

Discovery of a novel molecular mechanism controlling seed physical dormancy

Background

- Physical seed dormancy exists widely in higher plants, but its molecular mechanism has remained largely elusive.
- Seed dormancy is a contributing factor for slow seedling development and poor establishment of several prospective bioenergy species, including switchgrass.

Approach

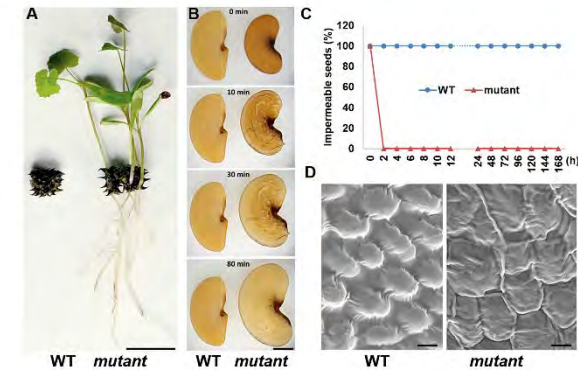
- We used the large mutant population for the model legume plant, *Medicago truncatula*, to study this trait.

Outcomes

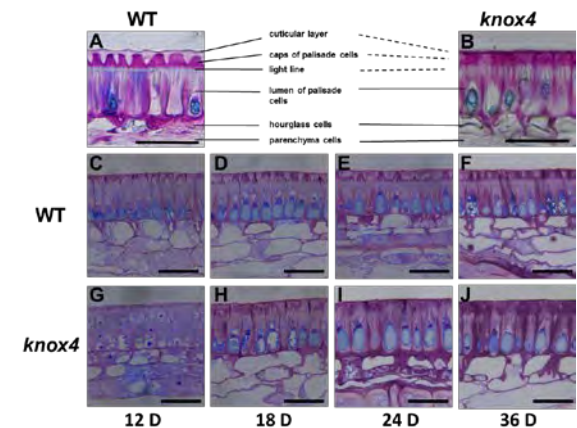
- By screening a large number of Tnt1 retrotransposon-tagged *Medicago truncatula* lines, we identified non-dormant seed mutants from this model legume species; unlike wild-type hard seeds exhibiting physical dormancy, the mature mutant seeds imbibed water quickly and germinated easily, without the need for scarification.
- Genetic and molecular analyses revealed that a class II KNOTTED-like homeobox (KNOXII) gene, *KNOX4*, was responsible for the loss of physical dormancy in the seeds of the mutants.
- Microscopic observations of cross sections showed that the mutant phenotype was caused by a dysfunctional palisade cuticle layer in the seed coat. Chemical analysis revealed differences in lipid monomer composition between the wild-type and mutant seed coats.

Significance

- This study elucidated a novel molecular mechanism of physical dormancy and revealed a new role of class II KNOX genes.
- Understanding the molecular basis of seed dormancy will be helpful in agronomic management and design of improved bioenergy crops.



Isolation and characterization of *M. truncatula* mutant seeds lacking physical dormancy.



Loss of function of *KNOX4* showed developmental defects in seed coat structure in *M. truncatula*.