

PEST CONTROL

Peppers trap worms

Agron. Sustain. Dev. 36, <http://doi.org/bs8x> (2016)

NIGEL CATTILIN / ALAMY STOCK PHOTO

Root-knot nematodes (*Meloidogyne* spp.) are a major agricultural pest, especially of crops grown under glass or other shelters. Nematicides are expensive and increasingly restricted on environmental grounds, while resistant crop varieties are few and only partially effective. Mireille Navarrete from the French National Institute for Agricultural Research, Avignon, and colleagues have field-tested an alternative approach, using nematode-resistant sweet peppers as a 'trap crop' in rotation with commercial crops.

The peppers carried two resistance genes: *Me1*, which induces a hypersensitive response

preventing the development of egg-laying females, and *Me3*, which causes cellular necrosis adjacent to infecting worms. Both strategies kill nematodes before they can reproduce, clearing them from infested soils, at least under experimental conditions. Over four years on a commercial farm in southern France, the researchers tested a cropping scheme in which peppers were grown every two years intercropped between Swiss chard, lettuce, tomatoes and melons. This regime reduced nematode infestation of the soil by over 80% and more than halved the occurrence of nematode-induced galls on the Swiss chard crops.

Despite the success of the trial, this approach will not suit everyone. Of 28 local farmers surveyed, 4 in 5 were worried that the peppers would interfere with their summer growing season and be too labour-intensive. Nevertheless, this trial shows that using resistant cultivars as trap crops could prove a practical defence against nematode pests. CS

VERNALIZATION

Memorizing the cold

Nat. Genet. <http://doi.org/bs6v> (2016)

Reproduction in many plants requires vernalization, which accelerates flowering by prolonged exposure to cold temperatures. The repression of *FLOWERING LOCUS C (FLC)* is essential to the vernalization mechanism. Recently, Yuehui He's group from the Shanghai Center for Plant Stress Biology, Chinese

Academy of Sciences, Shanghai, China, reported the identification of a cold memory DNA element and cognate reader proteins, which are essential for *FLC* silencing before and during vernalization.

Yuan *et al.* identified two Sph/RY DNA motifs in the nucleation region of *FLC* that are fundamental for *FLC* silencing, and investigated their importance in maintaining the silencing after cold exposure. A 47-bp element bearing Sph/RY motifs was designated the cold memory element (CME). Two *trans*-acting factors, VAL1 and VAL2, were characterized as *FLC* repressors. The VAL proteins read the CME as well as histone modification H3K27me3, marking a repressive state of *FLC*. Further, chromatin immunoprecipitation and quantitative polymerase chain reaction results suggest that the CME-VAL interaction mediates the induction and maintenance of *FLC* silencing during vernalization.

This study demonstrates an important epigenetic mechanism for how plants control when to flower in response to prolonged cold exposure. LL

KINASE SIGNALLING

Tanning with MYB75

The Plant Cell <http://doi.org/bs67> (2016)

Light is vital for plants to create sugars through photosynthesis. However, too much light can lead to photodamage. So, plants produce anthocyanins to protect themselves. As with many other danger signals, mitogen-activated protein kinases (MAPKs) are activated by excess light. Jin-Long Qiu and colleagues from Beijing and Copenhagen connect the two processes in *Arabidopsis*.

The authors used a constitutively activated form of MPK4 in a yeast assay to identify the transcription factor MYB75 as a MAPK substrate. MYB75 controls anthocyanin biosynthesis, is degraded in the dark through the constitutive photomorphogenic 1 (COP1) pathway, and both *mpk4* and *myb75* mutants failed to accumulate anthocyanin under high light. Multiple lines of evidence show that MPK4 is activated by light and phosphorylates MYB75, which can then escape proteasomal degradation and induce pigment synthesis.

This study shows that MYB75 is a post-transcriptional point of convergence between two opposite pathways; it is degraded by COP1 in the dark, and stabilized by MPK4 in the light. Given the wide occurrences of MAPK activation and anthocyanin synthesis in response to stress, it is significant to discover a molecular link between both pathways. GT

Written by Guillaume Tena, Chris Surridge, Lei Lei and Jun Lyu.

SMALL INTERFERING RNA

Hybrid revision

Proc. Natl Acad. Sci. USA 133, E6895-E6902 (2016)

The epigenetic reprogramming that occurs in plant hybrids involves altered levels of small RNAs (sRNAs) and DNA methylation (^mC). Trans-chromosomal methylation (TCM) and trans-chromosomal demethylation (TCdM) events were known to confer changes in ^mC levels, resulting in the epigenetic states of paternal and maternal alleles resembling each other. TCM/TCdM may also be important to heterosis. To gain insight into the establishment and features of TCM/TCdM events, a group of Australian researchers combined comprehensive epigenomic and mutant analyses for *Arabidopsis* parental lines, their F1 hybrids and the F2 generation.

The researchers identified hundreds of TCM/TCdM regions that were inherited by the F2 generation by comparing the methylomes among parental, F1 and F2 individuals. TCM events increased over time in F1 hybrids, suggesting the requirement of a build-up of inducing molecules, presumably small interfering RNAs (siRNAs). Another feature of the inherited TCM/TCdM regions is the enrichment of transposable elements.

The transgenerational stability of altered epigenetic states varies among F2 individuals and different genomic loci. Thirty-four candidate genes were found to show variable inheritance of the altered epigenetic states and associated variable expression, probably contributing to phenotypic segregation in the F2 population.

In some inherited TCM/TCdM regions, sRNA levels are significantly associated with altered ^mC states in hybrids. Genetic analysis showed that polymerase IV-dependent 24-nt siRNAs are required for the initiation of ^mC state change, as hybrids with a mutant *polIV* allele failed to establish TCM-mediated ^mC state change.

Although this study offers no evidence to suggest that TCM/TCdM affects heterosis, further studies will be needed to support or exclude this possibility. JL