HIGHLIGHTS

HIGHLIGHTS ADVISORS

KONRAD BASLER

UNIVERSITY OF ZURICH,
SWITZERLAND

WENDY BICKMORE

MRC HUMAN GENETICS UNIT,
UK

EWAN BIRNEY

EUROPEAN BIOINFORMATICS
INSTITUTE, UK

PEER BORK

EMBL, GERMANY

SEAN B. CARROLL

UNIVERSITY OF WISCONSIN,
USA

ADAM EYRE-WALKER

UNIVERSITY OF SUSSEX, UK

JANE GITSCHIER

UNIVERSITY OF CALIFORNIA,
SAN FRANCISCO, USA

SARAH HAKE

UNIVERSITY OF CALIFORNIA,
BERKELEY, USA

PETER KOOPMAN

UNIVERSITY OF QUEENSLAND,
AUSTRALIA

LEONID KRUGLYAK

FRED HUTCHINSON CANCER
RESEARCH CENTER, USA

GAIL MARTIN

UNIVERSITY OF CALIFORNIA,
SAN FRANCISCO, USA

BARBARA MEYER

UNIVERSITY OF CALIFORNIA,
BERKELEY, USA

TOSHIHIKO SHIROISHI

NATIONAL INSTITUTE OF
GENETICS, JAPAN

KEN WOLFE

UNIVERSITY OF DUBLIN,
IRELAND

RICHARD YOUNG

MASSACHUSETTS INSTITUTE
OF TECHNOLOGY, USA

PLANT GENETICS

Evolving mate recognition

Positive selection for genetic divergence is a well-known mechanism for driving speciation. One way to achieve this is to select for variation at loci that determine mate recognition — for example, at proteins that allow gametes of one species to specifically recognize each other. By analysing the proteome of *Arabidopsis thaliana*'s pollen coat, researchers have now found that the proteins that help pollen stick to a flower's stigma might also function as such mate-recognition molecules. Furthermore, the genomic arrangement of these genes provides new clues as to how speciation in flowering plants might occur.

Mate-recognition molecules must adapt to match the evolution of their target molecules. This requirement is likely to give them characteristic features, such as above average levels of polymorphism, and a genomic arrangement that facilitates allelic diversification, such as gene clustering. When Mayfield *et al.* analysed *A. thaliana*'s large pollen-coat proteins, they discovered that most are encoded by genes that reside in two genomic clusters. One cluster encodes six lipases, two of which are present in the pollen coat; the other encodes six oleosins, five of which are in the pollen coat. These proteins possibly determine the composition and size of the lipid droplets that coat pollen grains.

On closer analysis, the oleosin gene cluster showed some interesting features. Whereas exon 1 encodes a consensus oleosin domain in each gene, exon 2 varies considerably between

genes and contains a repetitive motif. In strains of *A. thaliana* collected from different geographical regions, Mayfield *et al.* found that insertions and deletions predominantly occurred in exon 2, often altering the number of repeats. Furthermore, all six genes were functional in these strains, indicating that their presence is selected for and that their exon-1 functional domain is tightly maintained, whereas exon 2 undergoes divergence.

If all these genes are required as a recognition haplotype, they should all be present in a related plant species but as divergent alleles. Mayfield *et al.* confirmed this in a distant relative of *A. thaliana* — *Brassica oleracea*, in which the oleosin cluster remains intact and the features of exons 1 and 2 are conserved, but the amino-acid identity between the two species'

oleosin genes is only ~50% and only in exon 1, despite conservation of function. This is considerably lower than the 85% amino-acid identity seen in the conserved genes in the syntenic regions that flank the cluster. Such small accumulated variations across these clusters, the authors suggest, might lead to speciation.

How these proteins function to maintain self recognition has yet to be resolved, but one way to test whether they confer species specificity will be to transfer such haplotypes between species.

Jane Alfred

References and links

ORIGINAL RESEARCH PAPER Mayfield, J. A. *et al.* Gene families from the *Arabidopsis thaliana* pollen coat proteome. *Science* **292**, 2482–2485 (2001)

WEB SITE Daphne Preuss' lab

Courtesy of Gregory M. Zinkl, University of Chicago, USA. Pollen grains are shown in pink.