Osteogenesis imperfecta type III: mutations in the type I collagen structural genes, COL1A1 and COL1A2, are not necessarily responsible

Gillian A Wallis, Bryan Sykes, Peter H Byers, Christopher G Mathew, Denis Viljoen, Peter Beighton

Abstract
Most forms of osteogenesis imperfecta are caused by dominant mutations in either of the two genes, COL1A1 and COL1A2, that encode the proα1(I) and proα2(I) chains of type I collagen, respectively. However, a severe, autosomal recessive form of OI type III with a comparatively high frequency has been recognised in the black populations of southern Africa. We performed linkage analyses in eight OI type III families using RFLPs associated with the COL1A1 and COL1A2 loci to determine whether mutations in the genes for type I collagen were responsible for this form of OI. Recombination between the OI phenotype and polymorphic markers at both loci was shown in three of the eight families investigated. The combined lod scores for the eight families were −10.6 for COL1A1 and −11.2 for COL1A2. Further, we examined the type I procollagen produced by skin fibroblast cultures derived from affected and unaffected subjects from the above eight families plus one further family. We found no evidence for defects in the synthesis, structure, secretion, or post-translational modification of the chains of type I procollagen produced by any of the family members. These results suggest that mutations within or near the type I collagen structural genes are not responsible for this form of OI.

Patients and methods

PATIENTS
The patients and relatives who participated in this study had been examined previously and were derived from reported series of affected persons in southern Africa. In general, recessive inheritance of this condition has been inferred on the basis of recurrence of the defined phenotype in sibs born to unaffected parents and the frequency of the phenotype. We performed linkage analysis and examined collagen synthesis and secretion in skin fibroblast cultures to determine whether mutations in the genes for type I collagen were responsible for this form of OI in southern African patients.

Osteogenesis imperfecta (OI) is currently subclassified into four major groups and several subtypes on the basis of clinical and genetic data. According to the original classification by Sillence et al., OI type III is characterised by a severe propensity to fracturing, marked short stature, progressive deformities, and white sclerae and, as the phenotype occurred sporadically, new dominant mutation or autosomal recessive inheritance was postulated. Subsequently, Sillence et al. identified seven families in a review of 345 pedigrees of different types of OI where the OI type III phenotype appeared to have an autosomal recessive mode of transmission. There is now accumulating evidence that the OI type III phenotype most often results from dominant mutations in either of the two genes that encode the proα1(I) and proα2(I) chains (COL1A1 and COL1A2, respectively) of type I collagen. In only one instance has a defect in the genes for type I collagen been shown to cause a recessive form of OI type III. In a further family postulated to have a recessive form of OI type III, linkage studies have excluded the involvement of the type I collagen genes.

In contrast to world wide figures, an autosomal recessive (AR) form of OI type III is comparatively common in the black population of southern Africa, where more than 70 affected persons have been studied. In general, recessive inheritance of this condition has been inferred on the basis of recurrence of the defined phenotype in sibs born to unaffected parents and the frequency of the phenotype. We performed linkage analysis and examined collagen synthesis and secretion in skin fibroblast cultures to determine whether mutations in the genes for type I collagen were responsible for this form of OI in southern African patients.

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Preparation and electrophoretic analysis of procollagens and collagens

Skin biopsies were taken from those subjects indicated in the figure by an asterisk and used to establish dermal fibroblast cell cultures. Dermal fibroblasts from unrelated, healthy subjects served as controls. Cell cultures were maintained under standard conditions in Dulbecco-Vogt Modified Eagle Medium (DMEM, Irvine Scientific) as previously described.29 Labelling of proteins with 2,3,4,5-[3H]proline (10 Ci/mmol, Amersham), harvesting of the medium and cell layer proteins, pepsin digestion of the procollagens to yield the collagen chains, and sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) were carried out as previously described.30-32

Results

Linkage analyses of families with OI type III

The pedigrees of the OI type III families studied are shown in the figure. The genotypes for the COL1A1 and COL1A2 associated RFLPs are indicated on the pedigrees and the lod scores at θ = 0.001 are given in table 2. A lod score was not calculated for family 9 as a DNA sample was available from only one of the sibs. Recombination between the OI phenotype and polymorphic markers at both loci was shown in three of the eight families investigated. In the remaining families, small positive lod scores were obtained at one or both of the loci. However, the combined lod scores for the eight families were −10.6 for COL1A1 and −11.2 for COL1A2.

<table>
<thead>
<tr>
<th>Pedigree</th>
<th>COL1A1</th>
<th>COL1A2</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>−3.2</td>
<td>−1.9</td>
</tr>
<tr>
<td>2</td>
<td>−4.8</td>
<td>−4.0</td>
</tr>
<tr>
<td>3</td>
<td>−1.4</td>
<td>−0.8</td>
</tr>
<tr>
<td>4</td>
<td>−2.0</td>
<td>−0.8</td>
</tr>
<tr>
<td>5</td>
<td>+0.6</td>
<td>+0.5</td>
</tr>
<tr>
<td>6</td>
<td>+0.2</td>
<td>+0.3</td>
</tr>
<tr>
<td>7</td>
<td>+0.6</td>
<td>+0.3</td>
</tr>
<tr>
<td>8</td>
<td>+0.1</td>
<td>0</td>
</tr>
<tr>
<td>9</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Total</td>
<td>−10.6</td>
<td>−11.2</td>
</tr>
</tbody>
</table>

Lod scores were calculated at a value of θ = 0.001. A lod score was not calculated (ND) for pedigree 9 as a DNA sample was available from only one of the sibs.

