TOUCHING BASE

QUESTIONS? THOUGHTS? IDEAS?
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Mutant of the Month

Photo courtesy of Purdue University

Mendel was able to formulate his laws of heredity because he studied traits that bred true. Since then, concepts of genetic inheritance have been gradually stretched to make room for things such as transposons and imprinted traits. But the *Arabidopsis hothead* mutant has the potential to push the laws of Mendelian inheritance to the breaking point. That is because it has the amazing ability to revert, at relatively high frequency, back to an ancestral state. This phenomenon isn't limited to mutations at the *HOTHEAD* locus; in mutant plants, other genomic markers also revert to an ancestral state, implicating some form of genomic instability. But what is the template and mechanism that allows specific reversion to ancestral alleles? Robert Pruitt and colleagues, who identified and characterized mutants at the *HOTHEAD* locus (*Nature* 434, 505–509; 2005), put forward a model in which a cache of ancestral RNA sequence provides a template and loss of *HOTHEAD* function increases the frequency at which the template is used. But others have proposed scenarios involving gene conversion from short regions of homology within the genome, inheritance of archival DNA in plant meristematic cells and strong selection for rare revertant cells. ***EN***

Where are they now?

We tip our hats to former editorial colleagues David Gresham and Michael Stebbins for their recent publishing achievements. David Gresham, working with David Botstein, Leonid Kruglyak and colleagues at Princeton, developed an array platform enabling genome-wide detection of polymorphisms in yeast at single-nucleotide resolution and then applied the tool to identify DNA variants underlying a range of spontaneous mutants and experimentally evolved traits. A paper describing the work appears in *Science* (published online 9 March 2006; doi:10.1126/science.1123726). Mike Stebbins, following a different path, carried his science and publishing experience into the political arena, spending a year as a congressional fellow in the office of US Senate Minority Leader Harry Reid before moving into his current position as the Director of Biology Policy for the Federation of American Scientists. Mike has also been busy at the keyboard: his first book, titled *Sex, Drugs and DNA: Science's Taboos Confronted*, is due out in April from Macmillan and promises to offer lively opinions on a range of science-related topics. You can learn more about the work through the book's website (http://www.sexdrugsanddna.com). *KV*

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

"Sometimes, you get a new idea that is better than the old idea. It wouldn't be the first time I've done that."

—J. Craig Venter, on plans to engineer microorganisms that convert plant material into ethanol as a fuel source (as quoted in *The Washington Post*.)

The next big thing

In the wake of reports of the first attempts to generate proteome-scale human protein-protein networks, Marc Vidal has issued a call for a Human Interactome Mapping Project (*The Scientist* **20**; 47–51; 2006). Estimating that the human interactome consists of 300,000 interactions, Vidal calculates that the project could cost from $100 million to $1 billion. Using the Human Genome Project as a model for the internationally coordinated effort he envisions, he points out several issues to be addressed, such as agreements for data availability and development of navigational tools and measures of data quality. He also raises an important question faced by the proponents of the Human Interactome Mapping Project: how will completeness be measured? Compared with the central mandate of the Human Genome Project—to generate sequence with only four possibilities (A, G, C or T)—the Human Interactome Mapping Project has a non-trivial challenge in the definition of its scope. Vidal suggests that if 80% of all predicted genes are interrogated with at least one splice variant, with 80% sensitivity and specificity, the resulting data will be complete enough to convey the global properties of the human interactome. *EN*

Drosophila species genomes

The assembly, alignment and annotation (AAA, see http://rana.lbl.gov/drosophila/) of twelve related *Drosophila* species will probe animal genome evolution to a depth of 60 million years in graded steps. The first comparative assembly freeze is now available for the latest ten species. Most species have been sequenced to deep whole-genome coverage, assembled and subjected to a process of 'reconciliation' that makes use of length discrepancies between alternative assemblies. *D. persimilis* and *D. sechellia* have been sequenced to lower levels (3–4×) of coverage and the sequences assembled with the help of synteny to other species. *D. simulans*, which is to be used for polymorphism discovery, has been sequenced to 2.8× coverage in one strain and 1× coverage in six other strains. As sequence data is posted in advance of publication of a set of definitive papers to reference, the question arises of how to give appropriate credit to these projects. The coordinating web resources are just starting points. As the *Drosophila* species genome page of FlyBase emphasizes (http://species.flybase.net/), "Please cite genome project web sites or publications from them referring to the genome sequence." It would be advisable as well to track the sequencing, assembly, reconciliation and annotation process of any region of interest, so that credit can be given to those involved. If in doubt, ask them. *MA*