

not confirm the predictions of topological defect models (11–13), and interest in these models decreased dramatically.

These measurements did not rule out topological defects, however. Rather, they only implied that defects could not be the dominant source of CMB anisotropies. There has, in fact, been a lot of recent interest in the possibility that cosmic strings produced by superstring theory might be seen in the sky [see, e.g., (14) for a review] and might contribute a fraction less than 10% to the overall anisotropies in the CMB sky. The main signature of cosmic strings in the sky would be lines across which the temperature jumps by an amount proportional to the tension of the string (see the figure) (15). The imprint of cosmic textures would be a distribution of hot and cold spots in the sky whose angular diameter depends on the time when the textures collapse (spots of between 1° and 10° are expected, with the smaller spots being more numerous) (16, 17). In the case of textures, the temperature deviation of the hot or cold spots from the average temperature depends on the energy scale of the texture, which in turn tells us the temperature at which the phase transition that generated the textures occurred. An important point is that these features of topological defects in the CMB maps, which can easily be identified when analyzing

the actual maps, get washed out when analyzing the data in the usual way, namely decomposing the maps into angular components and plotting the amplitude of each angular component (or, in more technical terms, when calculating the angular power spectrum).

Since the release of the CMB data from the Wilkinson Microwave Anisotropy Probe (WMAP) (7), some apparent anomalies in the temperature maps have been pointed out. Cruz *et al.* focus on a cold spot of angular size roughly 5° that had previously been identified. They performed two sets of numerical simulations of sky maps, one based on fluctuations from inflation only (“Gaussian maps”), the other assuming Gaussian maps (with reduced amplitude) plus a temperature template produced by a cosmic texture. Based on a Bayesian analysis, the authors find a probability ratio of 2.5:1 favoring the texture plus Gaussian model over the Gaussian model. The authors discuss follow-up tests with which to further test the hypothesis that the observed cold spot is due to a texture.

If confirmed, the identification of a cosmic texture in the sky will have provided us with good evidence that a phase transition in matter occurred at an energy of roughly 10¹⁶ GeV, many orders of magnitude higher than energy scales that can be reached in terrestrial exper-

iments. The energy scale involved in the candidate texture is close to the elusive Planck scale, an energy where quantum gravity becomes important. A lesson to be learned from this work is that Planck-scale physics may well be testable in the very near future in cosmological observations.

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PLANT SCIENCE

The Power of the Pyramid

William J. Moar and Konasale J. Anilkumar

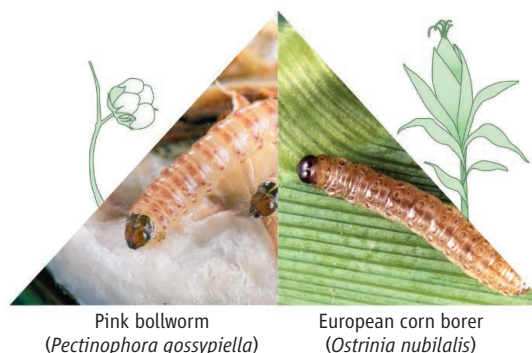
The use of crops that are genetically engineered to produce *Bacillus thuringiensis* (*Bt*) toxins has risen rapidly to more than 32 million hectares in 2006, resulting in substantially reduced use of insecticides and increased grower profit (1). However, with the increased use of *Bt* crops, such as corn and cotton (see the figure), comes the threat that target pests may develop resistance to these toxins. To date, there have been no reports of *Bt* resistance occurring in field populations of insects during the 11 years that *Bt* crops have been commercialized (2). Have we just been lucky, or have there been safeguards built in to the plants, and their use, to delay resistance development? To help answer this question, we need to know more about how *Bt* toxins kill insects. On page 1640 in this issue,

Soberón *et al.* (3) provide a breakthrough in understanding the mode of action of *Bt* toxins. The molecular details may be relevant for producing modified *Bt* proteins that are still toxic

Insects may be less likely to develop resistance when crops express proteins that have been modified to overcome resistance to other toxins.

to target insects, yet do not drastically affect the stability or host range of *Bt* proteins now in use, thus hopefully avoiding regulatory hurdles for registering novel insecticidal compounds.

In the United States, resistance-management strategies are mandated before *Bt* crops can be grown (4). First-generation *Bt* crops primarily use the “high dose plus refugia” option, whereby plants are engineered to express enough *Bt* protein to kill all target insects except for the very rare resistant individuals. These rare insects presumably have two copies (alleles) of the gene(s) that confer resistance. As for insects with recessive alleles for such genes, they are thought to be “diluted out” by susceptible insects from the refugia. However, even this strategy is not



Crop pests. Insects may develop resistance to plants that are genetically engineered to express *Bt* toxins or to insecticides containing *Bt* toxins. Pink bollworm (*Pectinophora gossypiella*) attack cotton (left) and the European corn borer (*Ostrinia nubilalis*) attack corn (right).

The authors are in the Department of Entomology and Plant Pathology, Auburn University, Auburn, AL 36849, USA. E-mail: moarwil@auburn.edu

expected to last forever, although the 11 years of utility (and still counting) for first-generation *Bt* crops already is remarkable (2).

