Clustering and frequency of mutations in the retinal guanylate cyclase (GUCY2D) gene in patients with dominant cone-rod dystrophies

Annette M Payne, Alex G Morris, Susan M Downes, Samantha Johnson, Alan C Bird, Anthony T Moore, Shomi S Bhattacharya, David M Hunt

EDITOR—Guanylate cyclase (retGC-1) is a key enzyme in the recovery phase of phototransduction in both cone and rod photoreceptor cells. Upon excitation by a photon of light, an enzymatic cascade of events occurs which leads to the hydrolysis of cGMP and the closure of the cGMP gated cation channels. This results in hyperpolarisation of the plasma membrane and the generation of a signal higher up in the visual pathway. Upon closure of the ion channels, the cytosolic levels of Ca\(^{2+}\) decrease because export by the Na\(^{+}\), K\(^{+}\), Ca\(^{2+}\) exchanger continues. This reduced Ca\(^{2+}\) concentration results in the activation of retGC by activating proteins (GCAPs) and the increased conversion of GTP to cGMP, thus restoring the level of cGMP in the photoreceptors to their dark level.

Mutations in GUCY2D, the gene encoding retGC-1, are a cause of Leber congenital amaurosis (LCA1), a recessive condition which manifests itself either at birth or during the first few months of life as total or near total blindness. Recently, we identified mutations in GUCY2D in four British families with autosomal dominant cone-rod dystrophy (ADCORD). Subsequent to this, mutations in this gene were shown to be responsible for ADCORD in a French, a Swiss, and a Norwegian family. In all seven families, the mutations are either in the same or in adjacent codons in a highly conserved region of the protein. In our four families and in the Swiss and Norwegian families, mutations were found in either codon 837 or 838, whereas codons 837-839 each encode for an amino acid substitution in the French family.

In order to determine whether ADCORD arising from mutations in GUCY2D are restricted to these codons and how important these mutations are to autosomal retinal disease in general, we have screened an additional group of unrelated patients diagnosed with autosomal dominant macular dystrophy or autosomal dominant cone or cone-rod dystrophy.

Methods

MUTATION SCREENING

The coding exons of GUCY2D were amplified using the intronic primers and annealing temperatures essentially as described previously and subjected to heteroduplex analysis. All fragments exhibiting band shifts were directly sequenced using the PRISM\textsuperscript{TM} Ready Reaction Sequencing Kit (Perkin Elmer PE Biosystems), and the products were visualised on an ABI Model 373 DNA sequencer.

HAPLOTYPE ANALYSIS

One of each primer pair was end labelled with 10 µCi of [\(\gamma^{32}\)P]ATP using polynucleotide kinase for 30 minutes at 37°C, followed by 10 minutes at 65°C. PCR was carried out using 1.5 mmol/l MgCl\(_2\), 0.2 mmol/l dNTP mix, KCl buffer, 0.05 U/ml Taq polymerase (Bioline), 0.1 mmol/l of each primer, and 0.1-0.2 µg of genomic DNA. The amplification protocol was 94°C for three minutes, followed by 35 cycles at 94°C for 30 seconds, 56°C for 30 seconds, and 72°C for 30 seconds. The resulting products were visualised on a 6% polyacrylamide/urea denaturing gel. The gel was dried down at 80°C under vacuum and autoradiographed over x ray film overnight.

The DISLAMB program\textsuperscript{7} was used to obtain an estimate of linkage disequilibrium.

Results

A group of 40 patients, 27 with autosomal dominant macular dystrophy and 13 with autosomal dominant cone or cone-rod dystrophy, was screened for mutations in all exons of GUCY2D. This group was drawn from the same panel that was used in our original study and is composed of unrelated patients with autosomal dominant macular dystrophies or cone or cone-rod dystrophies attending a Medical Retina Clinic at Moorfields Eye Hospital, London, UK. From this screen, three additional probands with mutations in GUCY2D were identified. Of these, two have the identical R838C substitution to that previously reported and one has a novel G2586A transition in codon 838, resulting in an R838H substitution (fig 1). In addition, a re-examination of our CORD6 family has shown a second mutation, a C2585A transversion again in codon 838 that results in the substitution of arginine by serine (fig 1). This mutation is in the adjacent codon to the originally reported E837D substitution. This is therefore a second example of a GUCY2D disease
allele carrying multiple mutations. In total, five of our families carry a C to T change in codon 838, one family has a G to A change in codon 838, and one family has a double mutation in codons 837 and 838. All these mutations were confirmed by restriction enzyme digestion, since all cause the loss of a \( HhaI \) site. None of these changes were observed in 50 ethnically matched controls. In each case, the diagnosis was confirmed as cone-rod dystrophy (D Bessant, personal communication). Excluding the original CORD6 family, the 90 unrelated patients screened in this and the previous study therefore yielded a total of six ADCORD patients with mutations in codon 838 of the \( GUCY2D \) gene. The above mutations, together with all previously reported mutations, are summarised in table 1.

Haplotype analysis was used to investigate whether there is evidence for relatedness among the five families with the R838C substitution (table 2). In order to determine the haplotype of the disease chromosome, additional family members were sought. However, family 5 could not be extended beyond the original proband; the disease associated alleles for markers D17S1881 and D17S1852 could not therefore be fully resolved. All families show some commonality for marker alleles adjacent to the \( GUCY2D \) gene; families 2, 3, 5, and 6 share allele 5 at D17S960, families 2, 4, 6, and possibly 5 share allele 2 at D17S1796, and families 3 to 6 share allele 5 at D17S1881. However, although family 3 shares the same allele as families 4, 5, and 6 at D17S1881, it is unlikely that this is part of a founder haplotype since it would require a double crossover within a very short map interval. An estimate of the likelihood of linkage disequilibrium was obtained from the DISLAMB program by using allele frequencies obtained from 20 unrelated “married in” subjects in the families. This is significant at the 5% probability level only for D17S960; the lower estimates of \( \lambda \) and \( p \) for the other markers reflect in part the common occurrence of the disease associated alleles in the “married in” subjects.

During our extensive sequence analysis of the \( GUCY2D \) gene, a number of single nucleotide polymorphisms (SNPs) were identified as follows: a silent C220A transversion in exon 2, coding G227A (A52S) and G227T (A52T) changes in exon 2 (the G227T transversion has been previously reported as a possible sequence polymorphism), a silent G2182A transition in exon 10, a coding G2584C (E837D) and C2585A (R838S) changes in exon 12, a G to A transition in intron 17, and a T insertion in intron 19. Unfortunately, in each of our R838C disease families, the more common nucleotide was present at each position. These SNPs do not therefore help to resolve the ancestry of the R838C mutations.

### Table 1 Dominant cone-rod mutations in the \( GUCY2D \) gene

<table>
<thead>
<tr>
<th>Families/probands</th>
<th>Mutation</th>
<th>Amino acid substitution</th>
</tr>
</thead>
<tbody>
<tr>
<td>1*</td>
<td>G2584C</td>
<td>E837D</td>
</tr>
<tr>
<td></td>
<td>G2585A</td>
<td>R838S</td>
</tr>
<tr>
<td>2-4**</td>
<td>G2585T</td>
<td>R838C</td>
</tr>
<tr>
<td>5-6‡</td>
<td>G2585T</td>
<td>R838C</td>
</tr>
<tr>
<td>7§</td>
<td>G2585T</td>
<td>R838C</td>
</tr>
<tr>
<td>8‡</td>
<td>G2586A</td>
<td>R838H</td>
</tr>
<tr>
<td>9*</td>
<td>G2586A</td>
<td>R838H</td>
</tr>
<tr>
<td>10**</td>
<td>G2584C</td>
<td>E837D</td>
</tr>
<tr>
<td></td>
<td>C2585T</td>
<td>R838C</td>
</tr>
<tr>
<td></td>
<td>C2589T</td>
<td>T839M</td>
</tr>
</tbody>
</table>

*Original CORD6 family.
†Kelsell et al.4
‡This study.
§Van Ghelue et al.7
¶Weigell-Weber et al.6
**Perrault et al.5
Table 2  Microsatellite markers in the vicinity of the GUCY2D gene

<table>
<thead>
<tr>
<th>Intermarker distance (cM)</th>
<th>Association with disease</th>
<th>Haplotypes or genotypes in families or probands</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>z</td>
<td>p</td>
</tr>
<tr>
<td>D17S796</td>
<td>0.13</td>
<td>0</td>
</tr>
<tr>
<td>D17S938</td>
<td>0.2</td>
<td>0.36</td>
</tr>
<tr>
<td>D17S960</td>
<td>0</td>
<td>0.57</td>
</tr>
<tr>
<td>GUCY2D</td>
<td>0</td>
<td>—</td>
</tr>
<tr>
<td>D17S1796</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>D17S1881</td>
<td>0</td>
<td>0.53</td>
</tr>
<tr>
<td>D17S1882</td>
<td>2.2</td>
<td>ND</td>
</tr>
</tbody>
</table>

The family numbers are identical to those in table 1. The numbers in parentheses are the frequencies of each allele on 40 chromosomes obtained from unrelated, "married in" subjects in the families. The statistic \( \lambda \) gives an estimate of linkage disequilibrium as determined by the DISLAMB program. Only D17S960 shows significant disease association.

Table 3  Frequency of mutations in codon 838 of the GUCY2D gene.

<table>
<thead>
<tr>
<th>Codon</th>
<th>Proportion of mutations</th>
<th>Family</th>
<th>Number of families</th>
</tr>
</thead>
<tbody>
<tr>
<td>838</td>
<td>0.2</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.3</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.4</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The family numbers are identical to those in table 1. The numbers in parentheses are the frequencies of each allele on 40 chromosomes obtained from unrelated, "married in" subjects in the families. The statistic \( \lambda \) gives an estimate of linkage disequilibrium as determined by the DISLAMB program. Only D17S960 shows significant disease association.

A further 40 patients, three additional patients with mutations in this codon have been identified, two with an R838C substitution and one with an R838H substitution.

The clinical phenotypes in the families with single (R838C or R838H) and double (E837D, R838S) mutations have been reported in detail elsewhere. In summary, the cone-rod dystrophy exhibited by the single mutation patients is less severe than that in the original CORD6 family with the double mutation, with mild variation in disease severity in the R838C families. In all cases, photophobia with decreased visual acuity and loss of colour vision is present from early childhood. However, during the early phases of the disorder when visual acuity is still good, a marked reduction in visual function in bright light is characteristically present. Funduscopic abnormalities are confined to the central macula with increasing central atrophy with age. Electrophysiological testing showed a marked loss of cone function with only minimal rod involvement in the single mutation families. This contrasts with expression in the CORD6 family where moderate to severe rod involvement is present. Different mutations in this region of the GUCY2D gene can result in differing severities of cone-rod dystrophy, especially with regard to the involvement of the scotopic system.

Pooling across our two studies, a conservative estimate of the overall frequency of mutations in codon 838 of GUCY2D among autosomal dominant patients with macular, cone, or cone-rod dystrophy is therefore 6.7%, although this rises to 23% if only the three new mutations found among the 13 cone and cone-rod dystrophy patients examined in this study are considered. It is important to emphasise that these two frequencies are estimates of the relative contribution that mutations in this codon make to the total frequency of autosomal dominant cone-rod disease in the population and that this conclusion is valid irrespective of the presence or absence of a founder effect for the R838C mutations. Whether such a founder effect is present is unclear from the present data. There is evidence for linkage disequilibrium between the disease allele and one of the flanking markers (D17S960) although, since the disease associated allele is relatively common (28%), this renders the test of association less powerful, and the situation is not further resolved by a number of SNPs scattered through the GUCY2D gene, since none was informative in our five families. Where a founder effect has been clearly established, for example for Sorsby’s fundus dystrophy, a highly significant disease associated haplotype covering 3 cM of the chromosomal region surrounding the disease gene was present. In contrast, the disease associated haplotype for the R838C mutations covers <0.2 cM. This indicates that either the R838C mutations have arisen separately from each other or that a single mutation occurred in a much more distant ancestor than the common mutation for Sorsby’s fundus dystrophy, with a consequent wider distribution in the population. Furthermore and again irrespective of the presence or absence of a common ancestor for our R838C families, the occurrence of the R838C mutation in a presumably unrelated Norwegian family, the R838H mutations in one of our British families and in a Swiss family, and the multiple mutations in codon 838 and adjacent codons in the original CORD6 family, as well as in a French family, all identify this codon as particularly mutation prone.

Two other dominantly inherited diseases have been associated with mutation prone regions: recurring C to T and G to A transitions were found in adjacent nucleotides within the MYH7 gene in hypertrophic cardiomyopathy and recurring G to A transitions and G to C transversions were found at the same nucleotide within the FGFR3 gene in achondroplasia. The recurring DNA transitions at these two loci are situated at CpG dinucleotides and a study of nucleotide substitution rates has confirmed the high mutability of CpG sequences. The spontaneous deamination of methylated cytosine, its relatively slow repair in mammalian cells, and the production of an intermediate susceptible to deamination in the enzymatic process by which cytosine itself is methylated, are all mechanisms which make CpG sequences preferential targets for spontaneous mutation. It is perhaps significant therefore that the C to T transitions and C to A transversions found in codons 838 and
Letters

383 of the GUCY2D gene all occur within a CpG dinucleotide (fig 2). What remains unclear is the mechanism responsible for the generation of multiple mutations in this region of exon 13 of the GUCY2D gene.

Recessive mutations in GUCY2D are a relatively common cause of LCA. However, the widespread distribution of LCA mutations (including missense, frameshift, and splice site changes) throughout the gene\textsuperscript{15} contrasts with the clustering of ADCORD mutations to codons 837, 838, and 839 encoded by exon 13. To date, no LCA mutations have been localised to exon 13. The causative ADCORD mutation has been shown to be recessive since the E837D substitution present in some families\textsuperscript{5} appears to have little effect on enzyme activity in vitro.\textsuperscript{19} In contrast, the changes in codon 838, R838H, R838C, or R838S, have all been shown to alter the sensitivity of the protein to Ca\textsuperscript{2+} inhibition via interactions with GCAPs.\textsuperscript{20-22} Substitution at this site may be the critical change in all cases so far reported, in causing ADCORD rather than recessive LCA. The effect of this dominant mutation is a change in function (altered Ca\textsuperscript{2+} sensitivity) whereas the recessive LCA mutations may represent loss of activity.\textsuperscript{22}

There have been reports of other retinal dystrophies mapping to regions of chromosome 17p which overlap with the position of the GUCY2D gene. These include two dominant cone dystrophies and dominant central areolar choroidal dystrophy, diseases which exhibit degeneration primarily of the cone-rich macular region only.\textsuperscript{23} As yet, there have been no reports of GUCY2D mutations in these disorders, despite screening this gene in patients with central areolar choroidal dystrophy.\textsuperscript{24}

We thank the patients for their cooperation in this study. This work was supported by the Wellcome Trust (grant numbers 019059 and 083940v3 and the Medical Research Council (grant number G9301094). We would also like to thank the Wellcome Trust for a Major Equipment Grant for the sequencing facility (grant number 039283).

