TOUCHING BASE

QUESTIONS? THOUGHTS? IDEAS?
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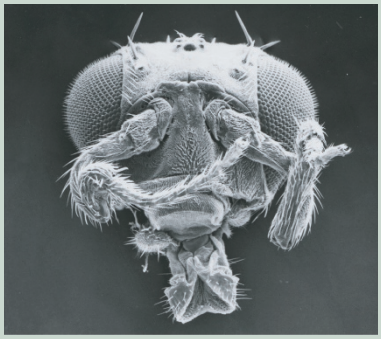
Mutant of the Month



Rudi Turner and FlyBase

This month we honor the spectacular *Drosophila melanogaster* mutant *Antennapedia*. Photos of the *Antennapedia* phenotype are frequently used to capture the interest of biology students (and with good reason—gain-of-function mutations cause a striking antenna-to-leg transformation, as shown above), but lessons learned from this and other homeotic mutations about mechanisms of segmentation and specification of segment identity should not be overlooked. On a basic level, the fact that appendages can be swapped implies that they are homologous and share a common origin. Molecular characterization of the function of homeotic genes, many of which encode transcription factors, has led to insights into the important role of regulation of gene expression in the control of development. And this knowledge is now being used to study evolutionary mechanisms of morphological divergence—quite a legacy for a mutant that at first glance looks like a sci-fi monster come true. ***EN***

ClinSeq Launched

The National Human Genome Research Institute recently announced the launch of a trans-NIH study, called ClinSeq, which aims to explore the use of individualized gene sequencing in a clinical setting. Led by Les Biesecker, the study will enroll 1,000 people, who will be evaluated for cardiovascular disease and will be followed for a number of years. In the pilot phase, 200–400 candidate genes for cardiovascular disease will be sequenced. In seeking to address the multitude of challenges that are likely to arise during clinical sequencing programs, from discernment of pathogenic variants to effective communication of results to participants, the investigators aim to develop the technological and procedural infrastructure necessary to implement clinical sequencing on a large scale. The insights that will come from this long-term study will be valuable to many in the medical genetics and genetic counseling communities, and for members of the research community, the insights into the relative contributions of rare and common variants will be greatly anticipated. *EN*

Touching Base written by Emily Niemitz and Kyle Vogan.

"I knew I was risking possible anxiety when I saw it. But it's much more [likely] that if I don't sleep at night it's due to thinking about Iraq rather than about my genome."

—James Watson, on being presented with a draft of his genome sequence (as quoted by The Associated Press)

Sporadic Traits

SNP, SNP, SNP, so passé
CNVs are here to stay
One FISH three FISH red FISH green FISH
Inversions too, if you wish
Mechanisms? Don't know how
But arrays in clinics here and now
Is recombination what we're after?
Base-pair changes are not always the answer!

J.R. Lupski and M.E. Hurles
(Inspired by Dr. Seuss)

iControlDB

As exemplified by the recent study from the Wellcome Trust Case Control Consortium (*Nature* **447**, 661–678; 2007), the use of shared controls across multiple diseases is a reliable and cost-effective strategy that can increase efficiency of large-scale genotype-phenotype association studies with minimal loss of power. Toward this end, Illumina has launched a new database, iControlDB (http://www.illumina.com/iControlDB), that makes freely available to researchers genome-wide SNP genotyping data from thousands of control samples, matched with information on age, gender and ethnicity. On the date of its launch, the site hosted data from more than 4,000 samples from The Children's Hospital of Philadelphia and 2,300 samples from the Feinstein Institute for Medical Research in Manhasset, New York. The database will continue to accept new submissions from registered users, subject to valid approval documentation and stringent quality control standards, and by the end of this year, iControlDB is expected to host data from more than 20,000 samples. Although the use of shared samples requires careful control measures to minimize potential sources of bias, the considerable savings in time and cost offer powerful incentives to incorporate this type of analysis into standard experimental designs. *KV*

"In the early days, databases were an adjunct to scientific publications and sequences were transcribed from the literature. Times have moved on. The databases are now the primary record for high-throughput science. We and our partners in Japan and the USA are custodians of that record, and proud of the long-standing collaboration which has kept all of the data available to scientists worldwide."

—EBI associate director Graham Cameron, on the occasion of EMBL-Bank's 25th anniversary in May 2007