TOUCHING BASE

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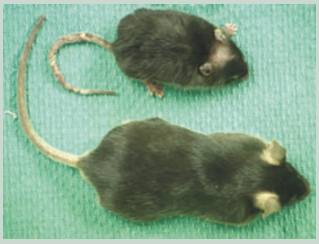
Mutant of the Month



Katherine Siminovitch

This month we revisit a mutant that first appeared in our pages in June of 1993; the *motheaten* mouse, first identified by Leonard Shultz at the Jackson labs (*J. Hered.* 66, 250–258; 1975). *Motheaten* mice were initially of interest for their immune deficiency and autoimmune phenotypes, and their name reflects their motheaten appearance which is caused by skin lesions leading to hair loss. The genetic defect underlying the motheaten phenotype is a mutation in the *Ptpn6* gene, which encodes the SHP-1 protein tyrosine phosphatase. While the original *motheaten* allele generates no SHP-1 activity, and the mice die with 2 months of birth, a less severe allelic mutation that produces a reduced amount of SHP-1 activity, called *viable motheaten*, was subsequently identified. *Motheaten* mice were initially used to elucidate the role of signal transduction pathways in hematopoietic cells, but these mice have subsequently proven useful for studying the physiological roles of signal transduction in other systems as well. For example, recent studies have shown that *motheaten* mice develop retinal degeneration (*Invest. Opthalmol. Vis. Sci.* 47, 1201–1209; 2006), indicating an essential role for SHP-1 in retinal homeostasis, and that SHP-1 negatively regulates insulin signaling (*Nat. Med.* 12, 549–556; 2006), indicating a role for SHP-1 in glucose homeostasis. If only all mutant mice proved so useful for elucidating fundamentally important biochemical mechanisms. ***EN***

Public housing

Most everyone would agree that knockout mice are a critical resource for biomedical research, and yet of the 4,000 or so lines described in the literature, fewer than 1,000 are available from public repositories. The others are maintained by individual labs, putting added strain on crowded university animal facilities, and slowing down the distribution of these mice to the wider community. As part of the Knockout Mouse Project (KOMP), which aims to mutagenize every gene in the mouse genome, the NIH is committed to expanding space in centralized repositories. The latest step came in the recent announcement of $800,000 in new grants to the University of California, Davis and the University of Missouri to house approximately 300 additional lines. The particular knockouts that will be included will depend on input from interested researchers. James Battey, director of the Trans-NIH Mouse Initiative, commented, "Getting these valuable models into the hands of a wide range of researchers will serve to accelerate our efforts to develop new strategies for understanding and treating human disease." Later this summer, the NHGRI will award cooperative agreements totaling $50 million over 5 years as part of the next stage of KOMP. *AP*

"While we understand and respect the sincerely held beliefs of those who oppose this research, we are equally sincere in our belief that the life-and-death medical needs of countless suffering children and adults justifies moving forward with this research."
—Harvard University President Lawrence Summers, on the university's decision to use private research funds to develop therapeutic stem cell lines from human embryos created by somatic cell nuclear transfer.

Conover Talbot Jr.

Getting it right

Under the guidance of HUGO president Leena Peltonen-Palotie, the 11th annual Human Genome Meeting took place between May 31st and June 3rd in Helsinki, Finland. In addition to the full scientific program, researchers were able to listen to Finland's acoustic roots band Värttinä (pictured), who combine ancient Finnish runo poetry with close Finno-Ugric harmonies. As always, we and the HUGO Gene Nomenclature Committee (HGNC) were on hand to help prevent communication between genome-based scientists from becoming a Babel-like chaos. The HGNC awarded prizes of subscriptions to *Nature Reviews Genetics* and to this journal for the two posters at the meeting that made correct use of the largest number of approved gene symbols. The winners were J. Ollila of the Division of Biochemistry, University of Helsinki and V.M. Kavsan of the Institute of Molecular Biology and Genetics, Kiev, Ukraine. The HGNC (http://www.gene.ucl.ac.uk/nomenclature/) is currently asking for your help and opinions: for instance, should they be responsible for assigning gene names for genomes without their own nomenclature committees? *MA*

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