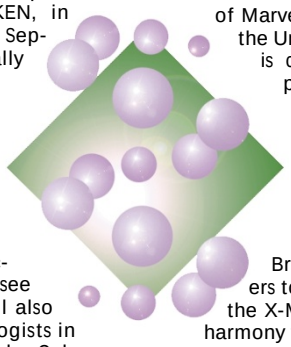
TOUCHING**base**

Autumn annotation



Two upcoming annotation jamborees promise to keep biologists off the streets until the new year. RIKEN, in Tsukuba, Japan, is hosting a meeting (28 August–8 September) of approximately 50 people to functionally annotate 20,000 full-length mouse cDNAs (see http://genome.rtc.riken.go.jp/FANTOM/). The acquisition of full-length clones was made possible by sequence analysis of 1 million cDNAs derived from tissues of the C57BL/6 mouse, in addition to several innovations, including one that reduces the secondary structure of mRNA during reverse transcription. The aim is to annotate according to ontologies recommended by the Gene Ontology Consortium (see *Nature Genet*. **25**, 25–29; 2000). The meeting will also host a much-needed discussion of the role of biologists in curating annotation, among other issues. Stateside, Celera Genomics is gearing up to annotate the human genome between the months of September and December. Whereas plans are preliminary as we go to press, slated for September is an assessment of the integrity and continuity of the sequence at hand. Predicted for October is an assessment of genome structure on a large scale. November's efforts, reckoned to be the most substantial in terms of bodies at monitors, will focus on gene families and genomic structure on a finer scale (for example, the distribution of repetitive elements), and December is dedicated to a comparison of the mouse and human genomes.

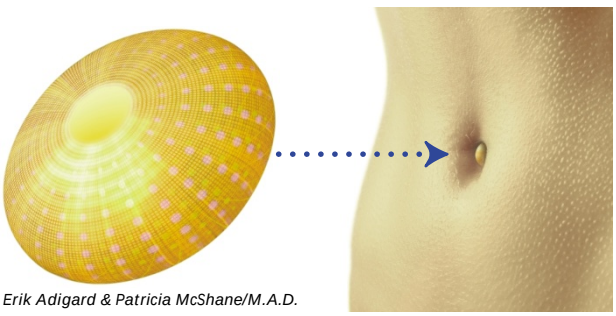
X-linked genophobia

The film adaptation of *X-Men*, conceived by Stan Lee (founder of Marvel Comics), has recently made its debut in theatres in the United States. For the purposes of the story, a 'mutant' is created by (macro)mutation, bestowing wondrous powers upon the individual—powers such as superhero strength, telepathy, instantaneous healing and ability to control the weather—without much by way of deleterious effects. (Many male mutants, however, sport truly grotesque facial hair.) The plot of *X-Men* centres on the efforts of two groups of mutants to be accepted by an uncomprehending and fearful humanity. The Brotherhood of Evil Mutants attempt to use their powers to force the world to accept their superiority, whereas the X-Men defend the masses in the hope that peace and harmony for all will eventually be achieved. By all accounts, the film remains true to the comics (which originated in the 1960s), but unfortunately, when it comes to the issue of mutation, all scientific credibility can be thrown to the wind. Never mind the question of how such massive mutations might have arisen so quickly, or the amusing contention that the next step in human evolution is a mutation-induced *Homo superior*. The film's assertion that an adult human could become a 'mutant' by the application of unspecified radiation, and that somehow this radiation would not affect 'natural' mutants, demonstrates a basic lack of understanding of fundamental scientific principles. But in a film in which the action careers from one cut-scene to another, the dialogue is dominated by groan-inducing one-liners and explosions occur frequently (at a volume that borders on overkill), science was probably the least—perhaps appropriately—of the producers' concerns. It seems a shame that such a depiction of the consequence of 'mutation' may so heavily influence public perception of a basic genetic process. But perhaps all will be explained in the sequel…'nuff said.

My kingdom for a genetic map!

Like Richard III on Bosworth Field, many today would give up just about anything for a horse. Yet, contrary to the desperate king of England, people seeking a mount have been and continue to be notoriously picky, carefully planning equine reproduction and jealously registering pedigrees. Knowledge accumulated through centuries of horse-breeding has had a major impact on the birth of modern genetics, most famously by fueling Charles Darwin's theory of natural selection. With the first comprehensive low-density horse linkage map (*Genomics* **66**, 123–124; 2000), horse-breeding has cleared a notable hurdle. Equine genetics has been hampered by long gestation, low birthrate and the heterogeneity of available pedigrees. Twink Allen, Matthew Binns and their collaborators at the Animal Trust in Newmarket (UK) have now cleverly produced two full-sibling reference families by crossing two pairs of identical twin mares with one stallion. They thereby generated a total of 68 individuals (removed as 30 day-old embryos), forming 2 full-sibling families, each being half-sibling with respect to each other. The grandparents were crossbred to maximize levels of heterozygosity and include Arabian, Thoroughbred, Welsh Cob and Icelandic Horse breeds. Families were genotyped with more than 350 markers, mostly microsatellites, and markers were assigned to all 31 autosomes and the X chromosome. Markers on the map thus generated are separated by 10 cM on average and form 42 linkage groups, covering 1,780 cM altogether. This will undoubtedly prove a valuable tool for veterinary medicine, but may also have implications for human genetics, given the great similarity between the genomes of horse and human, including a particularly high degree of orthologous synteny. As for improving horse-breeding decisions, and thus the wealth of kingdoms that depend on them, the ride might prove longer than some may hope. Indeed, a complex trait such as racing performance depends not only on bones and muscles, but also on lungs and guts and, as testified by many jockeys, psychology. The heritability of racing performance is reckoned to be about 30%, making the search for a 'speed gene' unrealistic. For the forseeable future, the outcome of a race will rely on the genetic dice and the skill of the jockey. As for those geneticists who ponder the existence of horses when flies or yeasts are so eminently alluring, ask the owner of Fusaichi Pegasus, the $4 million colt, what he thinks of the next *C. elegans* derby.

Post-genomic navel-gazing



Erik Adigard & Patricia McShane/M.A.D.

Forget piercing—think DNA-chip jewelry. According to *The New York Times Magazine* (9 July 2000), the recent announcements regarding the completion of human draft sequence herald an age in which everyone will "soon" have their 3-Gb genomes (affordably) sequenced and inscribed on a "computer chip". But of course, the real question is: how to carry it? In an article entitled "Biotech Chic," top designers show their solutions to that fundamental challenge to twenty-first century fashion—how to wear the precious "Gene Chip" in ways that will both protect privacy and allow access. For indeed, the chip is also an identification device, to be plugged into a computer for medical, administrative or judicial purposes. Various accessories are illustrated, ranging from belt buckles to suspended amulets to eye lenses. The vote at *Nature Genetics* unanimously endorses the "genegg," an oval, flexible capsule that fits over the belly button and conceived and designed by Erik Adigard and Patricia McShane. But why, pray tell, stop with conventional accessories? Instead of wearing an easy-to-steal computer chip, consider a "Gene Tattoo". But is it art?