TOUCHING BASE

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Mutant of the Month

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This month we highlight the mouse *inversus viscerum (iv)* mutant. Originally described in 1959 by Katherine Hummel and Dorothy Chapman at the Jackson Laboratory, this recessive mutation causes randomization of the orientation of the internal organs. The image above shows two young homozygous *iv/iv* pups; the milk-filled stomachs are visible through the translucent skin (the pup on the left has *situs inversus*). The *iv* mutation was identified as a mutation in the left-right dynein gene (*Lrd*), which encodes the microtubule-based motor ciliary dynein (*Nature* 389, 963–966; 1997). This mutation eventually helped establish that directional fluid flow at the embryonic node generated by cilia is critical for establishment of left-right asymmetry. *Lrd* has also recently been implicated in selective chromatid segregation, selective segregation of the 'older' DNA strands of a pair of chromosomes to daughter cells relative to the newly synthesized strands following semiconservative DNA replication. Mouse chromosome 7 undergoes selective chromatid segregation in specific cell types, such as embryonic stem and endoderm cells, and this is disrupted by knockdown of *Lrd* (*Science* 315, 100–101; 2007), suggesting that a microtubule-based motor mechanism is involved in this process. *EN*

Evidence-based conservation is an endangered species

Current genetic evidence used to register endangered species is insufficient, and standards of evidence need to be established, according to a recent survey by Silvia Fallon (*Conservation Biology* **21**, 1186–1195; 2007). The US Endangered Species Act provides protection to species and subspecies of wild animals and plants and 'distinct population segments' of vertebrate wildlife. Genetic distinctiveness is an increasingly popular criterion for deciding whether or not to provide legal protection to a putative taxonomic unit or population, but the effort expended on the genetic study is a strong determinant of whether or not a population receives protection. Listing decisions founded on genetic distinctions consistently had a greater amount of genetic data per marker type and used more markers. Only 37% of the population-level studies used microsatellites, which is not surprising, because probes often need to be established for each new organism under study. The number of individuals sampled from each unit ranged from 6 to 1,500, often without sufficient discussion of sampling statistics. Fallon recommends that genetic studies include markers from both the nuclear and mitochondrial genomes and that population-level studies include rapidly evolving markers such as microsatellites. Of course, conservation genetics currently makes use of neutral markers. If markers related to critical population adaptations and molecular markers of speciation itself become available, the regulatory landscape could change dramatically. *MA*

Written by Myles Axton, Orli Bahcall and Emily Niemitz

"As genomic research begins to touch more of us in our daily lives, it is essential that rigorous studies are undertaken to ensure that ethical, legal and social issues stemming from genetics and genomics are taken into consideration in the development and implementation of policies."

– Elizabeth Thomson, of NHGRI's ELSI Research Program.

ELSI centers for genetic research

Two new centers researching the ethical, legal and social implications (ELSI) of genetic research have recently been established by the National Human Genome Research Institute (NHGRI). The two new centers, part of NHGRI's Centers for Excellence in ELSI initiative, are located at the University of North Carolina at Chapel Hill and the University of Pennsylvania. These centers will each draw on interdisciplinary researchers from the fields of bioethics, clinical research, law, theology, policy and genetic research. Gail Henderson will lead the University of North Carolina at Chapel Hill's Center for Genomics and Society, and she plans to focus efforts on addressing ELSI issues unique to large-scale genomics studies and their impact on individuals, families and populations. Reed Pyeritz will lead University of Pennsylvania's Penn Center for ELSI Research and will focus on the ELSI issues arising from genetic technologies, particularly genetic testing, and how these issues are translated to patients, family members, doctors and insurers. *OB*

Annual Nobel haiku

Gene targeting wins
Stem cells go germline, happy
End of many tails

ENCODE goes full scale

The National Human Genome Research Institute (NHGRI) announced the next phase of the ENCyclopedia Of DNA Elements (ENCODE) project this past month. The initial pilot phase of the ENCODE project, which surveyed the functional landscape of 1% of the human genome, was reported in June of this year (*Nature* **447**, 799–816; 2007). The project will now be expanded to genome-wide coverage, with grants for this scale-up totaling $80 million over the next four years. The NHGRI has also announced grant recipients for additional pilot projects, including those on aspects of technology development and the establishment of a data coordination center. The data coordination center, which will collect and manage ENCODE data and access, will be led by Jim Kent (University of California Santa Cruz). Recipients of the ENCODE scale-up grants include Bradley Bernstein (Broad Institute), Gregory Crawford (Duke University), Thomas Gingeras (Affymetrix), Tim Hubbard (Sanger Institute), Richard Myers (Stanford University), Michael Snyder (Yale) and John Stamatoyannopoulos (University of Washington). *OB*