

HIGHLIGHT ADVISORS

SEAN B. CARROLL

UNIVERSITY OF WISCONSIN,
USA

NANCY J. COX

UNIVERSITY OF CHICAGO, USA

RALPH J. GREENSPAN

THE NEUROSCIENCES
INSTITUTE, CALIFORNIA, USA

YOSHIHIDE HAYASHIZAKI

RIKEN GENOMIC SCIENCES
CENTER, JAPAN

PETER KOOPMAN

UNIVERSITY OF QUEENSLAND,
AUSTRALIA

LEONID KRUGLYAK

FRED HUTCHINSON CANCER
RESEARCH CENTER, USA

STANLEY MALOY

SAN DIEGO STATE UNIVERSITY,
USA

BARBARA MEYER

UNIVERSITY OF CALIFORNIA,
BERKELEY, USA

JOHN QUAKENBUSH

THE INSTITUTE FOR GENOMIC
RESEARCH, USA

NADIA ROSENTHAL

EMBL MONTEROTONDO, ITALY

NORIYUKI SATOH

KYOTO UNIVERSITY, JAPAN

MARC VIDAL

DANA-FARBER CANCER
INSTITUTE, BOSTON, USA

VIRGINIA WALBOT

STANFORD UNIVERSITY, USA

DETLEF WEIGEL

MAX PLANCK INSTITUTE FOR
DEVELOPMENTAL BIOLOGY,
GERMANY

PHIL ZAMORE

UNIVERSITY OF
MASSACHUSETTS, USA

LEONARD I. ZON

CHILDREN'S HOSPITAL,
BOSTON, USA

PLANT GENETICS

Capitalizing on natural potential

Crop plants can be improved by genetic modification or by selective breeding that makes the most of natural variation. Two recent papers turn to nature to show how disease resistance naturally arose in barley and how tomato yield can be increased by tapping into the natural variation present in wild species.

Loss of function of *Mlo*, which encodes a transmembrane protein, makes barley plants resistant to powdery mildew fungus. Only one such allele, *mlo-11*, has been recovered from wild species. As Piffanelli, Ramsay and colleagues show by haplotype analysis, this allele probably arose only once after barley domestication.

Mutagen-induced *mlo*-null plants are completely resistant to the fungal infection. By contrast, the naturally occurring *mlo-11* allele is only partially resistant, allowing a low level of fungal infection. This partial resistance is associated with a complex tandem-repeat array, which lies upstream of the gene. The authors show that the repeat is made up of a truncated *Mlo* sequence, including some of its 5' regulatory sequence. Because these tandem repeats are transcribed and their removal restores susceptibility to fungal infection, the authors propose that the resistance is probably due to transcriptional interference at this locus.

As Piffanelli, Ramsay and colleagues uncover a new way of generating resistance (artificially induced resistance is usually a result of mutations in the coding sequence or at

the splice junctions), Gur and Zamir tap into natural biodiversity of the tomato family to maximize the yield of the crop. In a complex and lengthy breeding experiment, the authors show that it is possible to incorporate favourable quantitative trait loci from a wild species into genetic backgrounds of cultivated varieties to achieve increased crop yields. Although a single introgression is unlikely to produce significant improvements, they find that combining a number of independent introgressions into a single genotype can have a significant effect.

Gur and Zamir point out that the effectiveness of introgression indicates that alleles similar to those in the wild species are not present in the

cultivated varieties; long-term breeding has reduced the natural biodiversity of these varieties. The same of course applies to other crop plants, such as rice, wheat and soybeans; this indicates that — especially in light of the controversies surrounding genetic modification — for some traits at least, we are well-advised to explore natural variation first.

Magdalena Skipper

References and links

ORIGINAL RESEARCH PAPERS Piffanelli, P. *et al.* A barley cultivation-associated polymorphism conveys resistance to powdery mildew. *Nature* **430**, 887–891 (2004) | Gur, A. & Zamir, D. Unused natural variation can lift yield barriers in plant breeding. *PLoS Biol.* **2**, e245 (2004)

WEB SITES

Ralph Panstruga's laboratory: <http://www.mpiz-koeln.mpg.de/~panstrug/>

Paul Schulze-Lefert's laboratory: http://www.mpiz-koeln.mpg.de/schleif/PSL_webpage.html

