



TOUCHING BASE

QUESTIONS? THOUGHTS? IDEAS?
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Mutant of the Month

Al Hershey identified the *rII* mutant of bacteriophage T4 in 1946. It was Seymour Benzer's experiments in the 1950s, however, that conferred iconic status on December's MoM. The T-even bacteriophages (T4 shown here surrounding a microcolony of *Escherichia coli*) can inhibit bacterial lysis if superinfected. The *rII* is a host-range mutant and yields altered plaque morphology on the B strain of *E. coli*. It is also unable to grow on the K strains. In Benzer's *rII* tour de force (*Proc. Natl. Acad. Sci. USA* 41, 344–355; 1955), he exploited these mutants through simple crosses and selection to answer fundamental questions related to the fine structure of the gene (any gene), as well as its divisibility by recombination. In so doing, he contributed to the founding of molecular genetics through an approach that resounds to this day, a half-century later. **AP**

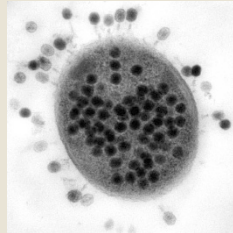


Photo courtesy John Wertz

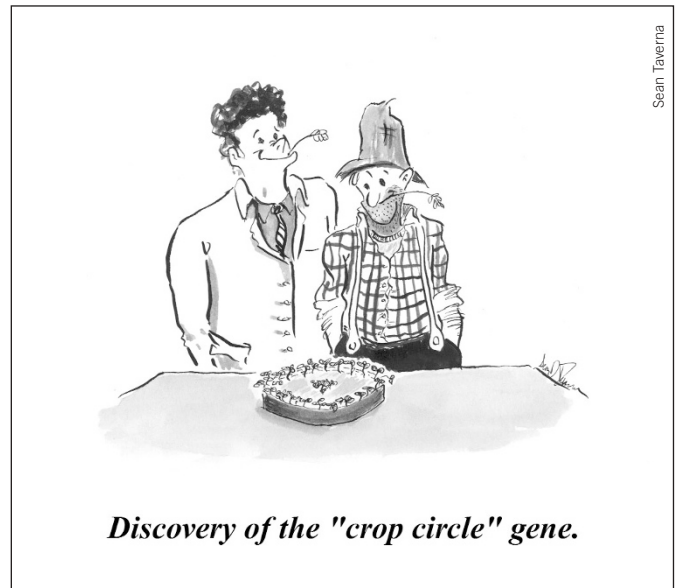
Mining the cancer transcriptome

Given that cancers arise in different tissues with multistep mutational histories and different cell biology, are there any common features of their programs of gene expression? Conversely, are there sets of genes whose expression is associated with particular tumor types? Examples of both were found by Rhodes *et al.* (*Proc. Natl. Acad. Sci. USA* 101, 9309–9314; 2004), who applied a statistical comparison called comparative meta-profiling to the existing transcription profiles of a number of cancers versus their matched normal tissue controls. Interpreting sets of genes that comprise statistically robust 'meta-signatures' will require the systematic application of a considerable amount of biological insight. The cancer literature needs to be interrogated for independent evidence supporting differential gene expression, and biochemical pathway information may be required to make sense of the relationships between the genes identified (*e.g.*, The Cancer Module Map; *Nat. Genet.* 36, 1090–1098; 2004). With so many types of information to be incorporated, hypothesis generation and testing requires a convenient common platform on which to work. That is why the Oncomine database (<http://www.oncomine.org>) and associated search tools were developed in a collaboration between researchers at the Institute of Bioinformatics in Bangalore and the University of Michigan. The site requires registration and is free to academic users. **MA**

Touching Base written by Myles Axton, Emily Niemitz, Alan Packer and Kyle Vogan

Arabidopsis 2010

The National Science Foundation recently awarded \$2 million to fund the Arabidopsis 2010 project, which aims to assemble the regulatory networks controlling development of *Arabidopsis thaliana*. This project brings together the strengths of four *Arabidopsis* research groups: the Grotewold, Lamb and Davuluri laboratories at Ohio State University and the Read laboratory at California State University, San Marcos. The goals of the Arabidopsis 2010 project are to identify direct targets of 31 transcription factors involved in flower development, validate target genes and determine transcription factor binding sites. The data will be integrated into the Arabidopsis Gene Regulatory Information Server (AGRIS), housed at Ohio State University, which contains two databases, the *A. thaliana* cis-regulatory database and the *A. thaliana* transcription factor database. These databases provide a publicly available web-based resource of promoter sequences, transcription factors and target genes. Materials developed through the project will be available through the Arabidopsis Biological Resource Center at Ohio State University. The list of selected transcription factors is available at the AGRIS website (<http://arabidopsis.med.ohio-state.edu>). **EN**



Discovery of the "crop circle" gene.

Allergen-free cats?

Allerca, a California-based biotech company, has announced plans to market a breed of hypoallergenic cats, the first in a line of so-called 'transgenic lifestyle pets'. They plan to use short interfering RNA (siRNA) technology to knock down expression of Fel d1, the most common protein allergen found in cat saliva and skin. Although they've yet to produce their first prototype, the company anticipates "the birth of these first special kittens" in 2007. And they're accepting reservations now: a \$250 deposit entitles you to be among the first to own one of these hypoallergenic felines (final price tag, \$3,500). Skeptics point out that the siRNA approach has yet to be validated in cats, and critics argue that eliminating Fel d1 won't remove all potential allergens and could have detrimental effects on the cat's health. But with demand for the designer pets expected to be high, the company should have little trouble finding willing scientists to assist them in their venture. **KV**