MEDICAL GENETICS: ADVANCES IN BRIEF

Parental origin and germline mosaicism of deletions and duplications of the dystrophin gene: a European study

One third of all cases of Duchenne muscular dystrophy (DMD) are new mutations; however it has been shown in some cases that a new mutation has not occurred as a single gamete but as a germline mosaic, thus further complicating risk calculations. This report provides evidence that germline mosaicism is far from rare. Twelve out of 52 cases of new DMD mutations, consisting of partial gene duplications or deletions, were found to involve maternal germline mosaicism. The study excluded the approximately 25% of cases which are probably caused by point mutations or very small deletions in the dystrophin gene, and the authors note that the risk of mosaicism for these types of mutation may be different. The study also shows no significant deviation from a 1:1 ratio of male to female origin of partial gene deletions. The authors also point out that haemophilia A studies suggest that point mutations arise preferentially in males. In conclusion, this study highlights the possibility that germline mosaicism may be a more important factor than has previously been thought in genetic disease.

ANDREW WILKIE

Characteristics and prognostic implications of myosin missense mutations in familial hypertrophic cardiomyopathy

Autosomal dominant hypertrophic cardiomyopathy (HOCM) is characterised by variable myocardial hypertrophy and symptoms such as effort pain, dyspnoea, syncope, and sudden death. Linkage has been established between HOCM and markers on 14q, and genes encoding α and β isoforms of cardiac myosin heavy chains have been mapped in tandem to the same region, making them candidate genes for HOCM. In 1990 Geisterfer-Lowrance et al found a β cardiac myosin heavy chain gene mutation in a HOCM family. Watkins et al have developed a ribonuclease protection assay which they used to screen β cardiac myosin heavy chain genes of probands from 25 unrelated HOCM families. Seven mutations were identified in 12 of the 25 families and nucleotide sequencing showed these were all missense mutations (that is, single amino acid substitutions) clustered in the head and head-rod junction regions of the molecule. Six mutations changed the charge of the amino acid. In these families mean age at death was 33 years, whereas in those with the neutral mutation survival was nearly normal. Different missense mutations can now be identified in the β cardiac myosin heavy chain gene in approximately half of HOCM families, allowing definite diagnosis in members of such families and suggesting better estimation of prognosis in future.

DAVID FITZPATRICK

Attitudes toward presymptomatic testing and prenatal diagnosis for adrenoleukodystrophy among affected families

This paper reports questionnaire responses of 136 subjects (18.4% affected, 72.8% first degree relatives) with a family history of an X linked disorder. The clinical spectrum of adrenoleukodystrophy ranges from rapidly fatal neurological degeneration to asymptomatic 'gene carriage' in most females and some male patients of the 'affecteds' kind. They asked their relatives if in the opinion of the patients and their treating physicians, we should consider the disease as a 'critical' disorder. Interestingly, 35% of patients would terminate a pregnancy if the risk of transmission were known. The authors suggest that the effect of prenatal testing needs to be 'explored', as many subjects would not terminate an affected fetus. More striking was that 95 to 100% of all responders would request carrier testing for their children. The results are obviously hypothetical, and in practice, as in Huntington's disease, the response may be different. How ever the results question many principles of genetic counselling, such as the freedom of choice for possible carriers of X linked disorders and the role of presymptomatic testing, in minors, for conditions without therapy. Are geneticists out of touch with reality? Are families in need of further counselling on the genetics, benefits, and consequences of their decisions? Perhaps the answer lies somewhere in between.

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D O ROBINSON

Levels of naturally occurring DNA polymorphism correlate with recombination rates in D melanogaster

In the rush to sequence individual genes, there is a tendency for the unifying principles of genome design (if there are any) to be forgotten. Why do linear chromosomes show regular variations in nucleotide composition, gene density, repeat sequence content, and many other properties, and what are the causes? The various genome projects will generate the data necessary to address these ‘global’ issues. This paper is an early attempt to examine one such problem, the variation in amount of naturally occurring DNA polymorphism in different parts of the genome. The authors collated data for the fruitfly Drosophila melanogaster, and found that local levels of nucleotide diversity correlated with the local recombination rate. There was no consistent relationship between sequence divergence with a closely related species, D simulans, and the local recombination rate, excluding a direct effect of recombination on mutation rate. The authors interpret their findings in terms of the ‘hitch-hiking’ of DNA flanking hypothetical advantageous mutations that have become fixed in the population. The authors note that the recombination rate, the wider the zone of linkage disequilibrium around the mutation, hence the lower the level of polymorphism. These are pre-liminary but interesting data, and in time a more rigorous analysis will be possible in a variety of species including the human.

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