

TROPICAL TREE GROWTH

No signs of stimulation

Nature Geosci. **8**, 24–28 (2015)



© MATHES/ISTOCK/THINKSTOCK

Forest inventory data point to a CO₂-induced stimulation of tree growth in the tropics, but direct evidence has been lacking. A tree-ring-based analysis spanning three continents suggests that tropical tree growth has remained stagnant on a centennial timescale, calling into question claims that old-growth tropical forests can help to soak up future CO₂ emissions.

Peter van der Sleen, of Wageningen University, and colleagues examined changes in the growth and water-use efficiency of canopy and understorey trees in Bolivia, Cameroon and Thailand over the last 150 years using measurements of the width and stable carbon isotope signature of tree rings. In conjunction with a marked increase in intercellular CO₂ concentrations, the researchers report a 30 to 35% increase in the water-use efficiency of the studied trees, indicative of a CO₂-induced increase in photosynthesis, reduction in transpiration, or both. However, they find no evidence for a concomitant increase in tree growth.

Why increased concentrations of CO₂ have failed to stimulate tree growth in the tropics remains unclear, but increasing temperatures, resource limitations and shifts in substrate allocation could hold the answer.

AA

INNATE IMMUNITY

Defence by transcription

Cell Host Microbe <http://doi.org/xmm> (2014)

Microorganisms are recognized by plants using membrane receptors sensitive to specific microbe-associated molecular patterns (MAMPs). This first line of defence produces multiple outputs, including the activation of a central MAP kinase cascade, and induces a massive transcriptional reprogramming.

Ping He, of Texas A&M University, and colleagues have found that during this response, two antagonistic pathways

modulate RNA polymerase II (RNAPII), a fundamental component of eukaryotic transcription. A genetic screen in *Arabidopsis* identified the phosphatase CPL3 as a negative regulator of the immune signalling network. CPL3 dephosphorylates residues on the long C-terminal domain (CTD) of RNAPII's largest subunit, altering the post-translational 'CTD code', which controls the recruitment of accessory proteins to orchestrate transcription. Although RNAPII is involved in global transcription, mutations in *CPL3* predominantly affect the expression of defence-related genes, making mutant plants more resistant to pathogens. The MAMP flg22 induces phosphorylation of CTD, suggesting the presence of an additional antagonistic pathway. Ping He and colleagues found two cyclin-dependent kinases that also counteract the effects of CPL3. These are substrates of MAP kinases previously implicated in plant immunity.

This work establishes RNAPII phosphorylation as a dynamic regulator of gene expression in the plant's response to microorganisms.

GT

GENETICS

Cucumber's bitter pill

Science **346**, 1084–1088 (2014)



© J.R. BALE/ALAMY

The bitter taste of cucumbers and squashes is due to cucurbitacins (CuCs), a class of triterpenoids involved in defence against herbivory. CuCs have been used in traditional medicine and possess cytotoxic and anticancer properties.

Yi Shang, of the Chinese Academy of Agricultural Sciences, and colleagues report a comprehensive genomic and biochemical study unravelling the pathway and regulatory mechanism underlying CuC biosynthesis. Through genome-wide association studies based on 115 cucumber lines, they mapped the previously reported *Bi* locus to the gene, *Csa6G088690*. Cucurbitadienol synthase activity of this gene was validated using yeast expression and gas chromatography–mass spectrometry assays. Analyses of mutants, gene expression patterns and genotype–phenotype association revealed two transcription factors, *Bl* (encoded by *Csa5G156220*) and *Bt* (*Csa5G157230*), binding to the *Bi* promoter, regulating its expression and, consequently, bitterness in leaves and fruits, respectively. *Bt* diversity has been reduced during the domestication of cucumbers, indicating that human selection has acted on this gene. A variation at *Bt*'s promoter is critical for its expression under stress. The researchers identified seven cytochrome P450s and one acetyltransferase whose genes cluster or are co-expressed with *Bi*, and regulated by *Bl* and *Bt*, which catalyse three of the reactions converting cucurbitadienol to CuC.

The CuC biosynthesis and regulatory networks, consisting of nine genes regulated by two transcription factors, could prove fertile ground for the engineering of anti-tumour drugs.

JL

Written by Anna Armstrong, Jun Lyu, Christopher Surridge and Guillaume Tena.

PLANT-MICROBE INTERACTIONS

Microbiome remote control

New Phytolog. <http://doi.org/xmn> (2014)

That the community of microbes associated with an organism affects its physiology is well established. But the distance over which these effects extend is underappreciated.

Studying lignin production in barley, Alison Bennett, of the James Hutton Institute, UK, and colleagues found that the soil microbiome has a stronger effect above ground than below it. They grew wild-type barley plants, and mutants impaired in their ability to synthesize lignin, on soils inoculated with two different microbial communities — one from a fertile agricultural land, the other from a nutrient-poor sand dune. Comparisons across the resulting eighteen treatments — six plant types and three soils, including sterile soil — found no effect of the plants grown on their colonization by soil microbes. However, the soil microbiome explained 6% of the lignin variation in roots and 21% of the variation in shoots, the most statistically significant effect the researchers detected.

Adjusting the properties of plants by grafting onto different rootstocks is commonplace; Bennett *et al.* have shown what is living on the roots deserves as much consideration as the roots themselves.

CS