Improved genetic mapping of X linked retinoschisis

N D L George, S J Payne, R M Bill, D E Barton, A T Moore, J R W Yates

Abstract

X linked retinoschisis (RS) causes poor vision in affected males owing to radial cystic changes at the macula. Genetic linkage analysis was carried out in 16 British families with X linked retinoschisis using markers from the Xp22 region. Linkage was confirmed between the RS locus and the markers DXS207 (lod score, Zmax = 17.9 at recombination fraction θ = 0.03; confidence interval for θ = 0.007–0.09), DXS1053 (Zmax = 18.0 at θ = 0.01, CI = 0.001–0.06), DXS43 (Zmax = 12.9 at θ = 0.03, CI = 0.004–0.09), DXS1195 (Zmax = 6.4 at θ = 0.00), DXS418 (Zmax = 8.2 at θ = 0.00), DXS999 (Zmax = 21.2 at θ = 0.01, CI = 0.001–0.05), DXS443 (Zmax = 14.2 at θ = 0.03, CI = 0.004–0.09), DXS365 (Zmax = 24.5 at θ = 0.008, CI = 0.001–0.04). Key recombinants placed RS between DXS43 distally and DXS999 proximally. Multipoint linkage analysis gave odds of 344:1 in favour of this location for RS and supported the map Xpter-(DXS207, DXS1053)-DXS43-1 cM-RS-1 cM-DXS999-DXS443-DXS365-DXS1052-Xcen.

Key words: retinoschisis; X chromosome; microsatellites.

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Patients and methods

FAMILIES

Sixteen families affected by X linked retinoschisis were examined by one ophthalmologist (NDLG). All available family members underwent a full ophthalmic examination including best corrected visual acuity, ocular movements, colour vision (Ishihara and City University plates), slit lamp examination, and ophthalmoscopy with dilated pupils.

The criteria for the diagnosis of X linked retinoschisis were: (1) typical foveal schisis and a reduced b wave on the ERG, occurring in at least one affected male member from each family, (2) X linked pattern of inheritance with affected males in more than one generation and transmission through unaffected females. Males were diagnosed as affected if they had either typical foveal schisis or a history of bilateral visual impairment since childhood associated with macular changes. Obligate carriers were diagnosed on the basis of having an affected father, or having an affected son plus an affected brother or other maternal male relative.

A total of 208 subjects were examined including 60 affected males, 46 obligate carriers, and 44 females of unknown status; 176 patients provided blood or mouthwash samples for DNA extraction.

Typing of microsatellite markers

DNA was extracted using standard methods.19 The microsatellite markers DXS207,19 DXS1053,24 DXS43,23 DXS999,26 DXS443,27 DXS365,27 and DXS105221 were analysed by polymerase chain reaction (PCR) in all 16 families. Each 10 μl reaction mix contained 100–200 ng of genomic DNA, 5–10 pmol of primer, 0.1 pmol of 32P end labelled primer, 0.25 U of Tag DNA polymerase, and...
which confirmed close linkage of all markers to RS.