Table: Codons and Amino acid substitutions

<table>
<thead>
<tr>
<th>Codons</th>
<th>Amino acid substitutions</th>
</tr>
</thead>
<tbody>
<tr>
<td>836</td>
<td>837 838 839 840</td>
</tr>
<tr>
<td>CGG</td>
<td>CGC ACG GAG</td>
</tr>
<tr>
<td>C</td>
<td>T ... T ...</td>
</tr>
<tr>
<td>. . .</td>
<td>E837D, R838C, T839M</td>
</tr>
<tr>
<td>C</td>
<td>A ... A ...</td>
</tr>
<tr>
<td>. . .</td>
<td>E837D, R838S</td>
</tr>
<tr>
<td>. . .</td>
<td>R838C</td>
</tr>
<tr>
<td>. . .</td>
<td>A ... R838H</td>
</tr>
</tbody>
</table>

Figure 2. Nucleotide and amino acid substitutions in exon 13 of GUCY2D associated with autosomal dominant cone-rod dystrophy.

9 Tierjagger JD. A powerful likelihood method for the analysis of linkage disequilibrium between trait loci and one or more polymorphic marker loci. Am J Hum Genet 1995;56:771-87.
A G339R mutation in the CTNS gene is a common cause of nephropathic cystinosis in the south western Ontario Amish Mennonite population

C Anthony Rupar, Douglas Matsell, Susan Surry, Victoria Siu

EDITOR—Nephropathic cystinosis (MIM 219800) is a rare autosomal recessively inherited lysosomal storage disorder with a newborn incidence of about 1 in 100 000-200 000 in the general population (OMIM). Cystine accumulates in lysosomes because of dysfunctional cystinosin mediated transport of cystine out of lysosomes. The accumulation of cystine results in damage to several organs with renal damage being the most pronounced in the first decade of life. Patients with cystinosis experience both tubular dysfunction (renal Fanconi syndrome) and glomerular deterioration. Renal Fanconi syndrome usually occurs within the first year of life with glomerular deterioration progressing throughout the first decade of life resulting in end stage renal failure.¹

The CTNS gene was mapped to chromosome 17p13 and subsequently isolated and characterised to have 12 exons spanning 23 kb of genomic DNA.²,³ The most common mutation that causes cystinosis is a large deletion that encompasses exons 1-10.⁴ Originally, this deletion was described as 65 kb long but the size has been recently refined to 57 257 bases.⁵ Forty four percent of 108 American based patients with nephropathic cystinosis were homozygous for this deletion.⁶

At least seven children in the Old Order Amish population in south western Ontario, Canada have been diagnosed with nephropathic cystinosis. This population is a culturally isolated population founded in 1824 by emigrants from Bavaria and Alsace-Lorraine. Within this Amish community, we have recently diagnosed four children with cystinosis, two sibs in two families not known to be related. In each family the parents are consanguineous. The proband presented at 14 months of age with protracted vomiting and dehydration, polyuria, polydipsia, and failure to thrive. On initial investigations he had a metabolic acidosis, hypophosphataemia, hyperkalaemia, and glucosuria. Slit lamp examination of his eyes showed corneal crystals. Urine amino acid analysis indicated a generalised amino aciduria. At presentation he had no evidence of renal insufficiency. A leucocyte cystine level done before the initiation of treatment was 1.99 nmol 1⁄2 cystine/mg protein. Patients with untreated cystinosis usually have greater than 2.0 nmol 1⁄2 cystine/mg protein (Dr J A Schneider, San Diego). His younger sister was diagnosed at 8 months when she presented with a similar clinical history and a leucocyte cystine of 1.19 nmol 1⁄2 cystine/mg protein before the initiation of treatment. Leucocyte cystine concentrations were measured at the Cystine Determination Laboratory, UCSD, La Jolla, CA using the cystine binding protein assay.

DNA was isolated from blood specimens that were obtained after receiving consent from the parents. Mutations were identified in the CTNS gene by PCR amplification and direct sequencing (ABI PRISM Model 377 sequencer) of exons 3-10 and PCR amplification for detection of the 57 257 base deletion using flanking primers as listed in table 1. A mutation, 1354 G→A, was identified in exon 12. This mutation results in the loss of an AauI restriction site. The proband was homozygous for the 1354 G→A mutation as shown in fig 1 and no other mutations were identified. This mutation results in a glycine 339 to arginine amino acid change in a transmembrane region of cystinosis. All four cystinosis patients from the two families were homozygous for this mutation and an unaffected sister was heterozygous.

The G339R mutation has been previously identified in one allele in a compound heterozygous patient of Italian ancestry.¹ Further evidence that this mutation is pathogenetic is that glycine 339 is an amino acid which is conserved between C elegans and humans in cystinosin.⁷ In our patients, homozygosity for the G339R mutation seems to be associated

Table 1 Primers for amplifying CTNS exons and testing for the 65 kb deletion

<table>
<thead>
<tr>
<th>Exon</th>
<th>Direction</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>Forward</td>
<td>5'- CAG ATT GTC TAC AAG GAG GAT TCT -3'</td>
</tr>
<tr>
<td>4</td>
<td>Forward</td>
<td>5'- CTT GGC AAC AAA CAG ATC AGT -3'</td>
</tr>
<tr>
<td>5</td>
<td>Reverse</td>
<td>5'- GAG CTT AGC ACA GCA GCG CCA -3'</td>
</tr>
<tr>
<td>6</td>
<td>Forward</td>
<td>5'- TCC AGT TCT TCA GCA GTA AT -3'</td>
</tr>
<tr>
<td>7</td>
<td>Reverse</td>
<td>5'- ACC TAG CAT TCC CCT ACC C-3'</td>
</tr>
<tr>
<td>8</td>
<td>Forward</td>
<td>5'- GCC GCG TCC TCG GTA ACT G -3'</td>
</tr>
<tr>
<td>9</td>
<td>Reverse</td>
<td>5'- CAG CAC GGC CCC CTT CT -3'</td>
</tr>
<tr>
<td>10</td>
<td>Forward</td>
<td>5'- AGT CTC CTT CAG AAG CCC AG -3'</td>
</tr>
<tr>
<td>11</td>
<td>Reverse</td>
<td>5'- ACC TAG CTT CAG AAG GCC GTG -3'</td>
</tr>
<tr>
<td>12</td>
<td>Forward</td>
<td>5'- GCT CTC CCG TGT CTG TC -3'</td>
</tr>
<tr>
<td>LDM-1*</td>
<td>Forward</td>
<td>5'- CAG AAG GAG CAG GAT AA -3'</td>
</tr>
<tr>
<td>D17S820*</td>
<td>Reverse</td>
<td>5'- GCC GAG TCT TTC TCT AT -3'</td>
</tr>
</tbody>
</table>

*Sequences from Anikster al.¹
with a relatively low concentration of leucocyte cystine.

Germany is likely to be the country of origin for the common 57 257 base deletion in the CTNS gene.\(^5\) The Amish Mennonite population originated in Germany but appears to have the G339R mutation exclusively rather than the 57 257 base deletion. This may reflect a founder effect but there are no data to indicate from whom or when the founder allele originated. Cystinosis does not appear to be present in the Amish population of Pennsylvania, suggesting that the mutation may have originated in a founder who emigrated to southwestern Ontario directly from Europe. A study of other populations that are related to the population from which this Amish community is derived would be helpful in this regard.

There are no data on the incidence of cystinosis or the prevalence of the G339R allele in the south western Ontario Amish Mennonite community. Our awareness of seven cases in the past 10 years suggests an incidence far greater than that of the general population.

There is evidence that the earlier that cysteamine therapy is started the less cystine accumulates in tissues. Markello et al.\(^7\) showed that the treatment of children with cystinosis with cysteamine before the onset of end stage renal disease resulted in a delay in the need for renal replacement therapy when compared to children not treated or not compliant with therapy. Early therapy has also been shown to prevent hypothyroidism\(^8\) and the accumulation of cystine in muscle.\(^9\)

If this Amish Mennonite community wishes, the determination of the frequency of the G339R allele within the population using the AvaI restriction site would enable the prediction of the population incidence of cystinosis. This incidence may be high enough to justify targeted newborn screening and early institution of management.

Electronic database information: Online Mendelian Inheritance in Man (OMIM), http://www.ncbi.nlm.nih.gov/OMIM (for cystinosis (MIM 219800)).

Technical assistance was provided by Roger Dewar and Sajid Shaikh.


Figure 1 Part of the DNA sequence of exon 12 showing that the patient is homozygous for the 1354 G→A mutation. The sequence is in the reverse direction with the normal sequence across this region being GAAGACCCGAGTC.
De novo terminal deletion of chromosome 15q26.1 characterised by comparative genomic hybridisation and FISH with locus specific probes

Holger Tönnies, Ilka Schulze, Hans-Christian Hennies, Luitgard Margarete Neumann, Rolf Keitzer, Heidemarie Neitzel

EDITOR—Reports of patients with terminal de novo deletions of chromosome 15q26 are rare. Excluding cases of ring chromosome 15 formation with different sized deleted chromosomal segments, only seven cases with solely distal deletions of 15q have been published.1–7 All other cases resulted from unbalanced reciprocal translocations involving different chromosomes and are therefore not comparable with de novo terminal deletions as described in our case.

With two exceptions, all de novo cases had interstitial deletions between chromosomal bands 15q21-q25. Only the patients described by Roback et al5 and Siebler et al6 had terminal deletions of 15q26.1. The deletions in these patients were not investigated by FISH, but molecular genetic techniques showed the loss of one copy of the insulin-like growth factor 1 receptor gene. IGF1R is a tyrosine kinase containing transmembrane protein that plays an important role in cell growth control. It has been assumed that monozygosity for this gene, which maps to distal 15q26, will directly disturb this pathway and inhibit normal growth of patients.8

Today, in addition to classical cytogenetic banding methods, FISH techniques including comparative genomic hybridisation (CGH) can be used to provide a powerful tool to characterise chromosomal aberrations. In this study, we present the molecular cytogenetic findings and the detailed clinical phenotype of a girl with deletion 15q26.1 and compare these with other published cases. Our patient described here is, to the best of our knowledge, the second patient with a de novo terminal deletion at 15q26.1 and the first one well characterised by molecular cytogenetic techniques.

Case report

The female infant was the first child of healthy, unrelated parents. An ultrasound examination at 15 weeks of gestation showed intrauterine growth retardation. At 39 weeks of gestation a caesarean section became necessary because of fetal heart rate deceleration. The Apgar scores were 6, 8, and 10 at one, five, and 10 minutes, respectively. Her birth weight was 1980 g (<3rd centile) with a length of 42 cm (<3rd centile) and a head circumference of 30 cm (<3rd centile).

The first chromosome analysis after birth in an outside laboratory showed a normal female karyotype. The girl had minor anomalies including micrognathia, low set ears, a broad nasal bridge, and a short neck (fig 1). Furthermore, there was a blood pressure difference between the upper and the lower extremities. Cardiac examination including cardiac catheterisation exhibited a complex heart defect with ventricular septal defect (VSD), atrial septal defect (ASD), preductal coarctation of the aorta, patent ductus arteriosus, and arteria lusoria. This complex congenital heart disease was corrected by several surgical interventions up to the age of 3 months. Laboratory findings including IGF1 and a screening for congenital infection were normal except for a transient hypothyroidism owing to maternal hypothyroidism. Renal ultrasonography showed a slight ectasia of the left renal pelvis from the age of 7 months. Neurological examination showed developmental delay but no other pathological findings. At the age of 15 months the infant could roll over but could not sit without support. Furthermore, she had severe feeding problems with gastrooesophageal reflux and vomiting. Because of increasing vomiting and a lack of weight gain, a gastrostomy feeding tube had to be inserted. For the whole period of time the girl continued to have poor development and severe failure to thrive. At the age of 16 months her weight was 5300 g (<3rd centile), length was 62 cm (<3rd centile), and head circumference was 39 cm (<3rd centile).

Figure 1 The patient at the age of 19 months.
Material and methods

Blood samples from the patient and her parents were drawn after informed consent. High resolution chromosome analyses from peripheral blood lymphocytes of the patient and both parents were performed using standard techniques. Preparations were GTG banded and karyotyped using the Ikaros system (Metasystems, Altussheim, Germany).

Whole chromosome painting (WCP) was initiated using the probe for chromosome 15 (VYSIS). YAC clones for chromosome 15 were selected from the CEPH mega-YAC library and obtained through the Positional Cloning Centre at the Max-Planck Institute of Molecular Genetics (Berlin, Germany). YAC DNA was amplified and labelled by degenerate oligonucleotide primed polymerase chain reaction (DOP-PCR) with minor modifications. YAC-FISH was performed according to standard protocols. Hybridisation of commercial probes for the subtelomeric region of chromosome 15q (TelVysion 15q, VYSIS) and the all human telomeres probe (ONCOR) were according to the manufacturers’ instructions. All probes used were directly labelled with fluorochromes.

