Localisation of the gene causing diaphyseal dysplasia Camurati-Engelmann to chromosome 19q13

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Abstract
Camurati-Engelmann disease, progressive diaphyseal dysplasia, or diaphyseal dysplasia Camurati-Engelmann is a rare, autosomal dominantly inherited bone disease, characterised by progressive cortical expansion and sclerosis mainly affecting the diaphyses of the long bones associated with cranial hyperostosis. The main clinical features are severe pain in the legs, muscular weakness, and a waddling gait. The underlying cause of this condition remains unknown.

In order to localise the disease causing gene, we performed a linkage study in a large Jewish-Iraqi family with 18 affected subjects in four generations. A genome wide search with highly polymorphic markers showed linkage with several markers at chromosome 19q13. A maximum lod score of 4.9 (0=0) was obtained with markers D19S425 (58.7 cM, 19q13.1) and D19S900 (67.1 cM, 19q13.2). The disease causing gene is located in a candidate region of approximately 32 cM, flanked by markers D19S868 (55.9 cM, 19q13.1) and D19S571 (87.7 cM, 19q13.4).

Keywords: Camurati-Engelmann disease; progressive diaphyseal dysplasia; chromosome 19q13; sclerosing bone dysplasia

Camurati-Engelmann disease (CED, MIM 131300) is a sclerotic bone disorder of unknown cause. This dysplasia was first described by Cockayne in 1920, but Camurati was the first to suggest its hereditary nature in 1922, describing a father and son, both with painful lower extremities, showing cortical thickening and sclerosis of the diaphyses on x ray examination. In 1929, Engelmann reported a single case with muscular wasting and marked bone involvement. Neuhauser et al named this disease progressive diaphyseal dysplasia, emphasising the progressive nature of the hyperostosis and the involvement of the diaphyses. However, Kaftori et al later proposed that the disease should be renamed progressive bone dysplasia since the metaphyses, skull, and even the vertebrae can be affected. Currently, the eponym Camurati-Engelmann disease is the most widely accepted, although recently the International Working Group on Constitutional Disease of Bone suggested naming this condition diaphyseal dysplasia Camurati-Engelmann.'

Besides muscle weakness, claudication, and severe pain in the legs, which affect the majority of CED patients, other observed clinical symptoms are easy fatiguability, reduced muscle mass, general weakness, exophthalmos, facial paralysis, hearing difficulties, and loss of vision. The first symptoms of the disease are mostly detected before the age of 30, but in many cases may be present in the first decade of life.

Routine biochemical parameters of bone and mineral metabolism, such as serum calcium and alkaline phosphatase, are usually normal. In order to localise the gene responsible for CED, we performed a linkage study in a large Jewish-Iraqi family with 18 affected subjects in four generations. A genome wide search with highly polymorphic markers showed linkage with several markers at chromosome 19q13. A maximum lod score of 4.9 (0=0) was obtained with markers D19S425 (58.7 cM, 19q13.1) and D19S900 (67.1 cM, 19q13.2). The disease causing gene is located in a candidate region of approximately 32 cM, flanked by markers D19S868 (55.9 cM, 19q13.1) and D19S571 (87.7 cM, 19q13.4).
analysed using an automated DNA sequencing apparatus (Applied Biosystems model 377). Extra markers for regions of interest were chosen from the Généthon Genetic Linkage Map.13 These were analysed using either radioactive isotope labelling or a 5'-IRD label. In the first protocol, radioactive end labelling of one oligonucleotide was performed before PCR using T7 polynucleotide kinase. Amplification products were separated according to size on a 6% polyacrylamide gel and analysed after autoradiography. In the alternative approach, one of the primers is synthesised with an M13 forward or reverse sequence at the 5’ end. An IRD labelled (800 nm) M13 primer is included in the PCR reaction and is incorporated from the second cycle, thus labelling the PCR product. Gel electrophoresis and pattern visualisation were performed using a LI-COR model 4200 DNA analyser (NEN).

LINKAGE ANALYSIS

Two point lod scores were calculated by use of MLINK (version 5.1).14 The disease frequency was set at 1/1 000 000. An autosomal dominant mode of inheritance was assumed with a disease penetrance of 100%. Allele frequencies were set at 1/n with n being the number of alleles detected.

Results

CLINICAL AND RADIOLOGICAL EXAMINATION OF THE FAMILY MEMBERS

In our current update of this family, we diagnosed 18 subjects as being affected with CED (fig 2). Both sexes were almost equally affected with CED (eight women and 10 men). Their diagnoses were mainly based on the presence of clinical symptoms. The most frequent symptoms were muscle weakness, reduced muscle mass, a waddling gait, exophthalmos, and thickening of the long bones. A few people (II.1, III.4, III.6, and III.9) were asymptomatic but based on the presence of affected descendants they must be obligate carriers. II.1 (currently 64 years old), for example, has no symptoms, while her daughter (III.1) suffers from pain and claudication. III.4, III.6, and III.9 all have a child showing typical symptoms of CED, including a waddling gait, inability to run quickly, and muscle pains. For two of these asymptomatic carriers (III.4 and III.6), radiological examination confirmed the affected status. Because of the presence of clinically asymptomatic gene carriers, all at risk subjects with no clinical symptoms and without radiological survey were assigned an unknown affected status (II.1, III.9, III.14, III.17, III.20, IV.6, and IV.7).

