



TOUCHING BASE

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Mutant of the Month

This month's mutant, *prometheus*, derives its name from the character in Greek mythology who, as punishment for stealing sacred fire and bestowing it upon mortal men, was chained to a rock and sentenced to the daily torment of having his liver eaten by an eagle. Identified

by Elke Ober, Didier Stainier and colleagues (*Nature* 442, 688–691; 2006) through a genetic screen for factors involved in endodermal organ development in zebrafish, *prometheus* (*prt*) mutants (right) show a profound but transient defect in the specification of the liver anlage. For comparison, the liver primordium in a wild-type embryo (left) is shown in red (upper right-hand corner); the gut endoderm is marked in green. Mosaic analyses showed that the *prt* gene product acts non-cell autonomously in the lateral plate mesoderm to promote liver specification in the adjacent hepatic primordium. *prt* encodes a homolog of *Wnt2b* expressed bilaterally in the mesoderm adjacent to the liver-forming region. Similar expression patterns have been reported in mouse and chick embryos, suggesting that *Wnt2b* homologs could have a conserved role in specifying the liver primordium in all vertebrates. **KV**

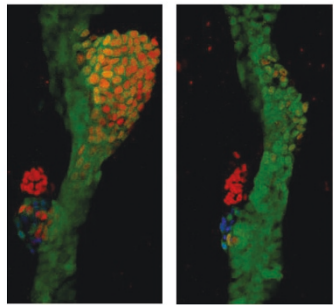


Image courtesy of Elke Ober and Didier Stainier

Sequencing diversity

The National Human Genome Research Institute (NHGRI) has recently announced a new list of organisms selected for sequencing. Among the targets chosen is the northern white-cheeked gibbon (pictured), representing the last branch of non-human primates not previously approved for whole-genome sequencing. The gibbon is of particular interest for its unusually high number of chromosome rearrangements relative to other hominoids. The NHGRI also plans to increase the density of coverage of seven mammals previously approved for low-density coverage, including the African savannah elephant and the domestic cat. It also announced plans to obtain the genomic sequence of five dermatophyte fungi, which cause human fungal diseases, and to sequence up to 50 strains of *Saccharomyces cerevisiae*. And, in a project aiming to shed light on the origins of multicellularity, the NHGRI has targeted ten unicellular protists related to the single-celled ancestor of fungi and animals. This follows a statement made earlier this year in which the NHGRI announced a project to identify structural variants in the human genome using a fosmid paired-end sequencing strategy. The proposal for the structural variation project includes genotyping identified variant regions in the full set of HapMap samples along with deep sequencing of a selected set of variant regions. The earlier announcement from NHGRI also included selection of three primates for high-density genomic sequencing—the rhesus macaque, the marmoset and the orangutan—along with the selection of eight mammals for low-density draft coverage, including the horse and the dolphin. **EN**



Photo courtesy of Jim Zuckerman

Gates Foundation refocuses with growth

In June, Warren Buffett announced a donation of \$31 billion to the Bill and Melinda Gates Foundation, doubling the assets of the Foundation. This came with an added stipulation that Buffett's contributions would be given annually and that each year's contribution must be spent in full that year. Since then, the Gates Foundation has considered how to manage a near-doubling of its annual distributions, to approximately \$3 billion. In order to handle this increase, the Gates Foundation is planning to double its staff to about 600 people and is considering reorganizing as the organization scales up to meet this latest challenge. The Foundation also plans to add a new area of global development in developing countries, encompassing financial and agricultural development. These projects came out of a review on how to expand the Foundation's operations in new directions that complement its current focus on global health issues. In their keynote address at the 2006 AIDS conference in Toronto this past month, Bill and Melinda Gates highlighted their commitment to the AIDS-related focuses of the Foundation, as evidenced by an additional \$500 million donation to the Global Fund to Fight AIDS, Tuberculosis and Malaria. They stressed the importance and urgency of efforts directed at HIV prevention and vaccine development. **OB**

Western Australia bets on a biobank

ABC Science Online reports that researchers led by Lyle Palmer at the University of Western Australia are proposing to create the world's biggest database of genetic and epidemiologic information. Palmer and colleagues hope to collect blood samples from two million volunteers and link genetic information with extensive health assessments of these individuals. "The obvious thing to do... is to study the whole population," says Palmer. The Western Australia Genetic Epidemiology Resource (WAGER) (<http://www.wager.org.au>), established in 2004 as a center for integrating health records and other types of data, will supply the infrastructure for the project. Palmer notes that Western Australia is ideally suited to a project of this scale, given its relatively isolated yet outbred population, large families, extensive existing health records, and an established DNA bank, based in Perth. WAGER itself already links family health records with longitudinal data, and efforts are being made to extend genealogical links back to 1840. **AP**

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