

SEED DORMANCY

A skeleton key to domestication

Nat. Genet. **50**, 1435–1441 (2018)

Crops share domestication traits, such as reduced seed dormancy, increased apical dominance and loss of shattering. However, whether orthologous genes contribute to parallel selection of domestication traits across plant families remains unclear. By studying a gene controlling seed coat colour in soybean, Min Wang from the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China, and colleagues fortuitously found a hidden function of this gene in regulating seed dormancy and demonstrated that parallel selection of this gene results in reduced seed dormancy during the domestication of multiple crops, including soybean, rice and tomato.

A dominant stay-green *G* locus is known to control green seed coat colour in soybean. By performing genome-wide association analysis, the researchers narrowed down the location of the *G* locus to a gene on chromosome 1. Additionally, the function of *G* in controlling green seed coat colour received support from transgenic data.

Interestingly, the region around the *G* locus exhibits selection signatures in soybean domestication. However, if the trait under selection is seed coat colour, it is then perplexing that all wild soybeans with black seeds contain the *G* allele conferring the green seed coat colour, considering that green is invisible against black. The researchers hypothesized that the trait controlled by *G* under selection is the reduction of seed dormancy. Indeed, overexpressing the wild-type *G* allele strengthened seed dormancy.

Intriguingly, selection signatures were also observed around the orthologues of *G* in rice and tomato, and genetic data suggested that in rice and *Arabidopsis*, *G* also controls seed dormancy. Moreover, the function of *G* in regulating dormancy proved to be conserved across plant families, as overexpressing the soybean *G* allele in *Arabidopsis g* mutants can rescue the dormancy phenotype. The authors concluded that *G* probably regulates seed dormancy by modulating the biosynthesis of abscisic acid.

Jun Lyu

Published online: 2 November 2018
<https://doi.org/10.1038/s41477-018-0305-8>