**Table 1 Results of two point linkage analysis in RS**

<table>
<thead>
<tr>
<th>Locus</th>
<th>Lod score Z at recombination fraction 0</th>
<th>Lod score Z at recombination fraction 0.001</th>
<th>Lod score Z at recombination fraction 0.01</th>
<th>Lod score Z at recombination fraction 0.05</th>
<th>Lod score Z at recombination fraction 0.1</th>
<th>Lod score Z at recombination fraction 0.2</th>
<th>Lod score Z at recombination fraction 0.3</th>
<th>Max Z</th>
<th>0max</th>
<th>Confidence interval for 0</th>
</tr>
</thead>
<tbody>
<tr>
<td>DXS207</td>
<td>-∞</td>
<td>14.6</td>
<td>17.2</td>
<td>17.8</td>
<td>16.6</td>
<td>13.1</td>
<td>9.1</td>
<td>17.9</td>
<td>0.03</td>
<td>0.007-0.09</td>
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<tr>
<td>DXS1053</td>
<td>-∞</td>
<td>17.3</td>
<td>18.0</td>
<td>17.3</td>
<td>15.7</td>
<td>12.0</td>
<td>7.9</td>
<td>18.0</td>
<td>0.01</td>
<td>0.001-0.06</td>
</tr>
<tr>
<td>DXS443</td>
<td>-∞</td>
<td>10.9</td>
<td>12.6</td>
<td>12.8</td>
<td>11.8</td>
<td>9.0</td>
<td>5.9</td>
<td>12.9</td>
<td>0.03</td>
<td>0.004-0.09</td>
</tr>
<tr>
<td>DXS418</td>
<td>8.2</td>
<td>8.1</td>
<td>8.0</td>
<td>7.5</td>
<td>6.7</td>
<td>5.1</td>
<td>3.4</td>
<td>8.2</td>
<td>0.00</td>
<td>0.00-0.07</td>
</tr>
<tr>
<td>DXS1195</td>
<td>6.4</td>
<td>6.4</td>
<td>6.3</td>
<td>5.8</td>
<td>5.3</td>
<td>4.1</td>
<td>2.8</td>
<td>6.4</td>
<td>0.00</td>
<td>0.00-0.09</td>
</tr>
<tr>
<td>DXS999</td>
<td>-∞</td>
<td>20.6</td>
<td>21.2</td>
<td>20.3</td>
<td>18.4</td>
<td>14.2</td>
<td>9.6</td>
<td>21.2</td>
<td>0.01</td>
<td>0.001-0.05</td>
</tr>
<tr>
<td>DXS443</td>
<td>-∞</td>
<td>12.2</td>
<td>13.9</td>
<td>14.0</td>
<td>13.0</td>
<td>10.2</td>
<td>6.9</td>
<td>14.2</td>
<td>0.03</td>
<td>0.004-0.09</td>
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<tr>
<td>DXS365</td>
<td>-∞</td>
<td>24.0</td>
<td>24.6</td>
<td>23.4</td>
<td>21.2</td>
<td>16.4</td>
<td>11.0</td>
<td>24.6</td>
<td>0.008</td>
<td>0.001-0.04</td>
</tr>
</tbody>
</table>

**Table 2 Details of individual recombinants in families with RS. Markers showing recombination with the disease are denoted by X; non-recombinant markers by O, and non-informative markers n. The dashed line indicates regions of probable exclusion of RS**

<table>
<thead>
<tr>
<th>Family</th>
<th>Subject</th>
<th>Sex</th>
<th>Status</th>
<th>DXS207</th>
<th>DXS1053</th>
<th>DXS443</th>
<th>DXS1195</th>
<th>DXS418</th>
<th>DXS999</th>
<th>DXS443</th>
<th>DXS365</th>
<th>DXS1052</th>
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<tbody>
<tr>
<td>6228</td>
<td>II.2</td>
<td>M</td>
<td></td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
</tr>
<tr>
<td>6165</td>
<td>III.4</td>
<td>M</td>
<td></td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
</tr>
<tr>
<td>6229</td>
<td>II.1</td>
<td>F</td>
<td></td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>n</td>
<td>n</td>
<td>n</td>
<td>n</td>
<td>X</td>
</tr>
<tr>
<td>6656</td>
<td>III.2</td>
<td>M</td>
<td></td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>7577</td>
<td>III.3</td>
<td>M</td>
<td></td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
</tr>
<tr>
<td>6228</td>
<td>II.5</td>
<td>M</td>
<td></td>
<td>O</td>
<td>n</td>
<td>n</td>
<td>n</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
<td>O</td>
</tr>
</tbody>
</table>

A = affected, OC = obligate carrier.

