research highlights

IMMUNITY

Parasite protection

Science **353**, 478-481 (2016)



Plants possess sophisticated innate immune systems. Defended by a vast repertoire of receptors waiting to be triggered by specific signals, plants can detect pathogenic organisms from other kingdoms of life that are very different from themselves, such as bacteria, oomycetes, fungi or insects. But how can they sense the presence of parasitic plants, which are biologically very similar? In the exact same way, says a study by Hegenauer and colleagues from Tübingen, Germany and Norwich, UK.

The lifestyle of dodder (*Cuscuta reflexa*) is aggressively parasitic, spanning a vast range of hosts. Without roots or leaves, these small vines wrap themselves around the stems of the host plant and insert structures called

haustoria to steal water, sugars and nutrients. The cultivated tomato is one of the rare plants that can mount an efficient immune response and fight off dodder.

Natural variation between wild and cultivated tomatoes allowed the authors to map one responsible gene. They identified a membrane receptor-like protein that is able to confer responsiveness to the still unknown *Cuscuta* peptide signal, and can be transferred to make susceptible plants more resistant. The levels of resistance achieved are not maximal, indicating that other layers of defence mechanisms are yet to be discovered in this fascinating interaction.

ECOPHYSIOLOGY

Adapting adaptation

Front. Plant. Sci. http://doi.org/bn8b (2016)

Arabidopsis thaliana has one of the largest geographical ranges of any plant species. It is a native of Eurasia and North Africa and can be found as a naturalized alien on all continents except Antarctica. Its ecotypes therefore provide a superb resource to study how a single species can adapt to various environments. William Adams III and colleagues at the University of Colorado Boulder have now demonstrated that this adaptability is itself adapted to local conditions.

The researchers investigated the physiological performances of three *A. thaliana* ecotypes originally collected at the same longitude, but separated by over 2,200 km, from Sweden in the north to Italy in the south. These were then grown under different day/night temperature regimes

approximating the normal conditions at the points of origin of each ecotype. A battery of physiological characteristics was measured for each plant including photosynthetic capacity, leaf thickness, levels of β -carotene, leaf vein density and many others.

The temperature regime affected all of these characteristics, however, the magnitude of the change varied with ecotype and the conditions of its native range. The researchers identified two classes of characteristics: one that included characteristics like photosynthetic capacity and extent of phloem, whose degree of acclimation related to the ecotypes' native temperature, and a second that included transpiration rate and leaf vein density, whose acclimation varied with the rainfall in the native range.

SYMBIOSIS

Triple trouble with lichen

Science **353**, 488-492 (2016)

Lichens are not single organisms but an intimate symbiosis of fungi, most often an ascomycete, and a photosynthetic alga or cyanobacterial species. Very occasionally the symbiosis will include a second photosynthetic partner (photobiont) but only one fungus (mycobiont) per lichen seemed an inviolable rule. Spribille *et al.* have rewritten this dogma by identifying lichen involving two mycobionts and demonstrating that such trinogamy is very common.

The closely related lichens *Bryoria fremontii* and *B. tortuosa* are distinguishable because the latter produces vulpinic acid, giving its thalli a characteristic yellowish colour. Previous genetic studies had failed to identify any differences between the symbionts constituting the two lichens and similarly Spribille *et al.* saw no discernable difference in the paired transcriptomes of 15 field-collected individuals. However, along with ascomycete and viridiplantae transcripts, they identified several hundred mRNAs of basidiomycete origin, present in both lichens but more abundant in the vulpinic-acid-producing *B. tortuosa*.

Having realized a basidiomycete was involved with the *Bryoria* lichens, the researchers proceeded to find basidiomycete mRNA in many other lichens; of 52 genera from six continents so far. These lichenassociated yeasts are part of the genus *Cyphobasidium*. As final confirmation, Spribille *et al.* used fluorescence *in situ* hybridization (FISH) to label the *Cyphobasidium* cells and locate them within the cortex of the lichens.

Written by Guillaume Tena, Chris Surridge and Jun Lyu.

FRUIT RIPENING

Targeting tomato softening

Nat. Biotechnol. http://doi.org/bn8c (2016)

Slowing fruit softening to extend shelf life remains a major challenge for tomato improvement, especially considering that the 'non-ripening mutations' currently used in production generally compromise the fruit flavour and colour. Selman Uluisik, at the University of Nottingham, UK, and colleagues now develop an effective approach to control tomato softening by manipulating a gene encoding a pectate lyase.

In strawberries, silencing pectate lyase reduces the rate of fruit softening, however in tomato, pectate lyase was the only major pectin-degrading enzyme hitherto lacking investigation. The researchers accordingly surveyed the pectate lyase genes in tomato and focused on one that is highly expressed during ripening. Downregulating this pectate lyase gene using RNAi increased fruit firmness without affecting other traits, such as yield and the contents of metabolites that influence colour, taste and flavour.

Examination of cell walls using microscopy and labelling techniques showed that the pectate lyase mainly acts in the tricellular junction regions where it breaks down the demethylesterified homogalacturonans to more degradable water-soluble pectins, resulting in rapid fruit softening.

The researchers suggest that manipulating the expression of this gene using natural variation or genomic editing can generate products for commercialization. Preliminary genomic editing experiments and quantitative trait locus mapping analysis demonstrated the feasibility of this strategy.