Genomic DNA of the patient was investigated by comparative genomic hybridisation using normal male reference DNA as a control. DNA was isolated using standard methods. Briefly, genomic DNA samples were differently labelled by nick translation with SpectrumGreen®-dUTP (VYSIS, test DNA) and SpectrumOrange®-dUTP (VYSIS, reference DNA). For each hybridisation, 200 ng of labelled test DNA, 200 ng reference DNA, and 12.5 µg Cot-1 DNA were coprecipitated, resuspended in 14 µl hybridisation mix containing 50% formamide, 2 x SSC, and 10% dextran sulphate, denatured at 70°C for five minutes, and hybridised to denatured normal male metaphase spreads. Slides were incubated at 37°C in a moist chamber for two days. Posthybridisation washes were performed as described previously. Images of the hybridised metaphases were evaluated using an epifluorescence microscope (Axiophot, ZEISS, Germany) fitted with different single band pass filter sets for DAPI, SpectrumGreen®, and SpectrumOrange® fluorescent. The microscope is equipped with a cooled CCD camera (Hamamatsu) for image acquisition. Image analysis and karyotyping (CGH) was performed using the ISIS analysis system (Metasystems, Germany). Diagnostic thresholds used for the identification of chromosomal under-representations (deletions) and over-representations (duplications) were 0.85 and 1.17.

Microsatellite markers on chromosome 15q were analysed in the patient and her parents. Marker loci were chosen from the Généthon final linkage map and from the Marshfield comprehensive human genetic maps. Marker loci were amplified by PCR in a final reaction volume of 10 µl containing 10 mmol/l Tris, 1.5 mmol/l MgCl₂, 100 µmol/l each dNTP, 0.4 U polymerase (Applied Biosystems), 7 pmol of each primer, and 20 ng of genomic DNA. One of the primers was end labelled with fluorescent dye. DNA amplification was carried out in an MJ Research PTC-225 thermal cycler. Reactions were electrophoresed on an ABI PRISM 377 automatic DNA sequencer (Applied Biosystems). Data were analysed using the computer programs Genescan v3.0 and Genotyper v2.5 (Applied Biosystems).

Results

Cytogenetic studies from the peripheral blood lymphocytes of the patient at the age of 9 months showed a female karyotype with a small deletion in the long arm of chromosome 15 at the 500-600 band level (fig 2). After conventional cytogenetics, the extent of the deletion was assumed to be from band 15q25–26 to the distal end of the chromosome, but it was impossible to decide whether the deletion was interstitial or terminal. Maternal and paternal karyotypes were normal at the same resolution level.

For further characterisation of the deletion, CGH was performed using total DNA from the patient as a probe. The averaged ratio profile analysis clearly indicated a terminal deletion (dim) of the chromosomal region 15q26 (fig 2). No other chromosome showed any profile imbalance.

This result was in agreement with the FISH analysis using a chromosome 15 specific whole chromosome paint (VYSIS) showing homogeneous painting of the whole deleted chromosome 15 without any hint of a translocation of the missing chromosome 15 material to any other chromosome (data not shown).

To define the proximal and distal boundaries of the deletion, FISH with different YAC clones was performed. Two of five YAC clones localised in chromosome band 15q25 (81-84 cM, table 1) showed signals on both chromosomes 15 on metaphase preparations of the patient (fig 3). Three YAC clones, 963d03, 895h10, and 882h08, localised distal to chromosome band 15q25 (98-110 cM), were missing from the patient’s deleted chromosome 15 (fig 3).

To delineate this chromosomal abnormality further, FISH with a probe hybridising to unique telomeric DNA sequences of chromosome 15q (TelVysion 15q, VYSIS) was performed. The investigation showed that a signal of this 100 kb sized probe for chromosome 15q is missing on the deleted chromosome 15 (fig 3). In contrast, FISH with an all telomeric probe (ONCOR) detecting the highly repeated (TTAGGG)n sequences located at the telomeres of all human chromosomes showed telomeric signals on both the normal and the deleted chromosome 15 as well as on all other chromosomes (fig 3). Thus the patient’s karyotype can be summarised as: 46,XX, del(15)(q26.1).ish del(15)(D15S130−, D15S207/D15S157−, D15S120/D15S203−, D15S936+)−.

In order to complement the FISH data and to substantiate the loss of the IGF1R gene locus, a microsatellite analysis was performed. Twelve polymorphic markers from chromosome 15q were analysed (table 1). All the
markers but those at D15S152, D15S1014, and D15S120 were informative for the family. Segregation of two different alleles clearly showed that the patient carries two copies of chromosome 15q proximal to D15S652 (table 1). Hence, the proximal boundary of the deletion is in the 10 cM interval between D15S652 and D15S130, so the deletion lies between D15S652 and the telomere. This finding is in accordance with the proximal boundary of the deletion defined by YAC hybridisation (table 1). Unfortunately, there is no true telomeric marker available on chromosome 15q, and the distance between the most distal marker at D15S642 and the telomere remains unclear. Additionally, it could be determined that the aberrant chromosome 15 was of paternal origin. The IGF1R gene is located close to D15S120 as shown by radiation hybrid mapping between D15S107 and D15S87.15 16 These two markers are within the deleted region of our patient who therefore exhibits monozygosity for the IGF1R gene.

**Discussion**

Terminal deletions of chromosome 15q are rare events or are seldom diagnosed. Only a few cases of de novo distal deletions of chromosome 15q without ring formation have been described and the vast majority have been characterised by standard banding only yielding breakpoints in the range from 15q24 to 15q26. We describe here a new case of terminal deletion 15q26. Even with high resolution chromosome analysis, it was difficult to determine the exact size of the deletion. Therefore, we used different molecular cytogenetic approaches like CGH and FISH with YAC clones and commercially available telomeric probes to refine the deleted chromosome region to chromosome band 15q26. However, even with the molecular cytogenetic investigation, it was impossible to differentiate between an interstitial versus terminal deletion. The result of the FISH analysis with the YAC from the subtelomere of 15q (Telvision, D15S936) clearly showed a deletion on the aberrant 15 while a signal could be detected on both chromosomes 15 with the all telomeric repetitive probe (TTAGGG)n.

Therefore, it cannot be shown whether the telomeric sequence (TTAGGG)n at the distal end of the deleted chromosome 15 was from the paternal chromosome, or whether it derived from another chromosome by translocation.

![Figure 2 Ideogram](image)

The normal chromosome 15 is to the left of the deleted chromosome 15. (C) Averaged CGH ratio profile of 12 measured chromosomes 15 of the patient.

### Table 1 Detection of chromosome 15q loci by FISH and microsatellite analysis

<table>
<thead>
<tr>
<th>STS</th>
<th>cM*</th>
<th>Probe (YAC clone)</th>
<th>Method†</th>
<th>Normal chromosome 15</th>
<th>Derivative chromosome 15</th>
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<tr>
<td>D15S153</td>
<td>62.1</td>
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<td>MS</td>
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<td>FISH</td>
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<td>−</td>
</tr>
<tr>
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<td>MS</td>
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<td>−</td>
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<td>—</td>
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<td>?</td>
<td>TelVysion 15q</td>
<td>FISH</td>
<td>+</td>
<td>−</td>
</tr>
</tbody>
</table>

*Genetic localisation according to Dib et al.12 The distance between D15S966 and D15S642 was obtained from Broman et al.13†Loci were studied either by FISH with YAC clones or by analysis of microsatellites (MS). +, allele detected; −, allele missing; NI, not informative.
Telomeres of all human chromosomes. Telomeres probe detecting the highly repeated DNA (TTAGGG)n sequences located at the ends of chromosomes. Telomeres are crucial for the maintenance of chromosome integrity and play a role in the regulation of cell growth and aging.

Figure 3 FISH images of YAC clones and commercially available probes hybridised to the patient’s chromosomes. (A) Fluorescence signals after hybridisation of the YAC clones 859c06 and 963d03. There is no signal for the latter clone in the patient’s deleted chromosome 15. (B) Magnification. (C) The subtelomeric TelVysion probe detecting the highly repeated DNA (TTAGGG)n sequences located at the telomeres of all human chromosomes.

New studies on terminal deletions also suggest that de novo telomere addition could occur either mediated by telomerase or by recombination-based mechanisms. In addition to the characterisation of the size of the deletion by in situ hybridisation, the deleted interval was determined by the analysis of microsatellites. These studies showed that the de novo deleted chromosome 15 was of paternal origin. This result is consistent with the paternal origin in the case described by Roback et al.

Most patients with deletions of distal 15q have intrauterine growth retardation (IUGR), microcephaly, abnormal face and ears, micrognathia, a high arched palate, renal abnormalities, lung hypoplasia, failure to thrive, developmental delay, and mental retardation. Apart from unbalanced chromosome translocations involving distal 15q and ring chromosome 15 syndromes, there are only seven previously described patients with de novo deletions of the distal long arm of chromosome 15. Most of these patients had interstitial deletions with different breakpoints indicating that the phenotypic discordance observed probably results from differences in the size and localisation of the deleted material.

Similarly to patients with distal deletion of 15q, many patients with ring chromosome 15 syndrome showed symptoms like IUGR, mental retardation, and microcephaly, but they more frequently had a triangular face, hypertelorism, café-au-lait spots, cryptorchidism, cardiac anomalies, and brachydactyly.

To the best of our knowledge there are only two comparable cases to our patient with a deletion of 15q26.1 (table 2) that have been investigated by molecular genetic techniques. These patients and our patient share intrauterine growth retardation, poor growth and development, and minor anomalies of the face. The female child described by Siebler et al also had a triangular face and brachydactyly and exhibited characteristics of patients with ring chromosome 15 syndrome and deletion of 15q26.1. Renal malformations were only reported in the case of Roback et al and our case. The patient of Roback et al also had lung hypoplasia, while our patient suffered from a complex heart defect. Feeding difficulties, as in our patient, were reported in four cases out of seven.

Only a couple of genes have been mapped to date in the distal part of chromosome 15, one of which is IGF1R. In vitro and in vivo studies of fibroblasts of the two patients described by Siebler et al showed that IGF1 receptor expression was decreased, while there was no evidence for impairment of the response to IGF1. Thus, Siebler et al suggested that the growth retardation might not be related to monozygosity for IGF1R. However, the authors conceded that extrapolation from findings in skin fibroblasts to the situation in vivo is difficult.

Peoples et al investigated five children with de novo ring chromosomes 15 with breakpoints in 15q26.3 showing monosomy of the IGF1R gene in three of them. These three children had significantly more severe growth retardation in the first few years of life than one patient who retained the IGF1R gene on the ring chromosome. These data support a correlation between monozygosity for the IGF1R gene and severe growth retardation in early childhood, while patients who have retained two copies of the IGF1R gene show milder growth retardation.

In vitro studies of fibroblasts of the two patients described by Peoples et al also showed that IGF1 receptor expression was decreased, while there was no evidence for impairment of the response to IGF1. However, the authors conceded that extrapolation from findings in skin fibroblasts to the situation in vivo is difficult.

De Lacerda et al were the first to describe in vitro and in vivo studies of a patient with ring chromosome 15 syndrome and monozygosity for IGF1R. The female child showed prenatal and severe postnatal growth failure, a slightly triangular face, high arched palate, café-au-lait spots, and delayed psychomotor development. The patient’s fibroblasts exhibited growth...
response in vitro to the addition of IGF1, similar to that of control fibroblasts. In contrast, the treatment of the child with short term recombinant human IGF1 (rhIGF1) caused no significant reduction in urinary urea nitrogen excretion, only 60% increase in calcium excretion, and no significant decrease in the GH secretion. Therefore, the authors suggested that the growth retardation could be the result of the absence of one IGF1R allele because of in vivo resistance to IGF1.

Studies on the effects of IGF1R in the cardiovascular system may support this assumption. These data showed evidence that IGF1 is an essential regulator of developmental growth and plays an important role in cardiovascular development. A variety of growth factors upregulate IGF1R on vascular smooth muscle cells and the data support the concept that IGF1R number per cell is an important factor for cellular growth response.

Therefore, monozygosity for IGF1R would be the best explanation for the complex heart defect seen in our patient. Thus, in addition to severe growth retardation, monozygosity for IGF1R might be a risk factor for the development of complex heart defects.

We thank the Max-Planck-Institute of Molecular Genetics, Berlin, for the YAC clones. The authors thank Antje Gerlach and Britta Teubner for excellent technical assistance in the molecular cytogenetic experiments.


Interstitial deletion of chromosome 11 (q22.3-q23.2) in a boy with mild developmental delay

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Editor—Deletions of the terminal region of the long arm of chromosome 11 (bands 11q23.3-11q24) are associated with a clinically recognisable phenotype, also called Jacobsen syndrome (JS). Reports on more proximal 11q deletions are rare. This is the second report describing a de novo interstitial deletion of the 11q22.3-23.2 region. The first described a de novo interstitial deletion of the 11q22.3-23.2 region in a mildly retarded male with minor

Letters

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dysmorphic signs (high and narrow palate, low set, dysplastic ears, small hands and feet, and slender fingers) and epileptic seizures. However, no FISH studies were performed in this patient.

In this report we describe a small de novo interstitial deletion in the long arm of chromosome 11 (bands q22.3-q23.2) in a 2 year 8 month old boy with mild developmental delay and without major associated dysmorphic features or a clinically recognisable phenotype.

**Case report**

The proband, a boy, is the second and youngest child of healthy, non-consanguineous parents. His 5 year old sister is normal. Pregnancy and delivery, at 39 weeks, were normal. Birth weight was 3130 g, length 49 cm, and head circumference 33.5 cm. Clinical examination in the neonatal period was normal, apart from mild axial hypotonia. Motor development was slightly retarded and he walked without support at the age of 17 months.

Now, at the age of 2 years 8 months, psychomotor development is borderline normal (2 years 2 months to 2 years 4 months on the Bayley Developmental scale). Social contact is adequate but expressive language is mildly retarded at a developmental level of 2 years. Height is 89.5 cm (10th centile), weight 12.5 kg (10th centile), and head circumference 48 cm (3rd centile for age). Except for the relative microcephaly and mild trigonocephaly, craniofacial dysmorphism is mild and non-specific, including a somewhat large mouth with a thin upper lip and everted lower lip and rather large and everted ears. Both thumbs are proximally implanted. Further clinical and neurological examinations were normal. Additional examinations including MRI scan of the brain, metabolic screening, and ophthalmological examination were normal.

Cytogenetic studies were performed using PHA stimulated lymphocytes according to standard cytogenetic procedures. G banded chromosome analysis showed an interstitial deletion of the long arm of chromosome 11 (q22.2→q23.1) (fig 1). The karyotype was 46,XY,del(11)(p<sub>ter</sub>→q22.3::q23.1→q<sub>ter</sub>). The parental karyotypes were normal.