The onset of the disease in this family varied, but was more common in childhood. There is considerable variability in the symptoms and clinical signs of the affected subjects; some patients are asymptomatic while III.15 and III.18, only teenagers, already complain of severe pains and muscle weakness in the lower extremities. Radiological examination showed symmetrical involvement of the long bones.

GENOTYPING

Genomic DNA was isolated from fresh leucocytes using standard techniques. The Cooperative Human Linkage Centre Human Screening Set (Weber version 6) was used for a genome wide linkage study. This set contains 391 fluorescently labelled, highly polymorphic markers covering the entire human genome with an average spacing of 10 cM. The markers were analysed by use of an automated DNA sequencing apparatus (Applied Biosystems model 377). Extra markers for regions of interest were chosen from the Généthon Genetic Linkage Map.13 These were analysed using either radioactive isotope labelling or a 5'-IRD label. In the first protocol, radioactive end labelling of one oligonucleotide was performed before PCR using T7 polynucleotide kinase. Amplification products were separated according to size on a 6% polyacrylamide gel and analysed after autoradiography. In the alternative approach, one of the primers is synthesised with an M13 forward or reverse sequence at the 5’ end. An IRD labelled (800 nm) M13 primer is included in the PCR reaction and is incorporated from the second cycle, thus labelling the PCR product. Gel electrophoresis and pattern visualisation were performed using a LI-COR model 4200 DNA analyser (NEN).

LINKAGE ANALYSIS

Linkage analysis in the Israeli family throughout the whole genome with markers of the Weber set excluded more than 70% of the human genome with lod scores below −2. D19S900 (19q13.2) was the marker most suggestive of linkage. To confirm these initial data and to delineate the candidate region, extra markers from this region were genotyped. The highest lod score of 4.9 (θ=0) was obtained with markers D19S425 and D19S900 (table 1). Four other markers in the same region (D19S416, D19S223, D19S879, and D19S867) also showed a lod score above 4 (θ=0). Besides these, three more markers (D19S876, D19S412, and D19S606) appeared to be free of recombination (table 1, fig 2). Together, these markers indicated a candidate region of approximately 32 cM. The
Camurati-Engelmann disease maps to 19q13

Figure 2  Pedigree reconstruction of the four generation Jewish-Iraqi CED family. Question marks represent subjects with an unknown affected status. Manually constructed haplotypes for the chromosome 19 markers are shown below the symbols. The haplotype consists of alleles from 13 marker loci. The black bars represent the haplotype that cosegregates with the disease.

Table 1  Two point lod scores (Z) at recombination fraction (θ) between CED and 13 markers from chromosome 19q13

<table>
<thead>
<tr>
<th>Lod score (Z) at recombination fraction (θ)</th>
<th>0.0</th>
<th>0.01</th>
<th>0.05</th>
<th>0.1</th>
<th>0.2</th>
<th>0.3</th>
<th>0.4</th>
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<tr>
<td>D19S225</td>
<td>−∞</td>
<td>−0.02</td>
<td>1.15</td>
<td>1.45</td>
<td>1.40</td>
<td>1.05</td>
<td>0.57</td>
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<td>D19S868</td>
<td>2.83</td>
<td>3.22</td>
<td>3.12</td>
<td>2.57</td>
<td>1.82</td>
<td>0.95</td>
<td>0.41</td>
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<td>4.83</td>
<td>4.75</td>
<td>4.43</td>
<td>4.00</td>
<td>3.10</td>
<td>2.12</td>
<td>1.08</td>
</tr>
<tr>
<td>D19S425</td>
<td>4.92</td>
<td>4.84</td>
<td>4.51</td>
<td>4.09</td>
<td>3.18</td>
<td>2.19</td>
<td>1.13</td>
</tr>
<tr>
<td>D19S888</td>
<td>2.30</td>
<td>2.28</td>
<td>2.16</td>
<td>1.96</td>
<td>1.47</td>
<td>0.93</td>
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<tr>
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<td>4.74</td>
<td>4.66</td>
<td>4.33</td>
<td>3.91</td>
<td>3.00</td>
<td>2.02</td>
<td>0.97</td>
</tr>
<tr>
<td>D19S900</td>
<td>4.90</td>
<td>4.82</td>
<td>4.50</td>
<td>4.08</td>
<td>3.17</td>
<td>2.19</td>
<td>0.13</td>
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<tr>
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<td>3.02</td>
<td>2.97</td>
<td>2.73</td>
<td>2.41</td>
<td>1.73</td>
<td>1.03</td>
<td>0.40</td>
</tr>
<tr>
<td>D19S606</td>
<td>3.28</td>
<td>3.25</td>
<td>3.10</td>
<td>2.86</td>
<td>2.26</td>
<td>1.56</td>
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<tr>
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<td>4.28</td>
<td>3.96</td>
<td>3.54</td>
<td>2.66</td>
<td>1.72</td>
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<td>3.54</td>
<td>2.66</td>
<td>1.72</td>
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<tr>
<td>D19S571</td>
<td>0.47</td>
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<td>0.67</td>
<td>0.67</td>
<td>0.49</td>
<td>0.26</td>
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</tr>
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</table>

