

SHOOTMERISTEMLESS: A GENE INVOLVED IN THE MAIZE SHOOT APEX INITIATION

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The regulatory mechanism of shoot apical meristem (SAM) initiation is an important subject of investigation in developmental plant biology. The establishment of the shoot apical meristem (SAM) during embryogenesis is a key event in plant development, because the above-ground body plan depends on the activity of the SAM through the production of leaves, axial buds and stem. A genetic approach utilizing developmental mutants is an efficient way to investigate on this topic.

Here we describe a mutation of the *shootmeristemless* (*sml*) gene disrupting shoot apical meristem maintenance and lateral organ formation. Introgression of this mutation in different genetic backgrounds has highlighted the epistatic interaction between *sml* and the unlinked *distorted growth* (*dgr*) gene. Seeds homozygous for both *sml* and *dgr* have a shootless phenotype whereas *Dgr*/-*sml*/*sml* seeds produce plants with many developmental abnormalities (*dgr* mutant).

sml lies on the long arm of chromosome 10, and its map position has been defined by linkage analysis with visible and molecular markers. To clone it we have adopted a candidate gene approach. The *SHOOT ORGANIZATION1* (*SHO1*) gene, recently isolated in rice, lies on a syntenic region. A mutant in this gene shows abnormal formation of the SAM. We have isolated the putative *SHO1* maize orthologue, that exhibits a significant sequence similarity. The correspondence between *sml* and *SHO1* will be revealed by polymorphisms detection and association studies.

The morphological and histological analysis of the *dgr* phenotype reveals a variety of plant abnormalities affecting different plant organ, including leaf, inflorescence, root and stem; the severity of defects may vary widely within a single mutant plant. Recessive mutations in the maize *leafbladeless1* (*lbl1*) gene lead to a very similar phenotype.

It is remarkable that both *SHO1* in rice and *lbl1* in maize are involved in the biosynthesis of the ta-siRNA, suggesting that a small RNA-mediated gene regulation operates at the critical step of SAM formation and maintenance in rice and maize. The analysis of the double mutant *sml*-*lbl1* will define the relationship between these two genes.