Exclusion of chromosome 9 helps to identify mild variants of acromesomelic dysplasia Maroteaux type

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Abstract

Acromesomelic dysplasia Maroteaux type (AMDM) is an autosomal recessive disorder belonging to the group of acromesomelic dysplasias. AMDM is characterised by severe dwarfism with shortening of the middle and distal segments of the limbs. An AMDM gene has recently been mapped to human chromosome 9p13-q12 by homozygosity mapping in four consanguineous families. Here, we show linkage of the disease gene to chromosome 9p13-q12 in four of five consanguineous AMDM families and its exclusion in a fifth family with two children affected with a mild form of the disease. This study suggests that genetic heterogeneity accounts for the variable clinical and radiological severity of AMDM.

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Keywords: acromesomelic dysplasia Maroteaux type; acromesomelic dysplasias; homozygosity mapping; chromosome 9

Table 1 Clinical profile of autosomal recessive acromesomelic dysplasias (AMD) and comparison with the mild AMD Maroteaux type variant

<table>
<thead>
<tr>
<th>Clinical features</th>
<th>Grebe type</th>
<th>Hunter-Thompson type</th>
<th>Maroteaux type, classical</th>
<th>Maroteaux type, mild</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adult size</td>
<td>100 cm</td>
<td>100–130 cm</td>
<td>120 cm</td>
<td>(?) (−2.5 to −3 SD at age 4)</td>
</tr>
<tr>
<td>Long bones</td>
<td>Severe shortening and deformed</td>
<td>Shortening progression proximal to distal, large joint dislocations</td>
<td>Severe growth retardation</td>
<td>Shortening of middle and distal segments</td>
</tr>
<tr>
<td>Hands and feet</td>
<td>Ball shaped fingers, occasional polydactyly, possibly absent joints</td>
<td>Normal distal phalanges</td>
<td>Normal distal phalanges</td>
<td>Shortening of middle and distal segments</td>
</tr>
<tr>
<td>Long bones</td>
<td>Short femoral neck, absent tibial and fibular diaphyses, hypoplasia of the ulna, malformed radial head</td>
<td>Bowing of the radius, hypoplastic femoral condyles</td>
<td>Ulna shorter than radius, bowing of the radius</td>
<td>Ulna shorter than radius</td>
</tr>
<tr>
<td>Hands and feet</td>
<td>Fusion of carpal and tarsal bones, absence of several metacarpal and metatarsal bones, absence of proximal and middle phalanges</td>
<td>Single phalangeal bone on digit 5, abnormally shaped carpal bones</td>
<td>Short and broad phalanges, metacarpal and metatarsal bones</td>
<td>Short and broad phalanges, metacarpal and metatarsal bones</td>
</tr>
<tr>
<td>Absent</td>
<td>Absent</td>
<td>Present</td>
<td>Minor</td>
<td>Unknown</td>
</tr>
<tr>
<td>Molecular findings</td>
<td>20q11.2 Homozygous missense mutation in CDMP1 (G1199A)</td>
<td>20q11.2 Homozygous 22 bp tandem duplication, frameshift mutation in the mature region of CDMP1</td>
<td>9p13-q12</td>
<td>Unknown</td>
</tr>
</tbody>
</table>
the vertebrae were almost normal. This mild AMDM variant was distinct from Grebe and Hunter-Thompson type AMDs, as none of the clinical criteria specific for these two AMDs was observed in our patients, namely joint dislocations, ball shaped fingers, and fused or absent bones (table 1).

DNA extraction and microsatellite analyses were performed as previously described and primers of the chromosome 9p13-q12 region were chosen from the Genethon map. Homozygosity mapping was performed according to Lander and Bostein and two point linkage analyses using the MLINK option of the LINKAGE package were performed according to Lathrop et al. The frequency of the disease allele was estimated to be 0.005 and penetrance was set at 100%, assuming an autosomal recessive mode of inheritance. Inbreeding loops but not allele frequencies were taken into account as no controls were available for the population studied. The mutation rate was set at 0. For homogeneity tests, the Morton likelihood ratio (LR) test was used. Linkage of the disease gene to chromosome 9p13-q12 was excluded in this family, as the affected subjects received different parental chromosomes in this region (fig 2). Linkage of the family to the CDMP1 region was tested by using microsatellites at flanking loci D20S191 and D20S195 and an intragenic [CA] dinucleotide repeat, but was inconclusive owing to a lack of informativity.

However, linkage analyses in four consanguineous AMDM families of Turkish and Lebanese ancestry supported the mapping of a gene for typical AMDM to chromosome 9p13-q12 (Zmax=3.27 and Zmax=3.23 at $\theta=0$ at loci D9S1878 and D9S1817 respectively). All probands presented with clinical features typical of AMDM including severe growth failure (−5.5 SD and −7 SD) (fig 1A). The Morton likelihood ratio test supported genetic heterogeneity between typical AMDM and...
mild variants (p<0.01, p<0.02, and p<0.03 for loci D9S1878, D9S165, and D9S1817, respectively).

The present study supports the mapping of a gene for typical AMDM to chromosome 9p13-q12 and shows that mild AMDM variants are unlinked to this region. It is worth remembering that the existence of mild AMDM was suggested by Borrelli et al., who described a boy moderately affected with AMDM with a birth length of 50 cm and a growth pattern of −2.6 SD at the age of 2½ years. Studies of additional families with mild AMDM will help to confirm whether genetic heterogeneity indeed accounts for the variable clinical and radiological severity of the disease.

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