**FISH** with chromosome 11 specific paint probe (Cambio) showed no translocation of chromosome 11 material (fig 2A). FISH analysis was performed with five YAC probes (878C12, 876G04, 901E11, 735B11, and 742F09), BAC442e11, and three cosmids probes that map to the 11q22-11q23 region.

**Discussion**

Chromosomal region 11q22-11q23 is apparently prone to instability (recombination, breakage, or rearrangement). The breakpoints of the classical constitutional t(11;22) and the breakpoints in the majority of cases with terminal 11q deletions and derivative chromosomes 11 are located in this region. This region is often involved in multiple tumour associated rearrangements of chromosome 11 and distally lies the MLL gene region that is frequently rearranged in haematopoietic malignant disorders. On the telomeric side of MLL is the fragile site FRA11B and also the Jacobsen syndrome breakpoints (11q23.3-11q24.2). Consequently the region could be considered as a hot spot of chromosomal recombination and breakage.

In this case, the deletion is smaller than the previously reported deletions on 11q, for example, deletions critical for the diagnosis of Jacobsen syndrome (MIM 147791) or larger deletions involving the 11q22-11q23→11qter region.

The fragile site at 11q23.3 (FRA11B) is linked to some Jacobsen syndrome breakpoints (10% of the cases) but the majority are located distal to FRA11B. It was proposed that JS is not a single disease but a collection of different genetic disorders with overlapping phenotypes. The phenotypic variability observed is because of the variation of breakpoints and the different genes involved. Thus, the 11q22.3-11q23.2 deletions in the present patient could be considered as a part of the spectrum of 11q deletions resulting from a similar mechanism, with the more distal deletions resulting in Jacobsen syndrome and the more proximal resulting in a milder phenotype.

In the present case, Bac442e11, which spans the t(11;22) breakpoint in 11q23, was deleted. This BAC clone is related to a palindromic AT...
The mechanism of formation of the deletion in the reported case could be consistent with the one proposed by Akgun et al. They proposed that in mammals palindromic DNA sequences can lead to the formation of unstable DNA structures, such as single stranded hairpin and double stranded cruciform structures, and they hypothesised that a small disruption of symmetry in the palindrome could stabilise the locus. To explain their results, they proposed two different models that could explain the formation of deletions and translocations. According to one model, replication slippage could result in two sided palindrome deletions spanning the tip of the hairpin and create a product with a deletion in the palindrome. This mechanism could explain the deletion in the present patient. According to the
Microdeletion in the FMR-1 gene: an apparent null allele using routine clinical PCR amplification

Madhuri R Hegde, Belinda Chong, Matthew Fawknner, Nikolas Lambiris, Hartmut Peters, Aileen Kenneson, Stephen T Warren, Donald R Love, Julie McLaughran

Editor—Fragile X syndrome is the most common chromosomal cause of inherited mental retardation. At the chromosome level, this syndrome is characterised by the presence of a fragile site at Xq27.3.1 The incidence of this disorder is approximately 1 in 4000 and 1 in 7000 in males and females, respectively. In most cases, the mutation responsible for fragile X syndrome is a CGG repeat expansion in the 5′ untranslated region (UTR) of exon 1 of the FMR-1 gene. People in the normal population have six to approximately 50 repeats.2-3 Those with 50 to 200 repeats correspond to the premutation class. Repeats in this class are meiotically unstable and can expand to a full mutation.2 The premutation class encompasses the “grey area” of 45-55 CGG repeats for which there is a variable risk of repeat expansion.2 Subjects with a full mutation have repeat lengths in excess of 200, which are associated with hypermethylation of the CpG island immediately upstream of the FMR-1 gene.4-5 This methylation correlates with transcriptional suppression of the FMR-1 gene, while the repeat expansion has been suggested to cause translational suppression by impeding the migration of the 40S ribosomal subunit along the 5′ UTR of the FMR-1 gene transcript.6-11

Fragile X syndrome has also been found to occur in a few patients without CGG repeat expansions. These mutation events fall into two classes, intragenic point mutations12,13 and deletion events.14-22 Of the latter class, five patients with microdeletions in the 5′ UTR of the FMR-1 gene transcript have been described.23,24

We report here a patient referred for fragile X testing who was found to carry an apparent null allele by PCR amplification of the CGG repeat region of the FMR-1 gene. This patient was analysed further using a combination of primers flanking the CGG repeat region, together with FMRP studies, in order to characterise the nature of the molecular defect underlying this apparent null allele.

Case report

The proband was born to healthy, non-consanguineous parents at 40 weeks of gestation. There was no significant family history. He weighed 4500 g (>90th centile), head circumference was 37.5 cm (>90th centile), and length was 57.5 cm (>90th centile). There...
was aspiration of meconium at delivery necessitating assessment in the neonatal unit. He appeared well initially but on the following day was noted to be irritable and hypotonic with an abnormal Moro reflex. A cranial ultrasound scan was normal. He required an inguinal hernia repair at a few weeks of age. His early development was felt to be normal. He had gastro-oesophageal reflux diagnosed at 8 months and was treated with ranitidine. He had mild plagiocephaly and a torticollis that required surgical correction at 18 months. He had persistent problems with drooling of saliva and tends to have an open mouthed expression.

In the second year of life he had problems with recurrent ear infections requiring insertion of grommets and adenoidectomy. An assessment of the language development to be significantly delayed. His parents felt his comprehension was limited and he had difficulty retaining information. The delay had been noted earlier but had been attributed to his recurrent ear infections. Full assessment at that time showed that he had developmental delay in all areas. He had some behavioural problems with trichotillomania and obsessive traits. He did not play well with other children.

On examination by a clinical geneticist, the proband was found not have any phenotypic features suggestive of fragile X syndrome, although he did have early features of joint laxity. His head circumference was on the 50th-90th centile, his height on the 75th centile, and weight on the 50th centile. He had mild clinodactyly and fetal pads. He had mild facial asymmetry and a deep crease between his malar eminences. The case was referred to the laboratory for fragile X screening.

Materials and methods

CYTOGENETIC AND DNA ANALYSIS

Cytogenetic analysis of a folate deprived culture of lymphocytes was performed as previously described. An estimation of the length of the CGG repeats, together with an analysis of the methylation status of the CpG gene sequence of the FMR-1 gene, were performed by PCR amplification and Southern blot analysis, respectively. In the case of the latter, 5 µg of genomic DNA was digested with respectively. In the case of the latter, FMR1 and FMR2 were carried out using the GC rich kit of Roche Diagnostics Ltd according to the manufacturer’s instructions. The sequences of the primers used in the amplification reactions were FMR1 (5'-GACGGAGCCGCGTCCAGG-3'), FMR2 (5'-GCTAGCGGCTATTCTTCTTTCG CCT-3'), FMR1 (5'-ATAACCGATGCA TTTGAT-3'), and FMR2 (5'-AGGC CCTAGGCGCTATTCCGAATGAGAGA-3').

Primers FMR1, FMR2, FMRB, and FMR2 were designed using the FMR-1 gene sequence deposited in GenBank (Accession number X61378), with their 5’ ends at base positions 2271, 2684, 2844, and 3106, respectively. The PCR cycling conditions comprised 95°C for two minutes followed by 30 cycles of 97°C for 30 seconds, 55°C for one minute, and 72°C for one minute. The reactions were held at 4°C following a final extension of 72°C for 10 minutes. Amplification products were electrophoresed in a 1% agarose gel, together with a 100 bp DNA ladder. In the case of radioactive amplification, the products were electrophoresed in a denaturing sequencing gel using a radioactively labelled M13 sequencing ladder for sizing purposes.

Amplification products were purified for sequencing using a PCR purification kit (Roche Diagnostics). Each amplicon was sequenced using the forward and reverse amplifying primers and an Applied Biosystems ABI sequencer. The sequences of the primers used were deposited in GenBank (Accession number X61378), with their 5’ ends at base positions 2271, 2684, 2844, and 3106, respectively. The PCR cycling conditions comprised 95°C for two minutes followed by 30 cycles of 97°C for 30 seconds, 55°C for one minute, and 72°C for one minute. The reactions were held at 4°C following a final extension of 72°C for 10 minutes. Amplification products were electrophoresed in a 1% agarose gel, together with a 100 bp DNA ladder. In the case of radioactive amplification, the products were electrophoresed in a denaturing sequencing gel using a radioactively labelled M13 sequencing ladder for sizing purposes.

Amplification products were purified for sequencing using a PCR purification kit (Roche Diagnostics). Each amplicon was sequenced using the forward and reverse amplifying primers and an Applied Biosystems ABI sequencing kit. DNA was recovered by ethanol precipitation and subsequently washed in 70% ethanol before the addition of denaturation buffer and loading in an ABI PRISM 377 DNA sequencer. The electropherograms were subsequently assembled using SeqMan DNA software.

PROTEIN ANALYSIS

An EBV transformed B lymphoblastoid cell line was established from a peripheral blood sample of the proband. FMRP and eIF4e levels were determined in whole cell lysates in a slot-blot based assay, using purified flag tagged murine Fmrp and purified human eIF4e as standards. Sample proteins and standards were applied to nitrocellulose membranes with a Bio-Rad slot blot apparatus. Using standard protocols, FMRP and eIF4e were detected with mouse monoclonal primary antibodies mAb 1C3 for FMRP, kindly provided by Jean-Louis Mandel, and anti-eIF4e (Transduction Laboratories) and HRP conjugated goat anti-mouse secondary antibody (Kirkegaard and Perry Laboratories). Signals were generated by Enhanced Chemi Luminescence (Amersham) and detected by exposure to Hyperfilm (Amersham). Signal intensities were quantified by analysis of digital scans using the program NIH Image 1.62b7f to plot signal profiles. Areas under the plot profile were calculated and used as signal intensities after subtracting out signals

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Figure 1  DNA analysis of the CGG repeat region of the FMR-1 gene. (A) EcoRI plus NruI digested genomic DNA from a normal male (lane 1), a male with a full mutation (lane 2), a normal female (lane 3), and the proband (lane 4) was probed with StB12.3. The 1 kb ladder is shown in lane 5, with the lengths of the unmethylated and methylated alleles in a normal subject indicated on the right hand side of the panel. (B) PCR amplification products encompassing the CGG repeat region of the FMR-1 gene are shown. The proband and normal males are represented by the filled and open symbols, respectively, while negative PCR controls are indicated by the letter N. The radioactively labelled products corresponding to PCR amplification using primers FMRA and FMRB were electrophoresed in a denaturing sequencing gel with a labelled M13 sequencing ladder, while the other amplification products were separated in 1% agarose gels with 100 bp ladders. (C) Electropherogram of the sequence of the proband’s FMR-1 gene encompassing the ATG initiation codon (indicated by a horizontal bar). The sequence is shown in the 3′ to 5′ direction. The vertical arrow indicates an arbitrary start site for the sequence presented in (D). (D) Partial sequence of the FMR-1 gene (GenBank accession number X61378) indicating the GAAGA direct repeats (in bold type and numbered horizontal arrows) and the ATG initiation codon (underlined). The location of the FMRA and FMRB primers are shown as horizontal arrows, together with their position with respect to the transcription start site. The nucleotide sequence derived from the electropherogram is shown starting at an arbitrary site, indicated by an arrow.
from the proband's genomic DNA. However, amplification products were obtained using primers FMRA and FMR2 (643 bp) and FMR1 and FMR2 (1 kb, fig 1B). The latter product was sequenced and showed a deletion of a 5 bp direct repeat, GAAGA, either immediately upstream, or encompassing the first base, of the ATG initiation codon of the FMR-1 gene (fig 1C, D). The mother of the proband was found to be heterozygous for this deletion event (data not shown). The deletion leaves the ATG codon unchanged and in phase with the remaining open reading frame of the FMR-1 gene.

FMRP quantitation, western blot analysis, and immunohistochemical studies were undertaken using the patient's lymphoblasts to determine the effect of the deletion event on translation initiation (fig 2). In order to assess the level of FMRP in the patient's lymphoblasts, quantitation studies were undertaken using the protein eIF4e as an internal control. The latter protein is the cap binding protein in eukaryotic translation initiation and is the rate limiting factor in translation initiation.34–36 FMRP levels were normalised with respect to eIF4e levels as a loading control. In seven cell lines from males with normal CGG allele lengths, the mean molar ratio of FMRP:eIF4e is 0.218 (standard deviation of 0.009). In the case of the cells from the proband, the molar ratio was 0.214, and thus the level of FMRP is not reduced compared to normal cell lines. In the case of the western blot analysis, normal sized FMRP was detected (fig 2A). Immunohistochemical staining of lymphocytes from the proband and his carrier mother showed FMRP staining in 80% and 98% of 100 lymphocytes examined, respectively (fig 2B).

Results

Cytogenetic analysis of the proband’s chromosomes indicated an apparently normal 46,XY karyotype. Southern blot analysis showed a positively hybridising 2.8 kb DNA fragment, suggesting a normal sized CGG repeat length in the FMR-1 gene (fig 1A). PCR amplification of this locus using previously published primers FMRA and FMRB yielded no product from the background and from the secondary antibody controls as appropriate. Standard curves were generated using data from the purified proteins, which then allowed the quantitation of protein levels in the samples. Quantitation data was calculated as the molar ratio of FMRP:eIF4e. Purified FMRP was obtained from Keith Wilkinson and eIF4e from Curt Hagedorn, both of Emory University.

In the case of western blot studies, total proteins were isolated from EBV transformed B lymphoblasts of the proband, as well as from a normal male control. The proteins were electrophoresed in a 7.5% non-denaturing polyacrylamide gel, and transferred to nitrocellulose and hybridised using mAb 1C3 as described above.

In the case of immunohistochemical staining of FMRP from blood smears, a modification of the method of Willemsen et al was used. Blood smears were counterstained with Nuclear Fast Red and 100 lymphocytes were examined for each person, together with positive and negative control blood samples. Less than 42% of lymphocytes are FMRP positive in affected males, whereas for carrier females this figure is 83%; the specificity of this assay is 100% for males and 41% for females.