One solution has been to engineer crops that express at least two toxic compounds that act independently, so that resistance to one does not confer resistance to the other. This approach, called gene pyramiding, became a commercial reality in 2003 with the introduction of Bollgard II, a transgenic cotton plant that expresses the original *Bt* protein, Cry1Ac, and a second *Bt* protein, Cry2Ab. The two proteins act independently in that they bind to different receptors in the insect's midgut. Of course, additional compounds for pyramiding are needed, but finding them is difficult. Each candidate must be encoded by a single gene (for transgenic plant development), must be toxic to the target pest, and must demonstrate a different mechanism of action from *Bt* toxin(s) already in the plant. Beyond those criteria, if the compound is novel, it must go through extensive regulatory testing.

So far, there are relatively few candidates for gene pyramiding in *Bt* cotton and corn for controlling target lepidopteran pests (5). One promising way to improve this is to determine how target pests develop resistance to specific toxins, and then modify these toxins so that resistance must occur in another manner. This would plausibly increase the time for resistance to develop and increase the life expectancy of insect-resistant *Bt* crops.

Soberón *et al.* confirm that active *Bt* toxins require additional enzyme cleavage before toxicity can occur (6, 7). Moreover, in the absence of a functional toxin receptor (cadherin) to properly bind the active forms of *Bt* toxin, cleavage does not occur. More importantly, Soberón *et al.* constructed modified *Bt* proteins (Cry1AbMod and Cry1AcMod) that were artificially "cleaved." These modified proteins were still toxic to insects that no longer expressed functional cadherin proteins, as well as to insects that were already resistant to native forms of the toxins (because they expressed mutated cadherin proteins that do not bind toxins). Thus, these modified proteins could potentially bolster a gene pyramiding scheme for delaying the development of insect resistance in crops.

One primary question arises: Can Cry1AbMod and Cry1AcMod be expressed at high levels in crops, and control target pests that have become resistant (due to mutations in cadherin) to the original *Bt* proteins they were derived from? Soberón *et al.* suggest that one possible reason Cry1AbMod and Cry1AcMod were slightly less toxic than native *Bt* toxins is that they could be less stable in the insect's midgut. If so, there might be concerns that they

won't be stable in plant cells and tissues, already one constraint in maintaining high *Bt* protein expression throughout the growing season (8). The knowledge that *Bt* toxins require additional enzymatic processing after binding to cadherin could hopefully lead to the design of a *Bt* protein that is specifically prone to enzymes in the midgut (without requiring cadherin binding), but not more susceptible to host plant enzymes.

Although *Bt* resistance has been the primary environmental concern with *Bt* crops in the United States, there are few laboratory-generated *Bt*-resistant insect model systems, and none have evolved from *Bt* crops. There are even fewer *Bt*-resistant model insects that have been selected for resistance to one particular *Bt* protein. For Cry1Ac, there are two such *Bt*-resistant insect models available in the United States—*Heliothis virescens* and *Pectinophora gossypiella*, both pests of cotton (9–11). Interestingly, and in support of the concept proposed by Soberón *et al.*, both *Bt*-resistant insects (and a third in China) (12) express altered cadherin. As more *Bt*-resistant insect model systems become available, it will be necessary to determine how universal mutations in cadherin are, and whether alterations in non-cadherin binding regions of *Bt* proteins could be made to delay other potential mechanisms of resistance.

As we continue to alter *Bt* proteins from their natural structure and composition, the question arises as to whether the selectivity or host range of these modified proteins will be altered as well. Clearly, this will need to be addressed, but the concept of designing *Bt* proteins to pyramid with other compounds to delay *Bt* resistance warrants further investigation.

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ECOLOGY

How Do Roots Interact?

Hans de Kroon

Plant roots recognize and respond to the identities of their neighbors.

The main function of plant roots is the acquisition of mineral nutrients and water from the soil. Roots do not encounter these belowground resources passively, but actively forage for nutrient hot spots (1) and avoid patches where root densities of competing neighbors are high (2). These responses can be driven by local nutrient concentrations in the soil (3). However, it is becoming increasingly clear that the world underground is even more complex and that elaborate root interaction mechanisms are at work.

Several studies have shown that roots respond to neighboring roots in a very specific

manner that depends on the identity of the neighbor (4–6). Root extension tends to be greater when roots grow into substrate containing "nonself" roots of a genetically different individual or a detached plant with the same genotype than when "self" roots of the same (physiological and genetic) individual are encountered. Dudley and File have recently shown that plants of the Great Lakes Sea Rocket (*Cakile edentula*) invested more biomass in fine roots when they competed with unrelated individuals than when they competed with siblings (7). This is one of the few cases (6, 8) in which root behavior has been shown to depend solely on the genetic identity of competing roots. Depending on the species, genotypic or physiological recognition processes appear to be involved in these root interactions.

The author is in the Department of Experimental Plant Ecology, Institute for Water and Wetland Research, Radboud University, 6525 ED Nijmegen, the Netherlands. E-mail: H.deKroon@science.ru.nl