# HIGHLIGHTS

#### **HIGHLIGHTS ADVISORS**

#### KONRAD BASLER

UNIVERSITY OF ZURICH, SWITZERLAND

# WENDY BICKMORE

MRC HUMAN GENETICS UNIT, UK

# PEER BORK

EMBL, GERMANY Steve Brown

### MRC MAMMALIAN GENETICS

UNIT, UK SEAN B. CARROLL UNIVERSITY OF WISCONSIN,

#### USA IANAN EPPIG

THE JACKSON LABORATORY, USA

# ADAM EYRE-WALKER

UNIVERSITY OF SUSSEX, UK CLAIRE M. FRASER

THE INSTITUTE FOR GENOMIC RESEARCH, USA

### YUJI KOHARA

NATIONAL INSTITUTE OF GENETICS RESEARCH, JAPAN

PETER KOOPMAN UNIVERSITY OF QUEENSLAND, AUSTRALIA

#### LEONID KRUGLYAK

FRED HUTCHINSON CANCER RESEARCH CENTER, USA **ROB MARTIENSSEN** 

COLD SPRING HARBOR LABORATORY, USA

GAIL MARTIN UC SAN FRANCISCO, USA

BARBARA MEYER UC BERKELEY, USA

## LAP-CHEE TSUI

THE HOSPITAL FOR SICK CHILDREN, CANADA

KEN WOLFE UNIVERSITY OF DUBLIN,

IRELAND RICHARD YOUNG

MASSACHUSETTS INSTITUTE OF TECHNOLOGY, USA

### TECHNOLOGY

# A bigger needle in a smaller haystack

For many decades, fruitfly chemical mutagenesis has followed a standard protocol: collect some flies, feed them a mutagen (such as EMS), select among their progeny those with a phenotype of interest, then breed and study the chosen few.

There are obvious shortcomings to this approach. If the aim is to mutate a specific gene sequence an increasingly common occurrence now that the Drosophila melanogaster genome sequencing project is complete — then the traditional approach requires sorting through thousands of mutagenized flies, to recover perhaps only a handful of mutations in the selected gene. A more reliable method of selecting specific mutations has become urgent in flies, and Bentley et al. report an economical and time-efficient way to recover mutations in any gene of interest.

The technique combines a classical chemical approach with a molecular detection technique. Flies are mutagenized in the traditional way, but the genomic region of interest is amplified from the mutagenized lines by PCR. The PCR product (or products) is then analysed by DHPLC (denaturing high performance liquid chromatography), which can resolve homoduplexes and heteroduplexes of DNA molecules. The presence of heteroduplexes suggests that the amplified region carries a point mutation.

But how well does it work? Bentley and colleagues tested the technique on the abnormal wing discs (awd) gene. Sixteen independent awd mutations were picked up from screening fewer than 5,000 flies. If this seems like a lot of flies, then consider that an average screen would recover mutations at a rate of one in several thousand flies. Because the DHPLC method identifies mutations irrespective of whether the mutation causes a phenotype (typically the result of a loss-of-function mutation), an allelic series of mutations can be obtained. In the case of awd, both loss-of-function and dominant alleles were found and will be valuable for studying protein function.

By tweaking the mutagenesis protocol, the new detection method should be just as useful for recovering mutations on other chromosomes and, indeed, it can also be extended beyond *Drosophila* to other genetically tractable organisms. A modified version of the technique has already been applied to *Arabidopsis* and to mouse embryonic stem cells.

For Drosophila, the snag lies in having to extract and analyse DNA from individual flies. Such problems should be ironed out, because clever shortcuts — such as pooling flies before PCR are expected to make the technique easier, quicker and cheaper.

# Tanita Casci Control Control

EB SITE Charles Dearoit's lab