0.25 mmol/l of each dNTP in buffer containing 1.5 mmol/l MgCl₂, 50 mmol/l KCl, 10 mmol/l Tris, and 0.1% gelatin (2 mmol/l MgCl₂ buffer was used in the case of DXS43). The reaction mixes were subjected to 30 cycles at 94°C for one minute, annealing (56°C for DXS999 and DXS43, 57°C for DXS207, 58°C for DXS443, DXS365, and DXS1052, 63°C for DXS1053) for one minute, and 72°C for one minute. PCR products were separated by electrophoresis on 4% or 6% denaturing polyacrylamide gels and alleles were visualised by autoradiography. The markers DXS1195<sup>24</sup> and DXS418<sup>28</sup> were analysed in the key recombinants only.

**LINKAGE ANALYSIS**

Genetic linkage analysis was performed using the computer program LIPED<sup>26</sup> for two point analysis and the LINKMAP option of the LINKAGE program<sup>26</sup> for multipoint analysis. The frequency of the retinoschisis gene was set at 0.0001. Confidence intervals were taken as the values of the recombination fraction at a lod score one unit below the maximum. For multipoint analyses the fixed map was (DXS207, DXS1053)-0.1 cM-DXS43-2 cM-DXS999-1 cM-DXS443-2 cM-DXS365 taken from published data.<sup>31</sup><sup>32</sup>

**Results**

**TWO POINT LINKAGE ANALYSIS**

Table 1 shows the results of two point analysis, which confirmed close linkage of all markers to RS.

**ANALYSIS OF INDIVIDUAL RECOMBINANTS**

In pedigree 6228 (fig 1), affected male II.2 was recombinant for DXS207 and DXS1053 having inherited the opposite alleles to his three affected brothers. DXS999 was uninformative and DXS43, DXS443, DXS365, and DXS1052 were non-recombinant. His affected grandson IV.1 has inherited the same recombinant haplotype. These data map DXS43 and RS proximal to DXS207 and DXS1053. In the same pedigree, affected male II.2 was recombinant for DXS1052, mapping RS distal to this marker.

In pedigree 6229, II.1 was an obligate carrier (having an affected brother and two affected sons) and was recombinant for DXS207 and DXS43. DXS1053, DXS999, and DXS443 were uninformative, but DXS365 was non-recombinant. This recombinant was inherited by her two affected sons, III.1 and III.2, and therefore maps RS proximal to DXS43.

In pedigree 6656, affected male III.2 was recombinant for DXS999, DXS443, DXS365, and DXS1052 having inherited different alleles to his affected brothers. DXS207, DXS1053, and DXS443 were uninformative. This result maps RS distal to DXS999.

Taken together these recombinants identify DXS999 as the proximal and DXS43 as the distal flanking markers to RS. DXS1195 and DXS418 map to the same interval<sup>29</sup> and were typed in the key recombinants (table 2) but were either non-recombinant or uninformative.

**MULTIPOINT LINKAGE ANALYSIS**

In the LINKMAP analysis the maximum location score was 125 with RS located at a point midway between DXS43 and DXS999. This position was favoured by odds of 344:1 compared to a location between DXS999 and DXS443 and by odds of 104:1 compared to a location between DXS43 and DXS1053.

**Discussion**

Using the microsatellite markers DXS207, DXS43, DXS1053, DXS999, DXS443, and DXS365 we have confirmed close linkage to RS. A recombinant in pedigree 6229 mapped RS proximal to DXS43. In pedigree 6656 a
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Pedigree 6228

Figure 1. Pedigrees 1, 2, and 3. Affected males are shaded and obligate carrier females are indicated by a central dot. The order of the markers for each haplotype is shown in the key.

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key recombinant mapped RS distal to DXS999. Together these data place RS between DXS43 distally and DXS999 proximally, a genetic distance of 2 cM. Multipoint analysis supported the map Xpter-(DXS207, DXS1053)-DXS43-1 cM-RS-1 cM-DXS999-1 cM-DXS443-2 cM-DXS365-Xcen. We have narrowed the genetic interval containing the RS locus from 5 cM to approximately 2 cM. This corresponds to a physical distance estimated at 2.5 Mb. The data presented represent a significant contribution to the effort to localise and ultimately clone the gene for RS. In addition we have identified highly informative microsatellite markers which can be used for accurate carrier detection.
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