



## ABRC: TRAINED Kit

### Molecular Control of Shoot Architecture

**Summary:** This kit can be used to demonstrate the concepts presented in the Teaching Tools in Plant Biology module “Molecular Control of Shoot Architecture”. This module explores plant growth, development and pattern generation. The ten stocks in this kit include one natural accession, and seven mutants with their corresponding reference strains. By growing and observing this set of seeds students will see the effect of various mutations on plant development.

**Recommended Grade Level:** College

#### Supporting Resources

All teaching materials related to this kit are available via *Teaching Tools in Plant Biology*, a publication of the American Society of Plant Biologists.

- Teaching Tools in Plant Biology - <https://academic.oup.com/plcell/pages/teaching-tools-plant-biology>
- Module - <https://academic.oup.com/plcell/article/30/12/tpc.118.tt1218/6100145>

#### Seed Strain Details

**Lov-1 (CS22574)** – This natural accession, originally collected from Lovvik, Sweden, displays a late flowering phenotype and requires a relatively long period of vernalization to induce flowering. LOV-1 carries the *flc-lov-1* allele of FLOWERING LOCUS C (FLC). FLC is a repressor of floral transition that can be silenced in response to vernalization. The *flc-lov-1* allele is not silenced by histone modification in response to vernalization as effectively as other alleles, resulting in a requirement for a longer period of vernalization and later flowering<sup>10</sup>.

**Landsberg erecta (Ler-0, CS20)** - This laboratory strain contains an X-ray induced mutation in the ERECTA gene, which causes the plants to have a more upright growth habit. Ler-0 is widely used to generate mutants, and is used as the reference strain for the *cuc1-1*, *ft-1*, *stm-2/+* and *wus-1* mutants used in this module.

***cuc1-1* (CS3869)** – This transgenic, homozygous mutation in the CUP SHAPED COTYLEDONS 1 (CUC1) gene results in a semi-dominant phenotype that includes slight fusion of the sepals, as well as a low frequency of fused stamens and cotyledons fused along one side<sup>1,2,5,8</sup>. The CUC1 protein is a transcription factor involved in establishing zonation in the meristem.

***ft-1* (CS56)** – This strain contains an ethymethane sulfonate (EMS)-induced recessive mutation in the FLOWERING LOCUS T (FT) gene. The FT protein acts in conjunction with TERMINAL FLOWER (TFL) to control the transition of the meristem from vegetative to flowering. Disruption of FT results in late flowering that is unaffected by vernalization and an increased number of rosette leaves<sup>6</sup>.

***stm-2/+* (CS8137)** – This strain contains an EMS-induced segregating, recessive mutation in SHOOTMERISTEMLESS (STM). The STM protein is a KNOX family transcription factor involved in regulation of cytokinin levels in the shoot apical meristem. Cytokinin is involved in maintenance of stem cells in the central zone, as well as interacting with auxin and GA to specify the identity of organs produced by the apical meristem. Loss of STM function results in a sterile bushy plant with aerial rosettes, a reduced number of flowers per inflorescence, as well as a reduced number of petals, stamens and carpels<sup>4</sup>.

**wus-1 (CS15)** – This strain contains an EMS-induced segregating mutation in the WUSCHEL gene. The WUSCHEL protein is expressed in the organizing center of the shoot apical meristem and acts in conjunction with CLAVATA to maintain cells in an uncommitted state in the apical meristem. The loss of WUSCHEL function in the mutant causes premature termination of shoot and floral meristems.

**Columbia (Col-0, CS70000)** - The genome of this laboratory strain has been completely sequenced and is used as a reference for comparison with the genome sequences of other strains of Arabidopsis. This strain has been maintained in the laboratory for many generations, grows well in laboratory conditions, and has relatively low levels of seed dormancy. Col-0 is used as the reference strain for the *max1*, *max2-1* and *arr1-3 arr10-5 arr12-1* mutants used in this module.

**max1 (CS9564)** – This strain contains an EMS-induced recessive mutation in the MORE AXILLARIES 1 (MAX1) gene. The MAX 1 protein is involved in strigalactone biosynthesis. The resulting phenotype demonstrates increased rosette axillary branches<sup>7</sup>.

**max2-1 (CS9565)** – This strain contains a homozygous EMS-induced recessive mutation in the MORE AXILLARIES 2 (MAX2) gene. The MAX 2 protein is involved in strigalactone signal transduction. Loss of MAX2 function causes increased shoot branching and hypocotyl length<sup>7</sup>.

**arr1-3 arr10-5 arr12-1 (CS39992)** – This transgenic, homozygous triple mutant was generated by crossing Arabidopsis response regulator mutants, *arr10-5*, *arr1-3* and *arr12-1*. The disruption of cytokinin responses in these mutants causes premature termination of primary root growth, altered vascular morphogenesis, reduced stature, increased light sensitivity and altered chlorophyll content<sup>3</sup>.

## Sources

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