Figure 2  FMRP analysis. (A) Western blot analyses of FMRP expressed by the proband and a normal male are shown in lanes 1 and 2, respectively. Molecular weight standards (expressed in kDa) are indicated on the left hand side of the panel. (B) Immunohistochemical staining of FMRP in lymphocytes of the proband (I), the proband’s carrier mother (II), a negative control (III), and a positive control (IV). FMRP staining is seen in the cytoplasm, with the nuclei stained with Nuclear Fast Red.
Discussion

The proband reported here carries an apparent null allele with respect to the primer pair FMRA and FMRB, which are used routinely for amplifying the CGG repeat tract of the FMR-1 gene. This case suggests that caution should be exercised regarding predictive testing for fragile X syndrome that relies solely on PCR amplification of the FMR-1 gene using one primer pair only. This reliance has been suggested as a first level predictive screen for fragile X syndrome in the general population.\(^5\) The need for caution with respect to single PCR amplifications of trinucleotide repeats has also been described with regard to predictive testing for the Huntington’s disease (HD) gene.\(^6\) Our data underline the need for complementing PCR analysis with Southern blotting or, at minimum, PCR amplification of the CGG repeat region with two primer pairs. Direct sequencing of amplification products using primers that map further upstream and downstream of FMRA and FMRB identified a 5 bp microdeletion near, or encompassing, the initiation codon of the FMR-1 gene. It appears that this deletion affects the annealing of the FMRB primer leading to inefficient amplification using this primer. The proband represents one of only a few cases that have been reported to have microdeletions in the FMR-1 gene.\(^7\)\(^8\) In these other cases, which were found in subjects with fragile X syndrome, the microdeletions ranged from 116 bp to 567 bp and were located in the 5' UTR of the FMR-1 gene. The deletions were expected to lead to a lack of the FMR-1 gene product, which was confirmed in some patients.\(^7\)\(^8\) A mispairing model for the generation of a 486 bp deletion was described by Schmucker et al.,\(^7\) which involved chi-like elements flanked by direct tandem repeats. In the case reported here, end joining, strand slippage, or indeed homologous recombination are possible molecular mechanisms that could account for the 5 bp deletion event.

Changes in the sequence of DNA upstream of an initiation codon can dramatically influence translation efficiency.\(^9\) Fragile X males with a full mutation have complete absence of FMRP. However, in the case described here, FMRP was detected of apparently normal size and at normal levels in the lymphocytes of the proband. This study leads to the suggestion that the proband does not have fragile X syndrome and that the 5 bp deletion in this patient’s FMR-1 gene is not causative of his phenotype. The FMRP detected in this patient appears to be qualitatively and quantitatively normal. Therefore, the comprehensive screening of genes implicated in disorders that are similar to fragile X syndrome may help resolve the cause of this patient’s phenotype.

We acknowledge Dr Hugh Lees of Waikato Tauranga for bringing this case to our attention and the technical assistance of Jane Iber. We further acknowledge the financial assistance of Laboratory Services of Auckland Hospital for running expensive testing, and the University of Auckland Research Committee and the Lottery Grants Board of New Zealand for funding an Applied Biosystems Model 377 DNA Sequencer.

- We report here a case that was referred for testing for fragile X syndrome. The patient was found to carry an apparent null allele by routine clinical PCR, but with CGG repeats that fall within the normal range.
- DNA sequencing showed that the patient carried a microdeletion of a 5 bp direct repeat immediately upstream, or encompassing, the translation initiation codon of the FMR-1 gene.
- Protein studies indicated that the patient expressed the protein product of the FMR-1 gene (FMRP), and that this expression was at near normal levels in the patient’s lymphoblasts.


Non-invasive evaluation of arterial involvement in patients affected with Fabry disease

Pierre Boutouyrie, Stéphane Laurent, Brigitte Laloux, Olivier Lidove, Jean-Pierre Grunfeld, Dominique P Germain

Methods and results
In the present study, we determined intima-media thickness (IMT) at the site of the radial artery, a distal, muscular, medium sized artery, in a cohort of 21 hemizygous male FD patients, with a mean age of 32 years (SD 13, range 13–56 years), compared with 21 age and sex matched normal controls. All patients were diagnosed with FD by the presence of both clinical signs and a markedly decreased α-galactosidase A activity in leukocytes (<4 nmol/h/mg protein, normal values 25–55 nmol/h/mg protein). No patient had end stage renal disease. Measurements of the radial artery parameters were obtained with a high precision echotracking device (NIUS 02, SMH, Bienne, Switzerland) as previously described. 

Briefly, the radiofrequency signal was visualised and the peaks corresponding to the blood-intima and media-adventitia interface were electronically tagged and followed over several cardiac cycles. Internal diameter and wall thickness were then measured with a precision of about 10 μm. Four to six measurements were averaged. Radial artery IMT was measured 2 cm upstream from the wrist.

Compared to controls, FD patients had considerably higher IMT values at the site of the radial artery (fig 1). IMT was twice as high in...
FD patients than in controls, even after adjustment for body surface area, age, and mean blood pressure (p<0.001). Radial artery IMT increased significantly with age in each group. However the slope was 2.3-fold higher in FD patients than in controls (p<0.001) (fig 1).

**Discussion**
In the present study, we describe evidence of a major, accelerated hypertrophy of the wall of a medium sized artery in a cohort of patients with FD. The magnitude of the difference in radial artery IMT was very large, with virtually no overlap between FD patients and controls. With age, the radial artery wall thickening was 2.3-fold faster in FD patients than in controls. The high definition echotracking system used in the present study has been previously validated in large subsets of patients with various diseases, and its accuracy and reproducibility are well accepted.

The most commonly proposed explanation for the pathogenesis of cardiovascular lesions in FD patients is the slow deposition of uncleaved neutral glycosphingolipids within the arterial and cardiac tissues. However, the hypothesis of
a sole lysosomal accumulation of sphingolipids is somewhat simplistic since in the most advanced reported cases of left ventricle hypertrophy in FD patients, the amount of uncleaved glycosphingolipids found in the cardiac tissue did not exceed 1.6% of tissue weight (10-20 mg/g wet weight). Other mechanisms are thus probably involved. First, although accumulation of globotriaosylceramide is the main mechanism in FD, the metabolism of other glycosphingolipids may also be disregulated. Among them, lactosylceramide, which mimics the biological function of cytokines, growth factors, and stress signalling molecules and accumulates in vascular tissues of FD patients, could act as a second messenger and potentiate the hypertrophy of the arterial wall. Second, the smaller internal diameter of the radial artery in FD patients may be the result not only of wall hypertrophy enroaching the lumen (fig 2), but also endothelial dysfunction. Deposition of glycosphingolipids occurs predominantly in the lysosomes of endothelial and smooth muscle cells, with consequent cellular dysfunction. An altered endothelium dependent relaxation of arterial smooth muscle could occur at the site of the radial artery or downstream, in arterioles, influencing the tonic flow dependent vasodilatation. The mechanism of flow dilatation is known to occur physiologically at the site of the radial and brachial arteries, and has been related to changes in basal and stimulated nitric oxide (NO) release. Finally, both in the media and intima, smooth muscle cells with glycosphingolipid inclusions secrete important quantities of extracellular matrix, notably elastic fibres. Proliferation of smooth muscle cells and extracellular matrix deposition may thus contribute to the hypertrophy of the radial artery observed in FD patients.

In conclusion, this study presents the first non-invasive demonstration of a major increase in arterial wall thickness at the site of the radial artery in a cohort of patients with confirmed FD. The assessment of the involvement of the large arteries, through non-invasive procedures, could prove useful in monitoring new therapies for FD in providing an intermediate phenotype or a surrogate marker. However, the prognostic significance of the radial artery wall hypertrophy and its ability to regress with emerging treatments, such as enzyme replacement or gene therapy, remains to be determined during follow up studies.

This study received financial support from the Institut National de la Santé et de la Recherche Médicale (INSERM) and from Vaincre les Maladies Lysosomales (VML).

Variation of iron loading expression in C282Y homozygous haemochromatosis probands and sib pairs

Catherine Mura, Gérald Le Gac, Virginie Scotet, Odile Raguenes, Anne-Yvonne Mercier, Claude Férec

EDITOR—Hereditary haemochromatosis (HH), a common autosomal recessive disease of iron metabolism, is more prevalent among populations of northern Europe with an affected rate of 1 in 200 to 400 and a carrier frequency of around 1 in 10.1 2 The disease is characterised by progressive iron overload, and the clinical onset usually appears after middle age. The phenotypic manifestations of HH are variable, and the severity of the disease is related to the iron loading; the most common symptoms of iron overload are fatigue, lethargy, arthropathy, and skin pigmentation, often along with more serious organ damage including cirrhosis, diabetes mellitus, myocardopathy, and endocrine dysfunction. The assessment of iron loading is currently based on the levels of biochemical iron markers such as transferrin saturation percentage, serum ferritin, and serum iron concentrations. However, the diagnosis of haemochromatosis can now be confirmed using direct HFE mutation testing. The diagnosis depends on early diagnosis and therapeutic venesections. Thus, population screening would allow early diagnosis during the asymptomatic phase and prophylactic treatment by repeated venesection to prevent the irreversible damage of iron overload,3 but predictive diagnosis requires a well established phenotype-genotype correlation.

The identification of the haemochromatosis gene,4 now referred to as HFE,5 enables the performance of direct genetic testing for diagnosis. The role of the HFE protein in iron metabolism has not yet been clearly established, but it seems that the complex of HFE with β2-microglobulin interacts with the transferrin receptor (TIR) on the cell surface, which decreases the affinity of TIR for transferrin.6 7 Some mutations characterised in the HFE gene and leading to a functional defect have been correlated with HH. Two missense mutations, 845G→A (C282Y) accounting for 80-90% of HH chromosomes,4 10-15 and 187C→G, (H63D) representing 40-70% of non-C282Y HH chromosomes,4 12-15 leading to the absence and decrease of HFE activity, respectively, have been described.14 17 Another variant, 193A→T, leading to the missense substitution S65C, has been reported to be increased in HH chromosomes, accounting for 7.2% of HH chromosomes, neither 845A (C282Y) nor 187G (H63D).18

The considerable heterogeneity of iron loading observed in HH patients has been correlated with their genotype. Several studies have confirmed that HH patients homozygous for the C282Y mutation are associated with a more severe form of the disease than those carrying other genotypes (H63D/H63D, C282Y/H63D, C282Y/S65C).12 13 19 Phenotype-genotype correlation studies have shown discrepancies. Some reports have mentioned patients diagnosed with haemochromatosis who did not carry known HFE mutations on both chromosomes, accounting for up to 21% of the HH population.1 12 13 Thus, the aetiology of the iron loading in these patients remains unclear. Non-HFE related patient cases may have been included in these HH subjects because of misdiagnosis owing to secondary iron overload or atypical juvenile haemochromatosis linked to chromosome 1q21-22; this point still needs to be clarified. In addition, despite the prominent role of the C282Y mutation in HH, population screening indicates that 17.6% of homozygotes for C282Y were asymptomatic patients.20 Thus, C282Y penetrance confronts one with a problem and requires more investigation.

In the present study, we assessed the biochemical expression of iron loading in HFE C282Y homozygotes. We thus examined the parameters indicative of iron loading in a series of probands homozygous for the C282Y mutation. Then we conducted a family case study of HFE identical sibs enrolled because one of them had HH. The whole study showed a variable biochemical expression of iron overload related to the patients’ age and sex, which was not correlated in subjects with an identical inherited genotype at the HFE locus.

Patients and methods

SUBJECTS
A series of 545 unrelated probands, all homozygous for C282Y, showing various symptoms of clinical haemochromatosis and referred from clinicians to our blood centre for treatment by venesection, was included in this study. Before treatment the diagnosis was confirmed by their iron status markers, and all of them showed at least two of the following criteria: (1) transferrin saturation higher than 60% in males and 50% in females, (2) serum ferritin concentration exceeding 400 µg/l in males and 300 µg/l in females, and (3) serum iron above 20 µmol/l. These iron status markers were measured by standard techniques.

SIB PAIR STUDY
As part of genetic counselling a family study was conducted. Partners and sibs of C282Y HH probands were screened for HFE mutations and biochemical iron markers. The study
group consisted of 53 subjects from 24 unrelated HH families in whom at least one sib had exhibited symptoms and an increased total body iron loading, indicative of HH. This allowed the examination of 18 same sex sib pairs, homozygous for C282Y, and composed of 13 male pairs and five female pairs; eight others were opposite sex pairs. At the time of the biochemical diagnosis, all these sibs were 32 to 64 years old. The mean difference in age within a set of sibs was 5.6 years.

**HFE MUTATION ANALYSIS**

DNA was extracted from peripheral blood leukocytes. C282Y, H63Ds, and S65C substitutions were analysed as previously described.18

**STATISTICAL ANALYSIS**

Measurements of transferrin saturation, serum ferritin, and serum iron are expressed as means (SD) and range is indicated. Comparisons between groups of subjects were made with Student’s *t* test and correlation between iron parameters was assessed. The relationship between the iron parameters and the age of patients was studied separately in males and females using linear regression analysis.

**Results**

A total of 545 unrelated subjects including 197 females and 348 males, all diagnosed with HH and homozygous for the C282Y mutation, were studied. Thus, the male to female sex ratio was 1.7:1 showing a reduced penetrance of the C282Y mutation in females compared to males. The difference in age at onset was recorded according to the sex of probands. The mean age was 44.1 (SD 10.9) and 49.8 (SD 12.5) in males and females, respectively. The difference in mean age at onset calculated between the males and the females using Student’s *t* test was significant (*t*=4.57, *p*=3.3×10⁻⁸) showing that, at onset, females were significantly older than males. Approximately 70% of the males were diagnosed with HH before the age of 50, whereas only 48.6% of females were; 90% of the males and 76.5% of the females were diagnosed with HH before the age of 60 (table 1). These results show that the biochemical expression of haemochromatosis strongly depended on both sex and age in C282Y homozygotes. Iron marker values ranged between normal and significantly increased compared with control values and regardless of the proband’s sex and age. However, transferrin saturation, serum ferritin, and serum iron values as a whole were significantly higher in males than in females (*p*=1.2×10⁻⁸, 6.7×10⁻³, 9×10⁻³, respectively).