proximal key recombinant can be seen with marker D19S868 (19q13.1) which recombines in IV.5. On the distal side, D19S571 (19q13.4) recombines in III.15 (fig 3).

Discussion

Bone is a dynamic tissue, which is constantly remodelled throughout life by two processes, bone formation and bone resorption. The balance of these processes is under control of both systemic and local factors. Disruption of this balance can cause a diverse spectrum of pathological conditions. At one end of the spectrum, we find the conditions with decreased bone density, of which osteoporosis is the most frequent. At the other end, there is a set of mainly rare, inherited conditions characterised by increased bone density. CED is an example of these sclerosing bone dysplasias.

The great majority of sclerosing bone dysplasias have not yet been characterised at the molecular level, with the exceptions of carbonic anhydrase II, which causes osteopetrosis with renal tubular acidosis, and of the cathepsin K gene which underlies pyknodysostosis. However, genetic linkage studies in extended pedigrees have recently localised disease causing genes for several of these conditions: An autosomal dominant and a recessive form of osteopetrosis were assigned to 1p21 and 11q13 respectively, whereas two related conditions, van Buchem disease and sclerosteosis, both presenting as endosteal hyperostoses, were assigned to 17q12-q21.

Taking into account the progress of the Human Genome Project, the identification of other genes responsible for sclerosing bone dysplasias can be expected soon.

CED presents in most cases with an autosomal dominant mode of inheritance but some so called skipped generations, in which carriers show no radiological abnormalities, have been described. Sparkes and Graham, for example, presented the case of a severely affected subject with asymptomatic parents and grandparents showing no definite radiological abnormalities. However, six additional cases of CED were discovered in the same
family rejecting the isolated status of this case. In our family, non-penetration was observed in several cases based on clinical examination, but, when available, radiological examination allowed us to confirm the affected status. The progression of the disease is highly unpredictable; stages of progression can alternate with quiescent and inactive stages. Onset of the disease seems to be more common in childhood, as is the case in our family.

So far, the cause of CED is unknown. Since CED is a progressive disease, the gene responsible is unlikely to be involved in bone development but rather is most probably involved in the regulation of bone metabolism and bone turnover throughout life. During skeletal growth and ageing, new bone is laid down on the periosteal surfaces of long bones and undergoes a process of maturation to form cancellous bone of the bone cortex. Simultaneously, bone is removed from the endosteal surfaces to create the marrow cavity. Both of these processes appear to be abnormal in CED, where the formation of periosteal bone is disorganised and the removal of endosteal bone is abnormal. In view of this, identification of the disease causing gene in CED will provide new insight into the mechanisms by which normal bone remodelling occurs and may also represent a therapeutic target for the prevention of osteoporosis or the healing of bone fractures.

The candidate region we have identified is large and contains several known genes. Among others, we feel that at least four genes need further consideration. These are “nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, beta” (NFKBIB on 19q13.1), human proto-oncogene BCL3 gene (19q13.1), transforming growth factor beta-1 (TGFβ1-1 on 19q13.1), and latent transforming growth factor beta binding protein-4 (LTBP-4 on 19q13.1-19q13.2). NFKBIB encodes the IxBβ protein, an inhibitor of NFkB. NFkB regulates the expression of a variety of genes involved in immune and inflammatory responses, but also plays a role in the generation and function of osteoclasts. BCL3 has a similar function. Transforming growth factor-β (TGFβ-1) is a multifunctional growth factor in bone with effects on cells of the osteoclast and osteoblast lineage, whereas LTBP-4 is a member of the LTBP-fibrillin family of proteins which are needed for the secretion and folding of TGFβ-1. It is of interest that glucocorticoids are known to regulate the activity of both Nfkbib2 and Tgfβ-1, which would make NFKBIB, BCL3, TGFβ-1, and LTBP-4 strong positional candidate genes.

In conclusion, the localisation of the disease causing gene for CED presented here will most probably accelerate its characterisation. This might result in a better understanding of the underlying pathogenesis and might contribute to our general knowledge of bone metabolism.

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