Metachromatich leucodystrophy (MLD) in a patient with a constitutional ring chromosome 22

M B Coulter-Mackie, J Rip, M D Ludman, J Beis, D E C Cole

Metachromatic leucodystrophy (MLD) is a neurodegenerative lysosomal storage disease resulting from a deficiency of arylsulphatase A. The arylsulphatase A gene is located on chromosome 22 at q13.3. An MLD patient is described who carries a common splicing mutation ("I" allele) and a de novo ring 22 deleted for the arylsulphatase A gene. The father was determined to be a heterozygous carrier of the "I" allele and the mother a heterozygous carrier of the arylsulphatase A pseudodeficiency allele. The ring 22 was shown by Southern blotting to be deleted in one copy of the arylsulphatase A gene. Minisatellite analysis showed the extent of the deletion and confirmed the biparental inheritance of chromosome 22 sequences. The carrier status of the parents and the patient's 46,XX,r(22) karyotype complicated the initial diagnosis in this family. However, the causal relationship of the ring 22 and MLD have implications for the recurrence risk in this family.

Materials and methods
CASE REPORT
This female child was born to non-consanguineous parents. She showed delayed development in her first year and was investigated for deafness at 14 months. Unusual physical features including large ears, high forehead, upward slanting eyes, microgathria, large extremities, and broad hands with short phalanges were noted at that time. She also had spina bifida occulta with a sacral dimple. Karyotype investigation showed a possible ring chromosome 22 in all cells examined. This was later confirmed in two subsequent karyotype studies. A partial spread of metaphase chromosomes from cultured fibroblasts is shown in fig 1. Neither parent showed the ring 22 formation. Because the child's condition was worsening more rapidly than would be expected from the ring chromosome alone, she was investigated for the possibility of metabolic errors. Enzymatic assay of arylsulphatase A in fibroblast extracts gave a diagnosis of MLD when the child was 2 years 3 months. She deteriorated rapidly becoming deacrebrate by the age of 2 years 4 months and died at 2 years 10 months.

MATERIALS
Taq polymerase was purchased from Promega. ID Pol, a heat stable DNA polymerase from *Thermus flavus*, was obtained from ID Labs Inc (London, Ontario). Restriction enzymes were
from Pharmacia Biotech (Baie d’Urfé, Quebec), New England Biolabs (Mississauga, Ontario), or Boehringer Mannheim Canada (Laval, Quebec). [α-32P]dCTP (specific radioactivity 3000 Ci/mmol) was from Amersham Canada. MapPairs™ for minisatellite analysis were purchased from Research Genetics (Huntsville, Alabama). A USB Random Primed DNA Labelling kit was purchased from Amersham Canada.

**DETERMINATION OF ASA ACTIVITY IN FIBROBLAST EXTRACTS**

Fibroblast cultures were grown under standard conditions and harvested at about 75% confluence for assay. Cells were homogenised and cell free supernatants were used in assays with a p-nitroctatehol sulphate substrate in an assay specific for ASA (J Rip and B A Gordon, manuscript in preparation) modified from Baum et al.12

**POLYMERASE CHAIN REACTION (PCR) AMPLIFICATION**

The following oligonucleotide primers are from a series designed for screening for common mutations in the ASA gene and were used in the PCR amplifications described below and in table 1:

1. 5’ GGGAGATTCTTGTGAGGCAACTGAGTGAC 3’
2. 5’ GCACAGCTGAAGCCTGAAAATCTGCTCC 3’
3. 5’ CTATGAGCAATTCCTGACACGGCAAG 3’
4. 5’ CACAGATTCCAGGACTCTGTCATGGTGCAG 3’
5. 5’ TGCTCAGCCTGCAAGAGCTCCTCAGGGTTGA 3’
6. 5’ GGAGGTAGGTCACAGCATAAAGCATTGTCAG 3’

**Restriction enzyme recognition sites were incorporated into primers 3, 4, 6, and 10 at the 5’ ends to facilitate cloning. Mismatched bases introduced in primers 11 and 12 to generate new restriction sites in the PCR product are underlined. All primers were synthesised using phosphoramidite chemistry on an automated DNA synthesizer.**

**PCR amplifications were performed using published procedures.**

The following amplification conditions were used for the ASA gene: Hot start (94°C for 30 s), followed by 30 cycles of 94°C for 30 s, 50°C for 30 s, and 72°C for 30 s. For PCR of chromosome 22, annealing was extended to 2 min. For reactions at 37°C, cycling parameters were: denaturation – 94°C; annealing – 37°C; extension – 2 min. PCR products were digested with restriction enzymes and separated on 3% agarose gels and visualised by autoradiography.

