Rapid diagnostic test for the major mutation underlying Batten disease

Irma Järvelä, Hannah M Mitchison, Patricia B Munroe, Angela M O’Rawe, Sara E Mole, Ann-Christine Syvanen

Abstract
Batten disease is the most common progressive neurodegenerative disorder of childhood in western countries. A novel cDNA responsible for Batten disease has recently been identified. We have developed a rapid diagnostic solid phase minisequencing test to detect the major 1.02 kb deletion which is responsible for 81% of affected chromosomes in Batten disease worldwide. In Finland, 90% of Batten chromosomes carry the major deletion owing to the enrichment of the CLN3 gene in the isolated Finnish population.

Key words: Batten disease; mutation; diagnostic test.

Batten disease (juvenile onset neuronal ceroid lipofuscinosis, Spielmeyer-Vogt) is the most common inherited neurodegenerative disorder of childhood with an incidence of 1:25 000 in western countries. The clinical features include visual failure, seizures, psychomotor deterioration, and premature death. At date, the presence of vacuolated lymphocytes and retinal degeneration have been the most reliable diagnostic criteria.1 The gene, CLN3, underlying Batten disease is located on chromosome 16p12.1.2 The cDNA which is defective in Batten patients was recently identified, and it encodes a protein with unknown function.3 The major mutation underlying Batten disease is a 1.02 kb deletion which removes two exons, and it is carried by 81% of the affected chromosomes from 16 different populations analysed so far.

We have developed a solid phase minisequencing based diagnostic test to identify the major mutation. The method4 originally developed to detect point mutations was devised to detect the 1.02 kb deletion. The strategy for the method is described in fig 1. Three PCR primers (table 1) were designed according to the previously determined genomic sequence of the CLN3 gene (H M Mitchison, personal communication). The result is expressed as the ratio (R) of radioactivity incorporated in the reaction with the 3H-dCTP defining the mutated allele to that incorporated with the 3H-dTTP defining the normal allele (table 2).

The genotype of each sample is unequivocally determined by the R values, which fall into three distinct categories (tables 2 and 3). The R values obtained were >6 for homozygotes for the mutation, 0.25-0.68 for heterozygotes, and <0.09 for normal subjects (table 3). All patients (n = 37) who were known to carry the “56” haplotype (as defined by the microsatellite markers D16S299 and D16S298 closely linked to the CLN3 gene) carried the 1.02 kb deletion. In addition, two sets of sibs homozygous for the haplotype “46” and “66”, respectively, and one patient with an unknown haplotype, were homozygous for the 1.02 kb deletion (table 4). The remaining patients showed R values identical to the carriers, indicating that they carry the major mutation on one of their affected chromosomes and other, rarer mutations on the other chromosome (table 4). Our results show that 80% of the Finnish Batten families carry the major mutation in homozygous form with the remainder being compound heterozygotes. In all, 90% of the Finnish CLN3 chromosomes carry the major deletion.

The test will be informative for more than 80% of cases worldwide.5 The test also identifies carriers of the deletion and excludes healthy subjects as carriers of the disease. We have recently reported the prenatal diagnosis in a case of Batten disease, in which the 1.02 kb deletion was detected by PCR followed by size analysis of the products.6 The two methods were compared by analysing 25 samples, representing homozygous and heterozygous genotypes and concordant results were obtained in each case (data not shown). The minisequencing method represents an improvement compared to previously used size based iden-

Table 1  Primers

<table>
<thead>
<tr>
<th>Name</th>
<th>Sequence 5' to 3*</th>
<th>Position on the CLN3 gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>6081</td>
<td>CATTCTGTTCACCCCTTGAAGCCC</td>
<td>nt 407–387 upstream of the 5' deletion breakpoint</td>
</tr>
<tr>
<td>B-51332</td>
<td>GGCATTCTGAGTCTCGATGCC</td>
<td>nt 51–31 downstream of the 3' deletion breakpoint</td>
</tr>
<tr>
<td>B-6302</td>
<td>TGACAGCGCAGCTCCGTC</td>
<td>nt 56–36 downstream of the 5' deletion breakpoint</td>
</tr>
<tr>
<td>6101</td>
<td>TGACAGGGCGAAGCTCCGTC</td>
<td>nt 20–1 upstream of the 5' deletion breakpoint</td>
</tr>
</tbody>
</table>

* The primers were synthesised on an Applied Biosystems 392 DNA Synthesiser. The 5' ends of the primers B-6302 and B-51332 were biotinylated during the synthesis.

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for 90 minutes in buffer, pH 7.5, Sample Homozygous normal DNA II 10
located located then washed six times with 350 mol/l, 0.08 µmol/l (Finnzymes Finland). The PCR was initiated by a “hot start”, and 33 cycles of one minute at 94°C, one minute at 56°C, and one minute at 72°C were carried out. (B) PCR products obtained from the normal (464 bp) and mutant (460 bp) alleles. Four 10 µl aliquots of the PCR product from each sample and 40 µl of 20 mmol/l sodium phosphate buffer, pH 7.5, 0.15 mol/l NaCl, and 0.1% Tween 20 were incubated at 37°C for 90 minutes in streptavidin coated microtitre wells with gentle shaking. The walls were then washed six times with 350 µl of 40 mmol/l Tri-HCl, pH 8.8, 1 mmol/l EDTA, 50 mmol/l NaCl, and 0.1% Tween20, at 20°C using an automated microtitre plate washer. The walls were treated with 100 µl of 50 mmol/l NaOH for three to five minutes, and washed as above. Fifty microlitres of the minisequencing reaction mixture containing 10 µmol/d of the deprotection step primer 6101, 0.1 µCi of either H-dCTP (TRK625, 71 Ci mmol, Amersham) or H-dTTP (TRKS76, 134 Ci mmol) and 0.05 unit of Dynazyme II DNA polymerase in the PCR buffer were added to the wells, and the plates were incubated for 10 minutes at 30°C. The walls were washed as above, and 70 µl of 50 mmol/l NaOH were added to each well, and the plates were kept at 20°C for three to five minutes. The eluted radioactivity was measured in a liquid scintillation counter.

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