Linkage analysis

The COL1A1 and COL1A2 genotypes were established using previously described restriction site dimorphisms.20-22 DNA was prepared from blood samples from all available family members and the samples were genotyped for the presence of the COL1A1 and COL1A2 dimorphisms using Southern blot hybridisation or the polymerase chain reaction (PCR).24 Two RFLPs for MspI and Rsal restriction sites were used as markers for COL1A1.25 Genotypes for each dimorphism were detected by Southern blot hybridisation using the probes pIAH17526 (MspI) and p2FC.6 (Rsal).22 RFLPs for the restriction enzymes EcoRI20 and MspI21 were used as markers for COL1A2. Two contiguous EcoRI genomic clones NJ-3' and NJ-3'20 were used to detect the EcoRI RFLP and a 4 kb EcoRI genomic clone25-26 to detect the MspI RFLP. The Rsal RFLP associated with the COL1A2 gene was not used in this study as it has not been detected in black southern African populations.27 The oligonucleotide primers used to amplify across the variable restriction sites in the COL1A1 and COL1A2 genes and the conditions of the PCR reactions were as previously described.28 Available subjects from the pedigrees were screened for the presence (+) or absence (−) of the COL1A1 and COL1A2 polymorphism restriction sites. Haplotypes were constructed according to the notation in table 1. Lod scores were calculated at a recombination fraction (θ) of 0.001 using the MLINK program.29 Other values of θ were not considered since the RFLPs were within or very close to the candidate genes.

<table>
<thead>
<tr>
<th>Haplotype</th>
<th>Rsal</th>
<th>MspI</th>
</tr>
</thead>
<tbody>
<tr>
<td>COL1A1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>2</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>3</td>
<td>−</td>
<td>−</td>
</tr>
</tbody>
</table>

Table 1 Haplotype notation. Combinations of variants used to assemble haplotypes are shown.

Table 2 Lod scores at each locus for each pedigree.

Pedigree | COL1A1  | COL1A2  |
---------|---------|---------|
1        | −3.2    | −1.9    |
2        | −4.8    | −4.0    |
3        | −2.0    | −0.8    |
4        | +0.6    | −2.1    |
5        | +0.2    | +0.5    |
6        | +0.6    | +0.3    |
7        | +0.1    | 0       |
8        | ND      | ND      |
Total    | −10.6   | −11.2   |

Lod scores were calculated at a value of θ = 0.001. A lod score was not calculated (ND) for pedigree 9 as a DNA sample was available from only one of the sibs.

Preparation and electrophoretic analysis of procollagens and collagens

Skin biopsies were taken from those subjects indicated in the figure by an asterisk and used to establish dermal fibroblast cell cultures. Dermal fibroblasts from unrelated, healthy subjects served as controls. Cell cultures were maintained under standard conditions in Dulbecco-Vogt Modified Eagle Medium (DMEM, Irvine Scientific) as previously described.29 Labelling of proteins with 2,3,4,5-[3H]proline (10 Ci/mmol, Amersham), harvesting of the medium and cell layer proteins, pepsin digestion of the procollagens to yield the collagen chains, and sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) were carried out as previously described.30-32
SCREENING FOR TYPE I COLLAGEN DEFECTS

Methods routinely used in the diagnosis of OI were used to examine the type I procollagen produced by the dermal fibroblast cultures established from affected subjects and their unaffected relatives. Examples of defects that have been identified using these methods have been previously published and show their efficacy. In all instances, the type I procollagen and collagen synthesised by the cell cultures migrated normally relative to that of controls, the ratios of the α1(I) to α2(I) collagen chains were normal, there was no intracellular retention of the chains, and there was no evidence for increased post-translational overmodification of the chains (results not shown).

Discussion

As a result of biochemical, molecular genetic, and linkage studies it is now evident that OI is in most instances caused by heterozygosity for mutations in one of the genes, COL1A1 or COL1A2, which respectively encode the proα1(I) and proα2(I) chains of the type I collagen molecule. In OI type III, biochemical studies are compatible with the presence of new dominant mutations that affect the structure of type I procollagen. Alterations to the structure of the type I procollagen molecule can in general be detected on PAGE gels as the procollagen chains are overmodified and poorly secreted. Molecular studies have shown heterozygosity for point mutations in both COL1A1 (gly526 to cys, gly415 to cys, gly844 to ser, gly1009 to ser, and gly154 to arg) and COL1A2 (gly259 to cys) that result in the substitution of triple helical glycine residues for other amino acids and cause forms of OI type III.

