The psychological consequences of predictive testing for Huntington's disease

This paper documents some of the psychological consequences of predictive testing for HD. All 135 participants in the Canadian programme of genetic testing to predict the risk of HD were followed prospectively in three groups divided according to their test result: high risk (37 participants), low risk (58), and a group for whom no change in risk could be given (40). Standard measures of psychological distress, depression, and well-being were administered before genetic testing and again at intervals of a week, six months, and 12 months after participants received their test result. At each assessment, the high risk group had lower scores for depression and anxiety than the control groups and the group with no change in risk. The high risk group showed statistically significant change on the Hamilton depression scale from before testing. The high risk group showed the highest levels of perceived threat over the year of the study. The group with no change in risk had scores lower than the baseline on the index of general well-being at each follow up. At 12 months both high risk and low risk groups had lower scores for depression and higher scores for well-being than the control group. A predictive test for HD has potential benefits for psychological health of people who receive results that indicate either an increase or a decrease in risk.

ANDREW NORMAN

The human Y chromosome: a 43-interval map based on naturally occurring deletions

The human Y chromosome: overlapping DNA clones spanning the euchromatic region

In a brace of articles from this special Genome issue of Science, David Page's group have produced the first complete physical maps of the euchromatic part of the Y chromosome. In the first article, two flow sorted Y chromosome phage libraries were used to generate unique Sequence Tagged Sites (STSs) which could be identified with PCR. Using their large collection of previously characterised abnormal Y chromosome clones, they then ordered by their presence or absence on these deleted or rearranged Y chromosomes. The result is a physical deletion map of 43 intervals which covers an average length of 800 kb. In the second article, an XXXY cell line was used to generate YAC clones to which the previously ordered STSs were assigned. A overlapping clones would share STSs which had already been ordered by deletion mapping, it was possible to build up a single array of YAC clones spanning 98% of the Y euchromatin. Landmarks within this array occur every 220 kb on average. These maps should be of great value in identifying Y linked genes as well as in elucidating the pathology and evolution of the human Y chromosome. The authors emphasise the ease with which this approach could be applied to other chromosomes.

JOHN C K BARBER

Effects of long-term calcitonin gene-related peptide on the incidence of fractures in osteogenesis imperfecta

Many therapeutic approaches aiming at a reduction in the incidence of fractures in osteogenesis imperfecta (OI) have been tried with little or no success. This paper reports the effects of calcitonin treatment on three children who were non-carriers of the OI A1 mutation and who were developing a high rate of fractures in the bones over the age of 11 years, and the results were normalized. The patients ranged in age from 1 month to 14.9 years and the diagnosis was established on the basis of frequent fractures at or near birth, multiple blue scleras, hearing disturbance, or a family history of this disease. Four of the patients were classified as type I OI and six as type II OI. They were receiving no other therapy, and all had normal dietary intakes of calcium, phosphorus, magnesium, and vitamin D. A reduction in the incidence of fractures per year was used as an indicator of treatment success. In the early stages of the trial porcine calcitonin was injected subcutaneously at a dose of 3 U/kg twice weekly; thereafter 50 or 100 U of salmon calcitonin were administered via nasal spray twice a week for two weeks followed by two weeks with no therapy. On these regimens the fracture rate decreased in all patients and this effect was dramatic in some of the group. No significant side effects were observed on nasal spray therapy whereas nausea and vomiting were seen in three patients receiving injections. This treatment would seem to offer the first significant therapy in the prevention of fractures in children with OI.

DAVID FITZPATRICK

A pseudodeficiency allele common in non-Jewish Tah-Sachs carriers: implications for carrier screening

Tay-Sachs disease (Gg, gangliosidosis type I) results from deficiency of function all β-galactosidase A (Hex A). An assay of Hex A activity using the synthetic substrate, 4-methylumbelliferyl-β-N-acetylgalactosamidase, identified affected subjects, carriers, and non-carriers. However, some healthy subjects are deficient in Hex A and were not identified in this assay. Molecular analysis of the HEXA gene in one subject identified a substitution on one allele that had not been reported before and a known disease mutation on the second allele. This substitution was found in other pseudodeficient subjects, both Jewish and non-Jewish. The inclusion of this substitution in the assays carried out on the subjects in the carrier range. They found that 20/62 non-Jewish biochemical carriers carried this substitution, but that 19/62 biochemical car- riers had this mutation. Biochemical screening of parents of known carriers could lead to the recognition of prenatal diagnosis of a subject with this mutation and confirm the feasibility of a pseudodeficient fetus. This paper raises awareness that in vitro assays do not always reflect the in vivo situation. It also reinforces that not all gene mutations cause disease. Finally, it has implications for testing partners of known carriers, particularly in non-Jewish families, where this mutation should be reconsidered in all subjects who fall in the carrier range of the assay.

JUDITH GOODSHIP

Genetic susceptibility to multiple sclerosis linked to myelin basic protein

That a genetic factor might be of etiological significance in multiple sclerosis (MS) has long been suggested. Early supportive evidence for this in 1990 centred on a possible association between the disease and a polymorphism adjacent to myelin basic protein (MBP) on chromosome 18. However, technical difficulties in relation to autoradiograph interpretation meant that corroborative evidence of this association would be required. Now a tetranucleotide repeat polymorphism 5' to the MBP initiation codon has been used to confirm a striking difference in allele distributions between MS patients and controls. When the allele frequencies in the MS cohort alone were considered with respect to variables such as familial MS versus non-familial, mode of clinical presentation, etc, no difference was observed between the subgroups in regard of allele frequency for the 1.27 kb band, which is the disease associated allele, apparently confirming that there is a broad association between MS and this polymorphism. Exploiting this observation and an extraordinary familial clustering of cases in western Finland, the authors proceeded to a linkage study. The families have been well characterised and investigated, although the precise allocation of affection status in some family members was clearly problematical, particularly where optic neuritis was the sole feature or where the MRI scan suggested an abnormality uncorroborated by any clinical evidence. The lack of a clear inheritance model necessitated several analyses using an autosomal dominant model with varying degrees of penetrance. The authors deal frankly with these problems and the difficulties posed by their resolution. The lod scores ranged from 2.2 to 3.4 over all the families and 1.9 to 2.5 in the clustered families only, with the highest score correlating with the highest estimate of penetrance in the clustered families and with the lowest penetrance estimate outside this group. This is an excellent paper and emphasises that the genetic component of the etiologically complex disease is amenable to study. Successful identification of such genetic factors requires technical expertise, excellent clinical documentation, as well as exploitation of naturally occurring resources such as case clustering. If a reservation is harboured, it is the use of a modified mono- genic model for the calculation of odds in a situation where multifactorial, possibly even polygenic, etiological influences apply.

W REARDON