



TOUCHING BASE

QUESTIONS? THOUGHTS? IDEAS?
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Mutant of the Month

With the recent publication of the genome sequence of the honeybee, *Apis mellifera*, this is a good time to highlight insights into the biological basis of social behaviors that can



Zachary Huang, <http://www.beatography.com>

come from synergies between research on social models, like the honeybee, and genetic models, like *Drosophila*. In *Drosophila*, naturally occurring allelic variants in the *foraging* gene, which encodes a cGMP-dependent protein kinase (PKG), result in 'sitters' and 'rovers'; the latter move over a larger area to collect food. Whereas fruit flies live a mostly solitary life, and feeding is an individual behavior, foraging in honeybees is a social behavior, since its purpose is to feed the colony. The onset of foraging behavior is socially regulated by the colony through pheromones. Drawing an analogy between foraging behavior in flies and bees led to a collaborative effort by Marla Sokolowski, Yehuda Ben-Shahar and Gene Robinson to determine if the *foraging* gene is involved in the social foraging behavior of bees. They determined that foraging bees have higher levels of *foraging* expression than bees working in the hive and that treating bees with cGMP to activate PKG causes foraging behavior. In addition, the onset of pheromone-mediated foraging is associated with elevations in *foraging* expression. This example highlights how the availability of the genome sequences of these diverse model systems will aid in the integration of different scientific fields into an emerging field of sociogenomics. **EN**

DNA database 'mission creep'

The United Kingdom's National DNA Database is the largest forensic DNA database in the world, containing samples from more than three million individuals. When launched in 1995, it was proposed as a way to identify repeat offenders more easily through matches in the database. Recent stories, however, have quoted Alec Jeffreys as wondering whether the database has grown in size to the point where it threatens the civil liberties of individuals who have come to the attention of the police for any reason, or whether it might be biased against young males and ethnic minorities. Recent changes in British law mean that anyone who has been arrested for a 'recordable offense' has a sample taken for the database, even if the person is not subsequently charged

Touching Base written by Orli Bahcall, Emily Niemitz, Alan Packer and Kyle Vogan.

with a crime. Jeffreys sees this as a sort of 'mission creep', and the Nuffield Council on Bioethics has announced that it will ask for public comment on the scope of the database and whether there is sufficient ethical oversight. **AP**

Contest for free sequencing

Roche Applied Science recently announced a contest with a prize of 1 gigabase of sequencing. The contest rules stipulate that the program is open to scientists in the USA and Canada, and the winner will be selected by an external panel of scientific experts. The contest will consider a wide range of projects with the aims of genome sequencing or resequencing, metagenomics, deep sequencing to detect variations, small RNA sequencing or transcriptome sequencing. Paired-end sequencing will be supported. The lucky winner will send samples to Roche, which will perform the sequencing runs on a new generation of sequencers developed by 454 Life Science Corporation. The winner will be responsible for the experimental design, data analysis and interpretation. The application calls for a 1,000-word proposal, and the winner will be announced in January 2007. May the best sequencing project win! **EN**

Serious nomenclature

Sue Povey, chair of the Human Genome Organization (HUGO) Gene Nomenclature Committee (HGNC), recently announced that the committee is renaming about ten genes that have potentially offensive names. This list primarily includes genes such as *fringe* and *hedgehog* that were discovered and named initially in *Drosophila*; subsequently, these names were used for homologs in other organisms. In some cases, multiple vertebrate homologs have been named with adjectives, such as lunatic fringe. This effort was prompted when Mark Ludman, a medical geneticist at Dalhousie University in Halifax, Canada, and his colleagues approached the HGNC with concern over referring to these genes in humans, citing an example of explaining to a patient that they had a mutation in lunatic fringe. In response, the HGNC conducted a survey to determine which genes to include and have now decided to change the potentially offensive gene names, while retaining the gene symbols. Previous gene names and aliases will be retained for reference. **OB**

Mouse resequencing milestone

Last month marked the completion of a joint effort between the US National Institute of Environmental Health Sciences (NIEHS) and Perlegen Sciences to collect resequencing and SNP discovery data for 15 commonly used inbred mouse strains. The project website, hosted by Perlegen (<http://mouse.perlegen.com/mouse/index.html>), includes basic information on the 15 selected strains and details on the array-based platform used for resequencing. The website also includes a simple browser for visualizing the strain variation, mapped onto the mouse reference C57BL/6J NCBI sequence build 36. The project's efforts contribute to the expanding list of genetic variation resources for the mouse community, which are powerfully complemented by a growing body of data-rich phenotypic information on individual inbred mouse strains (<http://www.jax.org/phenome>). The SNP data generated through the Mouse Genome Resequencing and SNP Discovery Project are also publicly available through dbSNP (<http://www.ncbi.nlm.nih.gov/SNP/>). **KV**