Despite the evidence for dominant mutations causing OI, recurrence of the phenotype in offspring born to phenotypically normal parents does occur. For the perinatal lethal form of OI (type II) the sib recurrence rate is about 6% and, in all families investigated, the mechanism of inheritance has been explained by parental gonadal, and often somatic, mosaicism for the mutant allele. In OI type III there is evidence that both recessive inheritance and gonadal mosaicism may be responsible for recurrence of the phenotype. Evidence for recessive inheritance has relied mostly on family studies. In a consanguineous pedigree in which a severe form of OI segregated as an autosomal recessive trait, a lack of linkage to both COL1A1 and COL1A2 was shown. In only one instance has homozygosity for a mutation in a gene for type I collagen been proven to cause a recessive form of OI type III.12-14 Germline mosaicism for a type I collagen mutation has been reported in three families with autosomal dominant (AD) OI type III.13,19,20 As AD OI type II and AD OI type III are caused by similar molecular mechanisms (both result predominantly from single base pair changes leading to the substitution of triple helical glycines by other amino acids) it is likely that, with further investigation, the frequency of recurrence of OI type III resulting from germline mosaicism will compare with that of OI type II. In the form of OI type III identified in the black population of southern Africa, AR inheritance of the condition has been proposed on the basis of the occurrence of multiple affected sibships with normal parents (recurrence of the phenotype has been recorded in 17 of the 44 families investigated), the defined phenotype, and the high frequency of this severe form of OI in this ethnic group. In addition, in the previously reported family of mixed ancestry with a similar form of OI, subjects were affected in two branches of the same family. As the frequency of recurrence of OI type III in the black population is far greater than the apparent frequency of recurrence in other populations, it seems unlikely that gonadal mosaicism is the mechanism responsible for the recurrent phenotype in all families.

We examined the type I collagen produced by skin fibroblast cultures derived from 15 affected and 12 unaffected subjects from nine black southern African families with the AR form of OI type III and in no instance were defects in the synthesis, structure, secretion, and post-translational modification of the composite chains detected. The absence of increased post-translational overmodification (increased lysyl hydroxylation and hydroxyprolyl glycosylation) is significant as this secondary abnormality is a useful marker for the presence of subtle mutation altering the integrity of the collagen helix and the extent of overmodification along the α chains of type I collagen has been used to localise mutations. On the basis of these results alone it would not be possible to exclude the involvement of type I collagen defects confidently in all families. In 16% of cell strains from subjects clinically diagnosed as having OI type III, Wenstrup et al. were unable to identify alterations in electrophoretic mobility of the chains of type I collagen synthesised. The reason for this may be that point mutations towards the amino-terminal end of the triple helix are difficult to detect owing to the paucity of potentially hydroxylatable lysyl residues. Alternatively, structural alterations may exist that affect molecular interactions or other aspects of the biological behaviour of type I collagen molecules without modification although no such mutations have as yet been identified. So, it is possible that somatic or germinal mosaicism for mutations within one of the type I collagen genes may cause recurrence of OI type III but in order for this mechanism to explain the frequency of recurrence of OI type III in the black population of southern Africa we would have to postulate that in each instance a new dominant mutation had occurred that did not alter the electrophoretic mobility or secretion of the type I procollagen chains and that the frequency of these kinds of mutations was greater in this population than has been recorded for other populations. The existence of autosomal recessive pedigrees allows a limited amount of linkage analysis using DNA polymorphisms associated with
both COL1A1 and COL1A2. A lack of linkage can be inferred if affected sibs do not share the same genotypes and this evidence provides a positive means for excluding the collagen genes as the site of the mutations. In three of the families with OI type III that we investigated, there was discordance between the phenotype and markers at both loci suggesting that a mutation within or near the type I collagen genes are not responsible for OI in these families. The concordant segregation with one or both of the COL1A1 or COL1A2 alleles that was evident in some families may be because of chance as the families were small. Further, this concordant segregation was not associated with the presence of any detectable protein abnormalities.

From phenotypic and genealogical data, OI type III in the southern African black population appears to be homogeneous. Proof of molecular homogeneity within this group, however, requires the elucidation of the cause of the bone fragility, deformity, and disturbance of growth in these patients. It is possible that genes controlling type I collagen processing or maturation might be involved. Equally, abnormalities in connective tissue components other than collagen could cause bone fragility and the bone specific, non-collagenous matrix proteins are possible candidates. Finding alternative causes for the OI phenotype may assist in the systematic exploration of the pathway between a mutation in one of the collagen genes and the phenotype and could lead to the identification of factors that modify the resultant phenotype.

We are grateful to Kathy Braun, Laura Suesserman, and Sue Schultz for technical assistance. We thank Dr Andrew Read of St Mary's Hospital, Manchester, for his assistance in calculating the lod scores. This work was supported in Cape Town by grants from the Medical Research Council of South Africa, the University of Cape Town Staff Research Fund, the Mauerberger Foundation, and the Harry Crossley Foundation, and in Seattle by grants from the National Institutes of Health (AR 21559), a Clinical Research Grant from the March of Dimes Birth Defects Foundation (6-298), and the Michael Giseman Memorial Fellowship from the Osteogenesis Imperfecta Foundation.