According to the age range, above 30 years old serum ferritin and serum iron concentrations were significantly higher in males than in females; transferrin saturation was significantly increased with age only after 40 years in males compared with females (table 1). A correlation analysis showed that, whereas transferrin saturation and serum iron remained stable with age in both sexes, there was a progressive increase of serum ferritin concentration with age in males (*r*=0.29) and females (*r*=0.23) (fig 1); it increased from 262 to 1349 µg/l in males aged from 30 to over 60 years of age. The linear regression analysis indicated a significant mean annual progression of serum ferritin of 39.9 µg/l (*r*=7.1×10⁻² in males (light line) and *r*=21.1×10⁻² in females (dark line)).

The biochemical data of families were reviewed following the discovery of one sib pair HFE identical by descent, in which one sib exhibited total body iron overload and was clinically diagnosed as HH. Sex matched sibs, homozygous for the C282Y mutation, were reviewed to determine the degree of iron loading in the other sib through transferrin saturation percentage and serum ferritin and serum iron concentrations. Opposite sex sibs were not compared because iron overload is known to be higher in male subjects compared to females. Therefore, 18 C282Y homozygous same sex sib pairs were examined; this showed that transferrin saturation ranged between 39 and 98%, serum ferritin between 159 and 4900 µg/l, and serum iron from 12.5 to 48 µmol/l.

**Table 1** Iron status in 545 probands homozygous for the C282Y mutation

<table>
<thead>
<tr>
<th>Sex</th>
<th>Age</th>
<th>No</th>
<th>Transferrin saturation (%)</th>
<th>Serum ferritin (µg/l)</th>
<th>Serum iron (µmol/l)</th>
</tr>
</thead>
<tbody>
<tr>
<td>M</td>
<td>&lt;30</td>
<td>11</td>
<td>68 (11.8) [55–82]</td>
<td>262 (104) [108–398]</td>
<td>37 (5.6) [28–42]</td>
</tr>
<tr>
<td>F</td>
<td>&lt;30</td>
<td>22</td>
<td>70.6 (16.7) [51–98]</td>
<td>598 (506) [83–2000]</td>
<td>38.4 (8.8) [21–49]</td>
</tr>
<tr>
<td></td>
<td>F &gt;40</td>
<td>30</td>
<td>79 (14.7) [57–99]</td>
<td>663 (944) [69–4000]</td>
<td>37 (11.3) [14–62]</td>
</tr>
<tr>
<td>M</td>
<td>&lt;40</td>
<td>105</td>
<td>76.2 (14.6) [34–100]</td>
<td>1341 (1078) [240–4800]</td>
<td>38.8 (7.8) [22–69]</td>
</tr>
<tr>
<td>F</td>
<td>&lt;40</td>
<td>63</td>
<td>70.5 (16) [34–95]</td>
<td>588 (764) [36–3300]</td>
<td>33.2 (6.6) [22–53]</td>
</tr>
<tr>
<td>M</td>
<td>&lt;40</td>
<td>117</td>
<td>82.5 (12.1) [44–100]</td>
<td>1822 (1672) [95–8890]</td>
<td>38.4 (6.3) [22–51]</td>
</tr>
<tr>
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<td>&lt;40</td>
<td>52</td>
<td>70 (16.9) [27–96]</td>
<td>847 (657) [77–2500]</td>
<td>31.8 (6.4) [22–48]</td>
</tr>
<tr>
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<td>&lt;40</td>
<td>71</td>
<td>81.8 (12) [47–97]</td>
<td>2133 (1601) [450–5368]</td>
<td>44.7 (25.2) [27–57]</td>
</tr>
<tr>
<td>F</td>
<td>&lt;40</td>
<td>65</td>
<td>75.8 (18.4) [37–98]</td>
<td>1649 (1525) [195–6680]</td>
<td>36.3 (8.4) [14–55]</td>
</tr>
<tr>
<td>M</td>
<td>&gt;60</td>
<td>33</td>
<td>70.6 (18) [37–95]</td>
<td>2349 (2059) [215–8800]</td>
<td>38.8 (6) [28–49]</td>
</tr>
<tr>
<td>F</td>
<td>&gt;60</td>
<td>54</td>
<td>75.8 (18.4) [37–98]</td>
<td>1649 (1525) [195–6680]</td>
<td>36.3 (8.4) [14–55]</td>
</tr>
</tbody>
</table>

Transferrin saturation, serum ferritin, and serum iron values are expressed as means (SD) and range (NS = not significant).

**Figure 1** Distribution and correlation of serum ferritin concentration in 348 males (*r*=0.29) and 197 females (*r*=0.23) according to age. The equation of the fitted regression line was *Y*=39.9*X*−43.4 in males (light line) and *Y*=21.1*X*−217.2 in females (dark line).
Transferrin saturation, serum ferritin, and serum iron means in probands were 79.4% (SD 13), 1382 µg/l (SD 1348), 39.5 µmol/l (SD 6.4), respectively, and in sib cases 74.2% (SD 19), 1069 µg/l (SD 1166), and 38.1 µmol/l (SD 8.1), respectively; these results were not significantly different. The concordance of these parameters between sib pairs was also assessed. There was no correlation of serum ferritin or serum iron levels between the HH diagnosed sibs and other sibs, while transferrin saturation level tended to be correlated, but remained non-significant (p=0.07); the mean differences in transferrin saturation, serum ferritin, and serum iron values in sib pairs were all significant (table 2). In addition, no significant correlation was found between the oldest and the youngest sibs for the three iron markers when all same sex pairs were considered, indicating that, in this case, the lack of correlation was not related to the age of the subjects. This intrafamilial study showed a variable level of iron overload for subjects with HFE genotype identical by descent. In addition, among the 18 same sex sibs, two, six, and one sibs were in the normal range of values for transferrin saturation percentage (<43%), serum ferritin concentration (<300 µg/l), and serum iron concentration (<20 µmol/l), respectively.

Moreover, in a family of five HFE identical sibs homozygous for the C282Y mutation, ranging in age from 53 to 61 years old, the sibs displayed variable biochemical expression of iron loading (fig 2). One 60 year old female had no significant increase of any of the iron parameters. Her two sisters (mother of four and two children, respectively) and two brothers, who were C282Y homozygotes, were affected with HH and showed iron overload according to their iron status parameters.

Another case of discrepancy between genotype and phenotype was discovered in a female homozygous for the C282Y mutation; she had five children. Her husband was genotyped to evaluate the potential risk for the children of having HH. He was found to be homozygous for C282Y and his biochemical iron status at 61 years of age did not show any sign of iron loading (fig 3). Their son, 35 years old and C282Y homozygous, showed signs of iron overload whereas of their four daughters, aged 30 to 40 years old, only the oldest showed raised transferrin saturation and serum iron concentration.

### Discussion

The present study reports on the relationship between the biochemical expression of iron loading and the homozygous genotype for the C282Y mutation. Iron loading was first examined in a series of 545 probands homozygous for the C282Y mutation. The iron loading was significantly lower in females than in males whatever the parameter investigated; moreover the study confirmed the reduced penetrance of C282Y in females with a male to female sex ratio of 1.7:1 in probands with clinical HH. The biochemical expression of HH, lower in females than in males, indicated that some C282Y homozygous females may not develop signs of iron overload. In a family study, one case of a female identical by descent to four sibs homozygous for C282Y and diagnosed with HH did not reach the threshold values for iron overload.
overload expression defined for haemochromatosis, which indicated that the C282Y mutation did not show complete penetrance in females.

In this series, iron marker values ranged between normal and significantly increased; transferrin saturation percentage seemed to be the best parameter to predict haemochromatosis in young C282Y homozygous subjects whereas serum ferritin, the only value to increase progressively, was proved better to show overloading extent. This study thus confirmed that the extent of iron loading in haemochromatosis C282Y homozygotes is strongly influenced by the C282Y mutation, an autosomal recessive trait. Although the expression of the disease is strongly influenced by the C282Y mutation, the lack of correlation between sibs and significant differences of the iron marker values between sib pairs clearly showed a variable biochemical expression of iron overload in sibs with genotype identical by descent at the HFE locus. Although the expression of the disease is strongly influenced by the C282Y mutation, an intrafamilial study of subjects also confirmed that an identical genotype for the HFE gene can show variable iron loading; thus, intrafamilial variations in iron loading do not only represent a variation in the genetic expression of the HFE gene. The cases of non-expressing C282Y homozygous males aged over 60 years old, and displaying iron parameters in the normal range, as reported here and by others, showed that the biochemical expression of HH is under the influence of other factor(s). In the families studied, transferrin saturation, serum ferritin, and serum iron variations could result from environmental and non-genetic factors or other genetic factors than those examined. Recent population studies have shown that, compared with non-carriers, any genotype group defined as carriers of a HFE mutation had higher mean serum iron concentration and mean transferrin saturation, whereas only C282Y homozygotes showed higher serum ferritin concentration; they also highlighted that some C282Y heterozygotes could be diagnosed as HH. Thus, despite a good correlation between HFE defined genotypes and phenotype in population studies, HFE genotyping does not show a clear level of iron loading in subjects and may have implications in genetic counselling.

Hereditary haemochromatosis (HH) is a common autosomal recessive disease characterised by progressive iron overload. The identification of the HFE gene and mutations involved in haemochromatosis allows direct genetic testing for diagnosis. However, correlations between phenotype and HFE genotypes showed discrepancies and mutation penetrance raises questions.

We examined the iron loading status in 545 probands and 18 same sex sibs, all homozygous for the C282Y mutation.

Our data support transferrin saturation percentage and serum ferritin concentration as the best biochemical iron marker for HH phenotype in young subjects and extent of overload in these patients, respectively. The results also confirm a clear correlation of the iron loading level with age and sex of the patients. However, the lack of correlation of the iron marker status between pairs of sibs, homozygous for C282Y identical by descent, indicated a variable phenotypic expression of iron loading independent of HFE genotype.

This work was supported by INSERM grants from CRI 9607 and Association de Transfusion Sanguine et de Biogénétique Gaetan Saleun.

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Haptoglobin genotype as a risk factor for postmenopausal osteoporosis

Gian Piero Pescarmona, Patrizia D’Amelio, Emanuella Morra, Gian Carlo Isaia

EDITOR—Some epidemiological and experimental data have shown a correlation between iron metabolism and calcium, phosphate, and magnesium turnover.1 2 In particular, previous reports have shown that iron availability can play a fundamental role in bone metabolism and that iron depletion can lead to bone demineralisation. For example, in patients who underwent gastrectomy3 4 or in rats treated similarly,5 osteoporosis was accompanied by laboratory and clinical signs of iron deficiency and was prevented by the administration of fructo-oligosaccharides, a substance that promotes iron absorption from the gut. In oophorectomised rats (a condition mimicking postmenopausal osteoporosis), a wide range of cells, including osteoblasts, displayed a reduced number of transferrin receptors and hence a reduced iron uptake.6 7 In humans, it has been assessed that out of 14 nutrients tested (including calcium), iron was the best positive predictor of BMD in out of 14 nutrients tested (including calcium), transferrin receptors and hence a reduced iron uptake.6 7 In humans, it has been assessed that out of 14 nutrients tested (including calcium), iron was the best positive predictor of BMD in 711 homochromatosis probands: evidence for S65C implantation in mild form of homochromatosis. Blood 1999;93: 252-2.8

On the basis of the above evidence, we searched for a genetic marker of iron disposal (haptoglobin genotype) as a risk factor for postmenopausal osteoporosis. Only about 5% of daily iron turnover comes from haemoglobin turnover, which requires haem oxygenase. We focused our attention on different genotypes of haptoglobin in normal adults. For example, in patients who underwent gastrectomy3 4 or in rats treated similarly,5 osteoporosis was accompanied by laboratory and clinical signs of iron deficiency and was prevented by the administration of fructo-oligosaccharides, a substance that promotes iron absorption from the gut. In oophorectomised rats (a condition mimicking postmenopausal osteoporosis), a wide range of cells, including osteoblasts, displayed a reduced number of transferrin receptors and hence a reduced iron uptake.6 7 In humans, it has been assessed that out of 14 nutrients tested (including calcium), iron was the best positive predictor of BMD in 711 homochromatosis probands: evidence for S65C implantation in mild form of homochromatosis. Blood 1999;93: 252-2.8

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On the basis of the above evidence, we searched for a genetic marker of iron disposal (haptoglobin genotype) as a risk factor for postmenopausal osteoporosis. Only about 5% of daily iron turnover comes from intestinal absorption, most of it coming from haemoglobin turnover, which requires three proteins, haemopexin, haptoglobin, and haem oxygenase. We focused our attention on haptoglobin since it is the only one with a well known polymorphism.

Haptoglobin (HP) is a serum α2 glycoprotein that exists as a tetramer, composed of two smaller identical alpha (α) and two larger identical beta (β) chains. At present, three main different genotypes of haptoglobin in normal adult plasma have been identified. Differences among the three haptoglobin genotypes are given by light alpha subunit structures: type 1.1, type 2.2, which has homozygous C282Y and H63D mutations on association with β2-microglobulin, intracellular processing, and cell surface expression of the HFE protein in COS-7 cells. Proc Natl Acad Sci USA 1997;94: 12384-9.

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The main function of haptoglobin is to bind free haemoglobin in a stable complex, which is later cleared from the plasma by the liver reticuloendothelial system. Haemoglobin binding capacity depends on the genetic haptoglobin type, on the amount of haptoglobin, and on the number of polymers. Functional differences between haptoglobin genotypes have been described; type 1.1 has the highest haemoglobin carrying ability, while type 2.2 is almost unable to carry it because the Hb binding site is buried by the polymerisation process.

In European populations, the genotype distribution is as follows: about 16% has genotype 1.1, about 48% genotype 2.1, and the remaining 36% genotype 2.2. Several authors have studied the haptoglobin haplotype frequency in different populations and different pathologies, and various haptoglobin genotypes have also been correlated with the serum iron. In spite of the large number of published reports on the topic, no study has been performed to investigate a possible difference in the incidence of haptoglobin genotypes in osteoporotic patients and non-osteoporotic subjects.

In order to investigate the possible correlations between postmenopausal osteoporosis and frequencies of haptoglobin genotypes, we studied a group of women affected by postmenopausal osteoporosis and a control group of non-osteoporotic postmenopausal women.