**SOUTHERN BLOT ANALYSIS**

DNA samples from plasmids and labelled with [α-32P]dCTP by random primed labelling. Genomic DNA samples (5 μg each) were digested with HindIII, and subjected to electrophoresis in 0·8% agarose, capillary blotting in neutral buffer, and hybridisation with probe by standard methods.17

**Table 1**  

<table>
<thead>
<tr>
<th>Site</th>
<th>Primers</th>
<th>PCR product size (bp)</th>
<th>Annealing temperature</th>
<th>Restriction enzyme</th>
<th>Restriction site in normal sequence*</th>
</tr>
</thead>
<tbody>
<tr>
<td>“I-1”</td>
<td>15/16</td>
<td>220</td>
<td>60°C</td>
<td>MvaI</td>
<td>+</td>
</tr>
<tr>
<td>“I-1/2”†</td>
<td>10/4</td>
<td>738</td>
<td>65°C</td>
<td>MvaI</td>
<td>+/+</td>
</tr>
<tr>
<td>“I-1; glycosylation†”</td>
<td>3/19</td>
<td>860</td>
<td>65°C</td>
<td>Bcl</td>
<td>+/-</td>
</tr>
<tr>
<td>Poly A</td>
<td>17/11</td>
<td>147</td>
<td>65°C</td>
<td>RsaI</td>
<td>–</td>
</tr>
<tr>
<td>Glycosylation</td>
<td>3/12</td>
<td>157</td>
<td>60°C</td>
<td>MauIII</td>
<td>–</td>
</tr>
</tbody>
</table>

*Normal sequence as per accession number X52150 (EMBL).
†Simultaneous detection of the two sites.

**Results**

ASA ACTIVITY IN FIBROBLAST EXTRACTS

Fibroblasts extracts from the patient, her parents, and controls were analysed for ASA ac-
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Table 2 ASA enzyme activity in fibroblast extracts*

<table>
<thead>
<tr>
<th>Sample</th>
<th>ASA activity</th>
<th>% control activity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mother</td>
<td>17.01</td>
<td>44.9</td>
</tr>
<tr>
<td>Father</td>
<td>10.14</td>
<td>26.8</td>
</tr>
<tr>
<td>Patient</td>
<td>0.009</td>
<td>0.02</td>
</tr>
<tr>
<td>Control</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Average</td>
<td>37.9</td>
<td>(22.3-49.6)</td>
</tr>
<tr>
<td>Range</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Activity measured with p-nitroacetyl sulphate as described in Methods.

Further support for this comes from PCR based analyses of the “I-2” and “I-3” polymorphisms and the pseudodeficiency mutations as outlined in Table 1. The “I-1” and “I-2”, and the “I-3” and glycosylation mutations can be detected simultaneously (data not shown). The glycosylation mutation can also be identified independently of the “I-3”. Results for the poly A signal mutations are shown in Fig 2B. The samples from the father and daughter were not cut by RsaI indicating that they were both homozygous negative for the mutation. The mother’s sample was partly cut by RsaI indicating that she is a carrier of the mutation. In summary, the father is heterozygous for all three “I” mutations and homozygous negative for the two pseudodeficiency mutations (glycosylation and poly A). The mother is homozygous negative for all three “I” mutations and a heterozygous carrier for the two pseudodeficiency mutations. The patient carries the three “I” mutations but not the two pseudodeficiency mutations. The finding of a pseudodeficiency allele in the mother accounts for her decreased level of ASA enzyme activity. Clearly none of the mother’s ASA markers, neither her pseudodeficiency mutations, nor her normal sequence at the sites of the “I” mutations, have been passed to her daughter, consistent with a complete deletion of the gene.

PCR/RESTRICTION ENZYME ANALYSIS
DNA from family members was tested for the “I-1” mutation using primers 15 and 16 and the restriction enzyme 1, as outlined in Table 1. Results shown in Fig 2A clearly indicated that the father’s PCR product was partly cut by 1, and thus he is a heterozygous carrier of this mutation. The patient’s sample appears to be homozygous for the “I-1” mutation; it was totally uncut. However, the mother’s sample was completely cut and therefore she does not carry the “I-1” mutation. This suggests that her daughter is probably deleted in one ASA allele and is actually hemizygous for the “I-1” mutation.

SOUTHERN BLOT ANALYSIS
DNA from family members was cut with restriction enzymes and subjected to agarose gel electrophoresis and Southern blot analysis. Results of HindIII digestion and hybridisation with a probe for the ASA cDNA are shown in Fig 3. Visually the patient’s sample appears to be about half the density of that of the parents,

Figure 2 PCR/restriction enzyme analysis. Genomic DNA was amplified by PCR and subjected to digestion. (A) “I-1” allele: lane 1, father (F); lane 2, patient (P); lane 3, mother (M). A 220 bp standard is indicated to the left. The 220 bp abnormal product is not cut by MvaI. The 175 bp product results from cutting of a normal 220 bp PCR product by MvaI. (B) Poly A pseudodeficiency mutations: samples are shown + additions of RsaI. Sample 1, pseudodeficiency homozygote control (PD); sample 2, father (P); sample 3, patient (P); sample 4, mother (M). The 147 bp normal product is not cut by RsaI. The 117 bp product results from cutting of an abnormal 147 bp product by RsaI. A 154 bp standard is indicated on the left.

