primarily during the maturation phase |
| ARR5 | lateral root formation |
| BA | root elongation |
| ABR4 | primary root tip |
| ARR4 | shoot formation |
| ARR15 | altered development |
| MTs | cell expansion |
| DC3000 | DC3000 |
| AUK2 | growth and development |
| AUK2 | seedling phenotype |
| AUK2 | growth and development |
| AUK4 | phosphate starvation |
| AUK2 | leaf phenotype |
| SLY1 | infertile |
| BELLA | plant growth |
| POLAR | cell expansion |
| CYTOKININ | shoot induction |
| CYTOKININ | cell division |
| AUK2 | inflorescence |
| AAR1 | longer hypocotyls |
| AAR1 | flower |
| C3 | organ development |
| IVS | shorter hypocotyls |
| Gene Symbol | Definition |
|-------------|------------|
| E3          | flower     |
| SA          | pseudomonas syringae |
| EDS1        | cell death |
| FCD         | plant defense |
| NPR1        | cell death |
| EDS1        | plant defense |
| PILS        | gravitropism |
| PHYB        | seed germination |
| NPR1        | hypocotyl elongation |
| PHYB        | gravitropism |
| PILS        | constitutive photomorphogenic phenotypes |
| PHYB        | far-red light |
| PILS        | hypocotyl elongation |
| PHYB        | seed germination |
| PEX5        | reduced auxin response |
| PEX5        | seed development |
| NCED        | a key regulatory enzyme in ABA biosynthesis |
| OF          | cell pattern |
| SCG         | epidermis development |
| GUS         | lateral root primordium |
| LATERAL     | vascular differentiation |
| INVOLVED    | cell wall biosynthesis |
| IN          | root elongation |
| LATERAL     | lateral root formation |
| DET1-4      | thermotolerance |
| DET1-4      | heat stress |
| RE          | pale-green leaves |
| FIB1        | cell death |
| POLAR       | required for vascular differentiation and patterning |
| POLAR       | auxin accumulation |
| CA2         | vascular development |
| ARR5        | circadian phenotype |
| PHYB        | reduced phyb signaling |
| PHYB        | long-hypocotyl phenotype |
| LEP         | curled leaves |
| LEP         | leaf development |
| LEP         | short-hypocotyl phenotype |
| LEP         | mutant seedling phenotype |
| GATA        | seed germination |
| ARBH1       | abi-hypersensitive |
| Li1         | abscisic acid |
| SA          | germination efficiency |
| SE          | root system |
| PHYA        | seed germination |
| PHYB        | far-red light |
| COBRA       | cell expansion |
| GUN4        | cell death |
| SAG12       | senescence |
| EDS1        | loss-of-function phenotype |
| BRs         | shoot elongation |
| AXR2        | root elongation |
| DET2        | hypocotyl elongation |
| Act1P       | physiological response |
| RCN1        | the regulatory subunit of protein phosphatase 2A |
| ARR5        | bushy phenotype |
| SEN4        | a marker gene for dark-induced and age-dependent leaf senescence |
| RABBITEARS  | a regulator of petal development |
| AP3         | cell division |
| AP2         | flower |
| LCG         | reduced number |
| FT          | inflorescence |
| GFP         | flower |
| POLAR       | auxin transport |
| GLC         | ethylene treatment |
| CHP         | plant growth |
| CDC48A      | as a monomer and may function in regulating plant growth |
| SA          | defense pathway |
| EDS1        | lacking a functional SA pathway |
| PPR         | control cytoplasmic male sterility |
| HPAEC-PAD   | high performance anion-exchange |
| BPM1        | structurally related |
| Cyelin B1   | promoter–GFP fusion |
| BOP         | lateral organ development |
| NPR1        | severe disease symptoms |
| CCA1        | expression had an altered phase |
| Gene | Description | ID |
|------|-------------|----|
| R    | a higher degree of pathogen-induced stress | 16623885 |
| LRP1 | produced an elongated root phenotype | 19835563 |
| PLC  | inhibits the expression of flowering-time integrators | 18849490 |
| WUS  | shoot stem cells and leaf development | 18950478 |
| YH1/BRL2 | repressed by ABA | 19000166 |
| ARF7 and ARF19 | LR formation | 19037657 |
| gs   | photorespiratory nitrogen metabolism | 19048287 |
| IPT  | increased secondary growth | 19074290 |
| ABI5 | the expression of the LEA gene | 191553448 |
| CVY  | aspects of floral specification | 19175771 |
| Erd15| induced under dehydration stress | 19210750 |
| MYB  | required for trichome initiation | 19223001 |
| BPTsa| essential for male gametophyte development | 19223514 |
| AGD10| root hair development | 19237690 |