**Methods**

The osteoporotic group consisted of 135 subjects (age range 40–73 years, postmenopausal age range 6 months–33 years) and the osteoporosis was diagnosed using the Double Emission X ray Absorptiometry (DXA) technique with a Hologic QDR4500 densitometer (Hologic Inc, Waltam, MA, USA). In particular, we considered as osteoporotic patients with a T score value of 2.5 SD or less, according to WHO (WHO Technical Report Series No 843 “Assessment of fracture risk and the application to screening for postmenopausal osteoporosis”, 1994). Secondary osteoporosis was excluded by history, physical examination, and measurement of calcium, phosphorus, and bone alkaline phosphatase (BAP) in the blood.

The control group consisted of 65 non-osteoporotic women (age range 47–76 years, postmenopausal age range 6 months–33 years) (T score >−1 SD).

The HP genotypes of patients and controls were analysed with SDS-PAGE electrophoresis (fig 1). Data were analysed by the χ² test using the Statistical Analysis System (SAS Institute Inc). The odds ratio and the corresponding confidence interval were also calculated for genotype 1.1 versus genotype 2.2 and 2.1. To avoid possible selection bias, we compared the patients and the control group for age, postmenopausal age, body mass index (BMI), and T score (table 1). The controls were, on average, older than the patients (p=0.01) with a longer postmenopausal period (p=0.05).

**Results**

The frequencies of the three haptoglobin genotypes are 32.6% for 2.2, 55.5% for 2.1, and 11.9% for 1.1 in the patient group, while in the control group they are 47.7%, 50.8%, and 1.5%, respectively, with significant differences between the two groups (p=0.0076, χ² test). The odds ratio between genotype 1.1 and genotype 2.2 was 12 (confidence interval = 1.34–106.7). The odds ratio between genotype 1.1 and genotype 2.1 was 7.04 (confidence interval = 1.21–2.9).

**Discussion**

It is well known that advancing age, a prolonged period of amenorrhea, and low BMI are risk factors for osteoporosis. Any possible bias in selection of subjects was excluded as the controls were on average significantly older and the BMI of the two groups was not significantly different.

Our data show that the presence of haptoglobin genotype 1.1 is an important risk factor for postmenopausal osteoporosis. The functional differences between haptoglobin genotypes, namely the fact that type 1.1 has the highest haemoglobin carrying ability and, hence, the highest elimination rate through the liver, while type 2.2 is almost unable to carry it to the liver, can account on a molecular basis for the increased risk for osteoporosis linked to the presence of haptoglobin genotype 1.1. In normal subjects, the amount of iron stores (namely ferritin) is significantly correlated with the HP genotype.

The daily requirement of iron intake to keep the body iron store stable is therefore strongly dependent on the ability of the organism to store iron (HP 2.2) or to waste it (HP 1.1) through the liver.

![Figure 1: Electrophoretic runs of haptoglobin: type 1 appears as a single band furthest from the origin, while types 2.1 (200 kDa) and 2.2 (400 kDa) appear as a series of bands nearer to the origin.](http://jmg.bmj.com/)

**Table 1**: Characteristics of the patients compared to the controls (age, postmenopausal age, BMI, T score). Shown are the mean values, the standard deviation (SD), and the result of Student’s t test.

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The finding that HP genotype may play an important role as a risk factor for osteoporosis may be useful in clinical practice to identify in advance the women who will probably develop postmenopausal osteoporosis and so allow primary prevention of the disease and reduce the social cost of its consequences.

This work was supported by a grant from the Ministero dell’Università e della Ricerca Scientifica e Tecnologica (MURST, 60%) of Italy.


**GDNF** as a candidate modifier in a type 1 neurofibromatosis (NF1) enteric phenotype

Michel Bahauad, Anna Pelet, Dominique Vidaud, Thierry Lamireau, Brigitte Le Bail, Arnold Munnich, Michel Vidaud, Stanislas Lyonnet, Didier Lacombe

**Editor**—Neurofibromatosis type 1 (NF1) is a common human disorder (1/3500 live births) with neuroectodermal involvement primarily resulting in dermatological manifestations of café au lait spots, cutaneous/subcutaneous neurofibromas, and freckling of major skin folds.1 Owing to diagnostic uncertainties, especially in young patients, an international scoring system has been discussed and agreed upon.2 Half of the cases result from new mutations, while others show an autosomal dominant mode of inheritance. The encoded product, referred to as neurofibromin, is a member of the so called GTPase activating proteins (GAPs), and is an upstream down-regulator of the RAS(p21)/RAF/MAPkinase3 and RAS/RA1 signalling pathways. Although locus homogeneity is a hallmark of this condition, phenotypic heterogeneity has been exemplified by a wide spectrum of diversity ranging from malformation or malignant variants to virtually benign dermatological changes.1 In particular, and among the many causes of gastrointestinal involvement in NF1 patients, the association with intrinsic intestinal dysmotility, resulting from intestinal neuronal dysplasia type B (IND B)4,5 or aganglionic megacolon (Hirschsprung’s disease, HSCR),5 has been documented and is now well established. Interestingly, a substantial fraction of the phenotypic variability seen in NF1 patients might be governed by non-allelic, trait specific, “modifying” loci.6 Although the action of such modifying loci has been primarily shown in the number of café au lait spots or the number of cutaneous/subcutaneous neurofibromas, it can be speculated that such a genetic phenomenon might also be operative in other phenotypic traits, especially in individual or familial cases with an enteric phenotype. The female proband from the family analysed here (fig 1A) had minor cutaneous manifestations of NF1, dysomorphic facial features (midface hypoplasia), congenital heart disease (ventricular septal defect, coarctation of the aorta), and congenital megacolon. She subsequently underwent a Duhamel abdominoperineal pull through and pathological examination of the whole colectomy specimen pointed to IND B (fig 2), because of findings of (1) abnormal submucosal plexuses showing focal hyperplasia (in terms of density and sizes), (2) occasional giant ganglia harbouring >10 neurons, and (3) nerve cell buds along afferent nerves.7 The older sister also had NF1 and congenital megacolon, while a brother was totally unaffected. NF1 was inherited from the mother and maternal grandmother, who both had a mainly cutaneous form of the condition. The father was healthy.8

Although IND B may segregate as a monogenic disorder, no specific locus has been

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of anomalous neural crest cell derived structures, especially parasympathetic enteric neurons, these genes were good candidate modifiers. For this reason, GDNF and NRTN gene exons were analysed for DNA changes by SSCP and sequence analysis, as previously reported. While NRTN showed no sequence variation (data not shown), a missense mutation was found within GDNF exon 2, changing codon 93 from arginine (CGG) to tryptophan (TGG) (R93W, fig 1B). The R93W mutation could be regarded as potentially pathogenic, since (1) it resulted in a non-conservative amino acid change at an evolutionarily conserved residue in the direct vicinity of a putative propeptide cleavage site and transforming growth factor beta (TGFB) related cystein rich motifs, (2) it was found in other patients with distinct neural crest cell related anomalies such as HSCR (in addition to mutations of RET), or the CCHS-HSCR association, and (3) it was conspicuously absent from a large number of control DNAs. Of interest, this is the first GDNF mutation seen in a patient with IND B without aganglionosis. The recurrence pattern of this mutation is probably explained by its relation to a CpG dinucleotide mutational hot spot. GDNF is probably the most powerful neurotrophin identified to date. It is the first identified member of a family of growth factors distantly related to TGFBs (see Bohn for a recent review and Ramer et al for an update on neurotrophic effects), whose action is mediated by binding to a multicomponent system composed of RET receptor tyrosine kinase (RTK), and glycosylphosphatidylinositol (GPI) linked cell surface adapter proteins (GFRA1, GFRA2). Signalling through RET can trigger phosphatidylinositol-3 kinase (PI3K), leading to activation of either members of the Rho family of GTPases (RHO, RAC, and CDC42) with ensuing rearrangements of the actin cytoskeleton and axon outgrowth, or protein kinase B (PKB) mediated effects on metabolism or gene transcription. Interestingly, in both these pathways, PI3K requires functional RAS. In addition, stimulation of RET leads to SHC-GRB2-SOS complex formation and RAS activation, the RAF and RAL families of GTPases acting as downstream effectors (fig 3). Although it is difficult to predict the exact outcome of the combination of mutations reported here for the subcellular signalling network, it can be speculated that certain pathways are markedly impaired while others are only mildly affected, especially since the NFI/GDNF double heterozygote infants depicted here have severe developmental alterations but only minor symptoms related to deregulated cell growth. Of special interest is that one might have expected functional recovery of the NFI mutation by the GDNF lesion, since NFI disruption generates activated, GTP bound RAS, whereas low GDNF maintains RAS in the GDP bound form. A possible rationale comes from the observation that RAF1 is able to induce growth arrest and differentiation of discrete human carcinoma linked to this recognised Mendelian entity (MIM 601223). However, since ∼30% of IND B patients have accompanying aganglionosis, that is, HSCR, the RET proto-oncogene, the genes encoding endothelin receptor B (EDNRE), or its ligand endothelin 3 (EDN3) are candidate genes for isolated IND B. Here, none of these genes was found to be mutated, suggesting that the NFI-IND B combination observed here was indeed an integral NFI variant.

However, the scarcity of this specific variant and the small family sizes has hindered the identification of modifying loci by phenotype and pedigree based analyses. The initial observation of an out of frame insertion within NFI exon 16 (2424-2425insCCTTCAC, fig 1B) favoured a null lesion, that is, it did not support causal genotype-phenotype correlation. The fact that only those relatives with the NFI mutation and a cytogenetically balanced reciprocal translocation t(15;16)(q26.3;q12.1) (fig 1A) had intrinsic intestinal dysmotility suggested that a modifier gene might have been altered at one of the translocation breakpoints. However, none of the breakpoint regions is known to harbour a gene involved in the development of the parasympathetic ganglion cells of the digestive tract and this family was the investigated further for putative modifiers lying elsewhere in the genome.

As changes in GDNFs and the neurutrin gene (NRTN) suggested polygenic causation
Murine models were generated for both NF1 and GDNF through disruption by homologous recombination in embryonic stem cells. Mice lacking Gdnf (Gdnf-) had total renal agenesis, resulting from defective induction of the ureteric bud and absent enteric neurones, also consistent with additional manifestations of pyloric stenosis, duodenal dilatation, and congenital megacolon. These models are highly reminiscent of Ret deficient mice (Ret-), providing a functional confirmation that GDNF is a ligand of RET. Heterozygotes (Gdnf+/) were indiscernible from wild type litter mates. However, heterozygous NF1 mutants (NF1+) do not replicate the human disorder (in particular, they do not develop obvious neurofibromas or pigmentation defects).41 42

Conversely, these mice are prone to age related tumours, in addition to malignancies reminiscent of human NF1 (especially phaeochromocytomas and myeloid leukaemia).42 Interestingly, homozygotes (NF1-) die in utero from severe cardiac malformation, especially involving the neural crest cell derived conotruncus,41 42 and show hyperplasia of the pre- and paravertebral sympathetic ganglia,41 indicating that the phenotype is both dosage sensitive, as in GDNF, and malformative rather than tumourous, eventually confirming the important role of neurofibromin during development. These models and the family presented here suggest murine NF1 x Gdnf- intercrosses for the phenotypic analysis of double mutants as an ultimate demonstration of a modifier gene effect.43

Modifying genes are not just hypothetical and HSCR families have provided particularly fruitful material for eliciting such entities. Two hitherto anonymous loci have been indicted in polygenic inheritance of HSCR. The first such example was illustrated by a large inbred Menonite HSCR pedigree that segregated a missense mutation in EDNRB and otherwise showed linkage disequilibrium with marker alleles mapped to 21q22.41 This finding is highly suggestive of a HSCR genetic modifier that links to this chromosomal region, which might elsewhere account for the high HSCR prevalence among trisomy 21 patients. More recently, genome wide non-parametric linkage was performed on a panel of HSCR pedigrees which selected a particular subgroup in the sense that these were either unlinked to RET or showed positive linkage but with no sequence alteration identified at that locus. From these families, significant linkage to a locus in 9q31 was found, suggesting that this genetic region contains a gene whose variation entails a specific susceptibility to HSCR, with or without concomitant linkage to RET.44 More straightforward evidence for a HSCR modifier was exemplified by the genes encoding glial cell line derived neurotrophic factor (GDNF) and, more recently, neurturin (NRTN), two highly homologous natural ligands of the RET tyrosine kinase receptor protein. Indeed, since GDNF and NRTN were found to be mutated in families also segregating well characterised RET alleles, it was postulated that alterations of these genes were not sufficient in themselves to

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Figure 2. Intestinal neuronal dysplasia. The colectomy specimen was fixed in Bouin’s reagent for 12 hours. Transverse sections were cut every centimetre, from both normal and pathological segments, and were routinely processed for histology. Four millimetre serial paraffin embedded sections were stained with haematoxylin-eosin-sa (HES). A distinctive neurones, as shown by characteristic vesicular nuclei and abundant amphophilic cytoplasm (HES).
cause HSCR, but that they probably contributed to the severity of the phenotype or to higher penetrance of the RET mutations.

Although molecular evidence for modification proper in the pathogenesis of human NF1 has not been provided to date, the possibility of epistatic interaction of the NF1 (Nf1) gene with other discrete loci was recently illustrated both in man and in a murine model for human NF1. Human pedigrees with hereditary non-polyposis colorectal cancer (HNPCC) have been reported in which children homozygous (doubly heterozygous) for an MLH1 mutation were shown to develop extracolonic malignancies of early onset and de novo NF1. These observations suggest that the NF1 gene is prone to common replication errors during mitosis and/or meiosis, and that MLH1 plays a particular role in monitoring these types of DNA lesions. These very important observations point to mismatch repair (MMR) genes as possible targets during NF1 tumour advancement and shed new light onto the rather unexpected microsatellite instability observed in NF1 derived tumours.

In mice, different combinations of mutations of Nf1 and/or Trp53 (homologous to TP53) were generated through intercrosses. The first remarkable observation was that, unlike their Nf1−/− or Nf1−/− congeners, mice that were haploinsufficient for both Nf1 and Trp53 developed benign or malignant peripheral nerve sheath tumours (MPNSTs) and malignant Triton tumours reminiscent of human NF1. In addition, permanent cell lines established from some of these mice showed a pattern of gene expression consistent with immortalisation of pluripotent neural crest stem cells, whether the original tumours were of seemingly mesodermal or of conspicuous neural crest origin. These data provide further evidence of linkage of RAS with the cell cycle machinery, especially with the pathways that are linked with the activation of TP53, and confirm the commonality of neural crest involvement in NF1 pathogenesis. In addition, these intercrosses clearly support the hypothesis that functional protein-protein interaction is a strong substratum for epistasis or modification.

