TECHNOLOGY

A fertile pursuit of sterility

Whether it is aphids or earwigs, wasps, spiders or cockroaches, most of us have a hate-list of pests we would happily have disappear from the planet. But, facts get in the way of our dreams. Insect pests in particular — which damage crops and transmit deadly diseases to humans and animals — are notoriously difficult to wipe out. The non-specificity of pesticides, as well as the cost of counteracting recurrent drug resistance, has made the chemical line of attack increasingly unpopular. A more economical and ecologically friendly strategy has been to release sterile insects into the wild. Unfortunately, despite its success, this sterile insect technique (SIT) isn't perfect — the ionizing radiation that sterilizes also reduces competitiveness in the wild. By developing a transgene-based method for sterilizing insects — in this case, for *Drosophila* — Carsten Horn and Ernst Wimmer have now built on the virtues of SIT while increasing its effectiveness.

Of the various ways of interfering with the reproduction of pests, the authors chose to engineer males whose genetic make-up caused them to produce lethal embryos. The strategy is conceptually simple: the flies to be released would be homozygous for a dominant-lethal gene that is active only in embryos. As the lethal effector, they chose an allele of the pro-apoptotic gene *hid*, the expression of which was controlled by the regulatory elements of the embryo-specific *sry-α* gene. The whole expression system was made conditional by using the tetracycline-controlled transactivator system: *hid* transcription is shut down in the presence of tetracycline, and so the laboratory flies can be reared unharmed by the lethal product of *hid* through adding the drug to their food. In the wild, where there is no tetracycline, the *hid* transgene is expressed and so can do its deadly deed.

The theory behind the new method translated well into practice: lethality occurred efficiently and was restricted to embryos. When a ninefold excess of sterile males was used, the transgene did not greatly affect the animals' competitiveness for mates in laboratory experiments, and the progeny from the competitive matings was reduced by nearly 90%.

In addition, although the system was established and tested in *Drosophila*, all the constructs, selectable markers and genes used in this study should be transferable to most other insect species — such as moths and butterflies — for which germline transformation is possible. As the SIT technique often works more effectively if only males are released, one plan is to aid the sex sorting of the engineered strain by integrating this transgenic method with a similar one that systematically kills adult females.

Transferring the new SIT technique from the bench to the field might take some time, but with luck it will give pests a much tougher bone to chew.

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References and links

ORIGINAL RESEARCH PAPER Horn, C. & Wimmer, E. A. A transgene-based, embryo-specific lethality system for insect pest management. *Nature Biotechnol.* **21**, 64–70 (2003)

IN BRIEF

GENOMICS

An active DNA transposon family in rice.

Jiang, N. *et al. Nature* **421**, 163–167 (2003)

The plant MITE *mPing* is mobilized in anther culture.

Kikuchi, K. *et al. Nature* **421**, 167–170 (2003)

Mobilization of a transposon in the rice genome.

Nakazaki, T. *et al. Nature* **421**, 170–172 (2003)

These three papers report the discovery of a family of active miniature inverted-repeat transposable elements (MITEs) in rice, which the authors call *miniature Ping* (*mPing*). This is an important finding as *mPing* is the first active MITE to be identified in any organism and the first active DNA transposon to be found in rice. A key feature of this transposon is that it reinserts with high frequency into low-copy coding regions of the rice genome. *mPing* mobilisation appears to be induced by stress such as gamma-radiation or cell-culture and relies on transposase activity provided *in trans*, probably to varying degrees by the related DNA transposons *Ping* and *Pong*. *mPing* might be suitable for use in developing gene-tagging programmes in rice. Such a programme could lead to the identification of genes controlling economically important rice traits and, therefore, facilitate the improvement of rice cultivars.

HUMAN GENETICS

Genetic structure of human populations.

Rosenberg, N. A. *et al. Science* **298**, 2381–2385 (2002)

The pattern of selection and migration of our ancestors is recorded in our DNA. In the largest survey of its kind, the authors have genotyped 1,056 individuals from 52 populations by using 377 autosomal microsatellite markers. Using a statistical analysis that clusters individuals solely on the basis of their genetic similarity, the authors were able to assign the individuals sampled to the five main geographical regions, and to subclusters that often corresponded to smaller populations. This work also confirms that most genetic variation exists within populations (93–95%) rather than between populations (3–5%).

BIOINFORMATICS

Modeling the percolation of annotation errors in a database of protein sequences.

Gilks, W. R. *et al. Bioinformatics* **18**, 1641–1649 (2002)

Functional annotation of protein databases often relies on sequence homology, the functional annotation of which might have also been determined on the same basis. Gilks *et al.* refer to this possible chain of misannotations as 'error percolation' and develop a way to model the annotation quality that clearly shows that this iterative approach quickly leads to decreased database quality. The authors use this as a starting point to build a scoring mechanism to qualitatively evaluate homology-based annotation.