that dHAND is still expressed in the same restricted segment of the heart tube, even when the tube is fated to loop to the left. This prediction can easily be tested by *in-situ* hybridization analyses of *iv* and *inv* mouse embryos.

Although transcription factors like dHAND and eHAND are good candidates to specify regional differentiation of the heart, the left-right asymmetry of heart development is probably orchestrated by extracellular signals that originate elsewhere in the embryo. A future challenge will be to understand how laterality signals are integrated with differentiation signals to coordinate the handsome choreography of cardiogenesis. □

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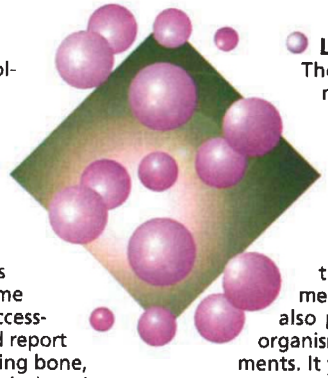
TOUCHING**base**



Two for Two

A pair of papers from researchers at the Baylor College of Medicine in *Nature* describing mice lacking disease-related genes once again point out the interesting similarities, and in some cases crucial differences, between humans and mice suffering the same primary genetic deficiencies. Last year, a Japanese group reported in *Nature Genetics* that some patients with the overgrowth disorder, Beckwith-Wiedemann syndrome (BWS), harbour mutations in the imprinted gene for $p57^{KIP2}$ on chromosome 11. Zhang, Elledge and colleagues have now successfully knocked out the equivalent mouse gene, and report a variety of developmental manifestations affecting bone, muscle and kidney, as well as cleft palate, although the mice do not show gigantism or enlarged tongue (macroglossia). Nevertheless, Elledge's team believes its findings support the conclusions based on clinical observations of a role for the cell-cycle regulator in at least some cases of BWS.

There is no doubt that mutations in *BRCA2* are associated with a significant portion of familial breast cancer cases, but would mice deficient in *Brca2* exhibit the same early developmental abnormalities as their homozygous *Brca1* brethren? Alan Bradley's group report in the 28 April issue of *Nature* that mice targeted for *Brca2* die at day 6.5 of gestation, around the time that *Brca2* expression is normally first detected; are hypersensitive to γ-irradiation (as are *RAD51*-deficient mice); and that Brca2 binds to Rad51 (as does BRCA1). The findings suggest a number of strong parallels between BRCA1 and BRCA2 function, perhaps as 'caretaker' genes, in the parlance of Kinzler and Vogelstein *(Nature* **386**, 762–763; 1997).

Life's a BLAST

The venerable words of the late Mark Bolan are more true today than ever before, with the announcement of a new and improved version of BLAST by Jinghui Zhang and Thomas Madden in the June issue of *Genome Research*. BLAST searches have been traditionally hampered by the amount of time it takes to search GenBank with repetitive elements and mega-long sequence slowing up search time. PowerBLAST provides masking and segmenting capacities to counter these obstacles. It can also process search results to generate up-to-date organism-specific data and more sensitive gapped alignments. It yields multiple alignments with annotated features; annotations can be cut and pasted onto the original sequence and once alignments are obtained, PowerBLAST enables the user to download data into other analytical programs. Anyone who's laboured with voluminous lists of unannotated sequence from primary BLAST searches after a night's query will testify that efficient and flexible searching matters . . . and may be heartened by the novel features of PowerBLAST.

"It is not often that the phrases "remarkably supple" and "deep silky nose" appear in Nature Genetics, but they do in the May issue . . . on a topic [the journal] obviously considers of great importance."

— **James Gorman**, science writer and wine connoisseur in the New York Times

Hear This

Two reports appearing elsewhere in this issue show that mutations in the gene for myosin VIIA, which has already been tied to a form of syndromic deafness known as Usher syndrome, can also lead to non-syndromic hearing loss. At the time of writing, both groups felt, with good reason, that they had stumbled on the first gene associated with this pure form of deafness, even though more than 30 genes for syndromic deafness are already known. But they have been pipped to the post (in print, at least) by Kelsell and colleagues. Writing in the May 1 issue of *Nature*, the British team showed that mutations in connexin 26 were associated with non-syndromic deafness in consanguineous families from Pakistan. Moreover, the trait can be inherited in either recessive or dominant fashion. In a *News & Views* in this month's *Nature Medicine*, Karen Avraham assesses the possible roles of these two cochlear transmembrane proteins.

Hot 100

Popular weekly magazines like to proclaim "Man of the Year" and "50 Most Beautiful People". Perhaps feeling a little bit left out, *Newsweek* recently compiled a list of its "100 Americans for the Next Century", saying "it's not too soon to identify some of the faces we'll be watching in the year 2000 and beyond". The results are curious, to say the least: rubbing shoulders with the likes of Tom Cruise and Tiger Woods are Margaret Pericak-Vance (the Duke University geneticist who is noted for helping to identify the genes for three major neurological disorders); Mark Skolnick (cancer epidemiologist and the co-founder of Myriad Genetics); and J. Craig Venter ('A pioneer in small-genome sequencing'). The magazine also spotlights AIDS researcher David Ho, and Steven Pinker, director of the Center for Cognitive Neuroscience at MIT.