In the family presented here, especially in the two infants who are doubly heterozygous for the NF1/GDNF lesions, it is questionable whether GDNF modification accounts for wider involvement of neural crest cell derivatives, such as midface hypoplasia (through disruption of the cranial crest mesectoderm) or conotruncal heart disease (VSD and coarctation of the aorta), also observed in the proband. Whatever the case, our findings seemingly confirm the previous speculation...
that genes whose products interact functionally with RAS are potential NF1 modifiers. Once identified, these modifiers will provide tools to understand interactions with the subcellular signaling network in NF1 patients and may lay the basis for new therapeutic approaches.

- A family with neurofibromatosis type 1 (NF1, MIM 162200) and congenital megacolon (intestinal neuronal dysplasia, IND B) was investigated for possible genetic modifiers. A germline mutation in the NF1 gene, c.2424InsCCTTCAC, and a germline GDNF variant R93W were found in this family.

- In this kindred, only members with both the paternally derived GDNF R93W and the maternally inherited NF1 mutation had megacolon.

- Such epistatic interaction between NF1 and GDNF is in keeping with functional cross-talk of the RET and RAS pathways in a complex subcellular signaling network.

The first two authors contributed equally to this work. We are grateful to Drs L. Taine, P. Vergnes, S. Gallet, and J-F. Chateil for their contribution to investigating this family, to I. Laurendeau and Taine S. M., for their contribution to investigating this family, to I. Laurendeau for establishing and maintaining lymphoblastoid cell lines. This work was supported by the Association pour la Recherche contre le Cancer (ARC) and the French Ministère de l’Éducation Nationale et de la Recherche, and the Association Française contre les Myopathies (AFM).


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Six novel mutations in the PRF1 gene in children with haemophagocytic lymphohistiocytosis

Rita Clementi, Udo zur Stadt, Gianfranco Savoldi, Stefania Varotto, Valentino Contar, Carmela De Fusco, Luigi D Notarangelo, Marion Schneider, Catherine Klersy, Gritta Janka, Cesare Danesino, Maurizio Aricò

EDITOR—The histiococytes represent a heterogeneous group of disorders including both hereditary and sporadic forms. The familial form of haemophagocytic lymphohistiocytosis (HLH) was originally described by Parquhar and Clarkeaux in 1952. The main features of this disease are fever, hepatosplenomegaly, cytopenia, hypertriglyceridaemia, hypofibrinogenaemia, and central nervous system involvement. PRF1 is a gene encoding a 7.8-kb protein in mice involved in the regulation of the immune response. PRF1 has also been implicated in the regulation of the immune response in humans. A human model for multigenic inheritance: phenotypic expression in Hirschsprung disease requires both the RET gene and a new 9q31 locus. Proc Natl Acad Sci USA 2000; 98:2846.

We report six novel mutations and also confirm three additional mutations which had been previously reported. They were observed in 10 patients of Italian, Turkish, and Ghanaian origin.

Materials and methods
We studied 10 families in which the index case fulfilled the diagnostic criteria for HLH and a careful family history was collected. Consanguinity was investigated and when not evident the parents were asked to obtain further information regarding their ancestry. Clinical data were obtained from the attending physicians and from thorough evaluation of records.

Natural killer activity was determined in one of the two reference laboratories (Dr Rita Maccario, Pavia, Italy and Professor Marion Schneider, Ulm, Germany) as previously reported. Molecular analyses were performed as reported by Stepp et al, sequencing exons 2 and 3 of the PRF1 gene. The sequences obtained were compared to the reported gene structure (gene number 190339 NCBI) using the BLASTN program (http://www.ncbi.nlm.nih.gov/BLAST). In order to
confirm the mutations found, the parents were also tested in all but three families, in which the mutations were confirmed by repeated experiments or by identification of the same mutation in the affected sib. In families in which consanguinity was considered possible on the basis of available information, polymorphic markers (D10S537, D10S676) were tested to confirm this.

STASTICAL ANALYSIS
The median age at diagnosis and quartiles were calculated for each group of children. The cumulative probability of diagnosis free survival was computed by means of Kaplan Meier estimation. Incidence rates expressed as events per person month were calculated for each group. Time to diagnosis distributions were compared between mutated and non-mutated subjects by means of the log rank test.

Results
We have identified six novel mutations in the PRF1 gene; three additional mutations that we observed had been previously reported by Stepp et al.\textsuperscript{10} Two novel mutations (C657A in case 3 and 1182 ins T in case 6) (table 1) introduced a stop codon in the sequence which resulted in a truncated protein. The other novel mutations (T283C in case 2, G658A in case 4, C662T in case 5, and C694T in case 6) caused an amino acid change. The mutations we observed are scattered along exons 2 and 3 without any obvious clustering. Four mutations were located in the second transmembrane domain while two occurred within or close to the EGF-like domain of the protein.\textsuperscript{14} It is remarkable that all the four patients of Turkish origin had the same mutation, G1122A. In 21 additional caucasian patients with HLH a mutation was not found. In 231 cases enrolled in the Registry with information on this, the median age at diagnosis was 5.3 months (range 0-254 months) (p=0.05); 32% were diagnosed within three months and 80% within two years. One of our patients with PRF1 mutations remained asymptomatic until the age of 6 years when he developed full blown HLH. Among the Registry patients, 17 (8.1\%) presented when older than 5 years of age, with an estimated risk of being diagnosed when older than 5 years of 8.1\% (SE 1.8).

Although difficult to quantify, all patients had a very severe presentation and clinical course. They had to be aggressively treated and showed early relapse after disease control was initially achieved. All six patients who underwent BMT remain asymptomatic.

Discussion
We have described six novel mutations in the PRF1 gene in children with HLH; two introduced a premature stop codon in the sequence which resulted in a truncated protein, while the other four caused an amino acid change. Caution should be exercised in interpreting a missense mutation which causes an amino acid change to be responsible for the disease and is not just a population polymorphism. In our cases, these mutations modified a conserved amino acid and were never found in other subjects tested. These mutations were scattered along exons 2 and 3 without any obvious clustering, in keeping with the previous report by Stepp et al.\textsuperscript{10} The same mutation, G1122A, was observed in the four patients of Turkish origin. This mutation had been observed twice by Stepp et al\textsuperscript{10} in patients of unspecified origin and was also reported in patients of Turkish origin.\textsuperscript{15} Altogether these data indicate that, at least in a subset of patients of Turkish origin with HLH, a founder effect is possible. Further analysis of affected children from the same geographical region should be undertaken to confirm this. No founder effect can be hypothesised in patients of Italian origin.

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Table 1  Details of mutations in the perforin 1 gene observed in 10 patients with HLH

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<td>Turkey</td>
<td>*</td>
<td>1122</td>
<td>3</td>
<td>g&gt;a</td>
<td>W 374 stop</td>
<td>EGF-like</td>
</tr>
</tbody>
</table>

**/*** = heterozygous/homozygous mutation.
† The same mutation was also observed in his brother with an identical clinical picture.
‡ These mutations have been previously described by Stepp et al.\textsuperscript{10}
2nd TM = second transmembrane domain.
EGF-like = epidermal growth factor-like domain.
Fs = frameshift.
Table 2 Presenting features and treatment outcome in 10 patients with HLH and PRF1 gene mutations

<table>
<thead>
<tr>
<th>Case</th>
<th>Gender</th>
<th>Ethnic origin</th>
<th>Age at diagnosis</th>
<th>Fever</th>
<th>Hepatosplenomegaly</th>
<th>Skin rash</th>
<th>Lymphadenomegaly</th>
<th>CNS alterations</th>
<th>Oedema</th>
<th>Jaundice</th>
<th>Associated infection</th>
<th>Present status</th>
<th>Haemoglobin (g/dl) mth after BMT</th>
<th>Platelets (1000/mm3) ×</th>
<th>Neutropenia</th>
<th>Hypertriglyceridaemia</th>
<th>Hypofibrinogenaemia</th>
<th>CSF pleiocytosis</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>M</td>
<td>Ghana</td>
<td>2 mth</td>
<td>++++</td>
<td>+</td>
<td>−</td>
<td>++</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>E coli, EBV</td>
<td>Asymptomatic</td>
<td>5.5</td>
<td>15</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>2</td>
<td>F</td>
<td>Italy</td>
<td>3 mth</td>
<td>++++</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>EBV, URI</td>
<td>Asymptomatic</td>
<td>6.4</td>
<td>46</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>3</td>
<td>M</td>
<td>Italy</td>
<td>1.5 mth</td>
<td>+++</td>
<td>+</td>
<td>+</td>
<td>++</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>EBV</td>
<td>Asymptomatic</td>
<td>7.8</td>
<td>7.8</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>4</td>
<td>M</td>
<td>Italy</td>
<td>1.5 mth</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>URI</td>
<td>Asymptomatic</td>
<td>46</td>
<td>ND</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
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<tr>
<td>5</td>
<td>F</td>
<td>Turkey</td>
<td>6 mth</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>CMV</td>
<td>Asymptomatic</td>
<td>28</td>
<td>35</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>6</td>
<td>M</td>
<td>Turkey</td>
<td>6 y</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>CMV</td>
<td>Asymptomatic</td>
<td>8.4</td>
<td>9.6</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>7</td>
<td>F</td>
<td>Turkey</td>
<td>3 mth</td>
<td>++</td>
<td>+</td>
<td>+</td>
<td>++</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>CMV</td>
<td>Asymptomatic</td>
<td>7.8</td>
<td>8.4</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
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<td>M</td>
<td>Turkey</td>
<td>2.5 mth</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>CMV</td>
<td>Asymptomatic</td>
<td>18</td>
<td>ND</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>9</td>
<td>F</td>
<td>Turkey</td>
<td>12 mth</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>CMV</td>
<td>Asymptomatic</td>
<td>42</td>
<td>ND</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>10</td>
<td>M</td>
<td>Turkey</td>
<td>4 mth</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>CMV</td>
<td>Asymptomatic</td>
<td>4.4</td>
<td>ND</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
</tbody>
</table>

Note: Items in bold are among the diagnostic criteria for HLH. P: possible; URI: upper respiratory infection; NA: not applicable; ND: not determined; ↓: decreased.

In conclusion, our data confirm that PRF1 mutations can occur throughout the coding region of exons 2 and 3 and suggest a founder effect for HLH in Turkey but not in Italy. HLH resulting from PRF1 mutation usually presents in infancy but occasionally may occur in older patients. Identification of a genetic defect in patients with HLH has diagnostic, prognostic, and therapeutic implications and should be pursued whenever possible. Despite frequent concordance of the age at onset within each family, asymptomatic sibs (including potential stem cell donors) cannot be safely defined as unaffected, unless their genetic status for HLH is assessed. Lack of this information may risk...
A novel mutation in the endothelin B receptor gene in a patient with Shah-Waardenburg syndrome and Down syndrome

J P Boardman, P Syrris, S E Holder, N J Robertson, N Carter, K Lakhoo

EDITOR—A case of Down syndrome, total gut Hirschsprung disease (HSCR), and segmental hypopigmentation is described in a neonate presenting with bowel obstruction. In addition to having trisomy 21, this patient was homozygous for a novel mutation in the endothelin B receptor (EDNRB) gene.

A term female infant with karyotype 47,XX,+21 presented on day 3 of life with bowel obstruction. She was of Somali origin and had large areas of segmental hypopigmentation affecting the left side of the face and trunk, the left upper limb, including the hair follicles, and had white scalp hair. At laparotomy she had an annular pancreas, duodenal web, and inspissated meconium in the ileum and colon, for which she underwent a duodenal and colonic resection. Histology of the rectal biopsy and appendix was inconclusive at this stage. Intestinal obstruction persisted and on day 20 she underwent a further laparotomy, which showed breakthrough of the original anastomosis. Intraoperative frozen sections showed complete aganglionosis throughout the entire large and small bowel, sparing only the stomach and oesophagus; this is incompatible with life. An ileostomy was fashioned, intensive nutrition was given, and the patient had an undulating course leading to death at 10 days of age.

This work was supported in part by the following grants: Telethon Italy, grants C30 (CD) and E795 (MA); Ricerca Corrente 390/RCR7/01 and 80291, IRCSS Policlinico San Matteo, Pavia (Italy); MURST (c分工ination 1999) (LDN), and by the “Associazione Antonio Panino” (Petralia, Palermo, Italy). The authors are grateful to Dr Michaela Allen and Dr Michaela Müller-Rosenberger for their help in data collection and manuscript preparation.

References


crested cell lineages: epidermal melanocytes and enterocytes.

A number of susceptibility genes for HSCR alone have been identified from the 5% of HSCR cases in whom there is an associated chromosomal or hereditary disorder and from HSCR affected kindreds.1 Susceptibility to Shah-Waardenburg syndrome is conferred by variations in this axis in both rodent models and in the endothelin-3 gene (EDN3 receptor) mutations in three genes, the endothelin B receptor (EDNRB) gene, a mutation of the RET proto-oncogene and disrupts receptor function, suggested by the finding that several other mutations in the transmembrane domains of the protein are known to cause a phenotype of aganglionosis and hypopigmentation; the human manifestations are the spectrum of Shah-Waardenburg phenotypes.7 The exact position of the mutation in the homozygous state is likely to produce the pleiotropic features observed in these patients.

There are case reports of patients with Down syndrome in association with both HSCR and/or Shah-Waardenburg determining genes.9 10 However, this patient had the coexistence of Down syndrome and a new homozygous mutation of the EDNRB gene. This case emphasises that although HSCR has a well recognised association with Down syndrome, other causes of HSCR should be considered. Mutation analysis of known susceptibility genes might be helpful in cases of long segment HSCR, especially in those patients with pigmentary abnormalities and those with a positive family history of bowel dysfunction.

A G339R mutation in the CTNS gene is a common cause of nephropathic cystinosis in the south western Ontario Amish Mennonite population
C Anthony Rupar, Douglas Matsell, Susan Surry and Victoria Siu

J Med Genet 2001 38: 615-616
doi: 10.1136/jmg.38.9.615

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