Figure 3 Hybridisation with an ASA cDNA probe. Lane 1, father (F); lane 2, patient (P); lane 3, mother (M); lane 4, control (C). Sizes of the restriction fragments are given in kb.
suggestive of deletion of one allele. Analysis of the same blot with a probe for the proximally located D22S55 site, pH9118 (data not shown), gave a similar result with a single band of 5.5 kb, again consistent with a deletion and suggesting that the loss of material from C22q extends proximal to the ASA gene at least as far as D22S55. The approximate location of D22S55 relative to the ASA gene is shown in fig 4.

MINISATELLITE ANALYSIS

Minisatellite analysis was performed on this family and the results are shown in fig 5. Approximate locations of all markers used are shown in fig 4. Amplification with the primers for the markers D22S315 and TOPIP2 clearly indicated inheritance of unique alleles from both parents in the child. The markers D22S283 and CYP2D also showed probable inheritance from both parents; however a common allele is shared by all three family members. Thus, these markers are proximal to the breakpoints involved in the ring formation. These data, in conjunction with the "I" allele inheritance pattern, confirm that there is bi-parental inheritance of chromosome 22 sequences and that the ring with the deletion is of maternal origin.

ASA SPECIFIC mRNA TRANSCRIPTION

The production of ASA specific mRNA in the patient was tested using RT-PCR as described in Methods. Virtually no product was detectable in the child's sample although appropriate sized products were detected when primers for an unrelated gene (aspartylglucosaminidase) on another chromosome were used (data not shown). These results are consistent with the expectation of essentially no functional ASA specific mRNA where one allele is deleted and the other carries a major splicing mutation.

Discussion

We have reported here a case of a female patient with MLD who has inherited a paternal chromosome 22 carrying the infantile onset "I" allele and has a de novo constitutional ring chromosome 22 of maternal origin, deleted for the ASA gene. The deleterious "I-1" mutation is a splicing defect and is not expected to produce any active enzyme of functional mRNA. The deletion of the other ASA allele would also preclude production of functional mRNA. This was indeed the case, as no RT-PCR products of appropriate size were detectable in this child although the mRNA was able to support transcription of an unrelated cDNA and PCR product.

A typical clinical picture of a patient with a constitutional ring 22 includes significant mental retardation, microcephaly, growth failure, hypotonia,19 and perhaps a predisposition to meningioma formation.20-22 In this particular case the child referred for cytogenetic analysis because of dysmorphic features, several of which have been noted in other cases of ring 22. De novo ring chromosomes affecting chromosome 22 are relatively rare, comprising approximately 9 to 10% of all constitutional autosomal rings.23 Autosomal rings occur in about 1/50 000 live births although they have also been detected as isolated findings in men-

Figure 4 An ideogram of chromosome 22 showing the approximate locations of the markers described.17,18

Figure 5 Minisatellite analysis: 2 μl aliquots of 10 μ reactions were loaded onto the gel. The samples are from the father (F), patient (P), and mother (M) respectively in each set of three. Alleles are designated a, b, c, and d.
At the time of presentation here, the coinheritance of a severe allele from the father resulted in infantile onset MLD.

Children with infantile onset MLD usually develop clinical signs between the ages of 15 months and 2 years. They lose the ability to walk or stand and show ataxia, weakness, and progressive spastic quadriparesis. Blindness, seizures, and loss of speech are commonly seen. Neurological function declines rapidly to a de cerebrate state and the disease culminates in death usually within one to seven years of onset.

There are not usually striking dysmorphic features associated with MLD.

A metabolic error was not initially suspected in this child. It was not until it became obvious that she was deteriorating much more rapidly than would have been expected for ring 22 alone that she was investigated for possible metabolic errors. Subjects with documented ring 22 alone\(^\text{19}\) have usually survived longer.

Those with one deleted arylsulphatase A gene would not have been expected to display any signs of MLD since they would have had a normal copy of the ASA gene on the other chromosome and therefore would have had heterozygote carrier levels of ASA enzyme activity and none of the clinical problems associated with MLD.

In considering this family's risk for future pregnancies, there is a 25% chance of having a child with a combination of the father's "\(1\)" allele and the mother's pseudodeficiency allele but this would not result in MLD. Compound heterozygotes for MLD and pseudodeficiency alleles have been identified in other laboratories\(^\text{20}\) as well as our own and are usually without any clinical symptoms. However, the risk for late onset or neuropsychiatric disorders associated with this combination of alleles remains a contentious issue in some laboratories\(^\text{19,21}\). Such a combination of alleles would also complicate prenatal diagnosis by enzymological means alone since it is not always possible to distinguish unequivocally a compound heterozygote fetus from one that is affected with MLD. DNA analysis would be necessary to provide an unambiguous result. The risk for a second ring chromosome event in this family is very small and thus there is essentially no risk of a second MLD child.

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