Letters to the Editor

Can hair be used to screen for breast cancer?

EDITOR—The use of hair as a biopsy tissue has been considered for some time. For instance, in the case of breast cancer, raised zinc levels in head hair have been reported.\(^1\) Besides, x-ray diffraction patterns of hair are rich and have attracted much attention for 70 years.\(^2\) However, its potential use as a diagnostic indicator of disease was only suggested a short time ago.\(^3\) Most recently, James et al\(^4\) reported that x-ray diffraction of hair taken from women diagnosed with breast cancer (and those at high risk by virtue of a proven \(BRCA1/BRCA2\) mutation) showed a diffuse ring. They claimed a 100% correlation with the disease, advocating the use of pubic hair as a simple non-invasive screening method for breast cancer. The use of pubic hair was suggested in view of possible damage to the head hair from cosmetic treatments. Despite this note of caution, the study of James et al\(^4\) was based on 12 pubic hair samples with only eight from cancer affected subjects. Here, we report a detailed double blind study from 109 women belonging to five clinically distinct groups as well as a normal population group and show that there is no correlation between the diffuse ring and breast cancer or breast cancer predisposition.

The present work was initiated in November 1998 to provide an independent double blind study on clinically well controlled samples because of our concerns with the study of James et al\(^4\) for which a major proportion of the samples was provided by two of us (AH and DGRE). Both diffraction and x-ray fluorescence data have been obtained. Diffraction data were collected on station 2.1 with the multiwire area detector and the fluorescence data on station 7.1 of the UK Synchrotron Radiation Source (SRS). The use of a multiwire detector allowed on-line alignment of hair within seconds and enabled high resolution data collection on a large number of samples. Six groups of subjects were selected including a normal population group. For each subject, head and pubic hair were collected and reference numbers assigned in a random manner. The identities of samples were kept blinded until all data were analysed. Each woman was asked to provide information on whether they had had any hair treatment (perm, dye, etc) or were on medication. No hair treatment was reported for pubic hair and thus here only results from pubic hair (108 samples) are discussed. Results of head hair are included in table 1 for completeness. The groups consisted of 27 unaffacted controls aged 26-60 years, 21 isolated cases of breast cancer (<31 years) who had been screened negative for \(BRCA1/BRCA2\) mutations, and three cases aged over 60 years not so tested. The remaining groups came from a set of 43 families with proven \(BRCA1/BRCA2\) mutations: 25 affected mutation carriers, 10 unaffected mutation carriers, and 23 unaffected close female relatives who tested negative for the known mutations in the family.

Diffraction patterns could be grouped into two categories: one characterised by a diffuse ring at 4.78 ± 0.10 nm and one with no ring present (fig 1). The occurrence of this ring is well known from x-ray patterns of both keratins and muscle and is ascribed to lipid crystals resulting from degradation processes.\(^3\) Contrary to the observation of James et al\(^4\), the pubic hair of only 12 of 49 (25%) women with breast cancer showed the diffuse ring. This is only slightly larger than in the normal population group, where about 20% of the pubic hair samples showed the ring. In the case of the affected group who tested positive for a \(BRCA1\) or \(BRCA2\) mutation, 56% of the pubic hair samples showed no ring and only 24% of the pubic hair samples showed the ring. Table 1 provides a detailed summary of diffraction results for all six groups. A statistical analysis for pubic hair samples was performed to determine

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**Table 1 Proportion of subjects in each of six groups whose diffraction patterns show or do not show the diffuse ring**

<table>
<thead>
<tr>
<th>Pubic hair</th>
<th>Head hair</th>
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<tr>
<td></td>
<td>N</td>
</tr>
<tr>
<td>Ring* (%)</td>
<td>5</td>
</tr>
<tr>
<td>No ring (%)</td>
<td>22</td>
</tr>
<tr>
<td>Total = 217</td>
<td>27</td>
</tr>
</tbody>
</table>

N = control from normal population. U = unaffected (known not to have breast cancer). A = affected (known to have breast cancer). +/- = tested positive/negative for mutations in \(BRCA1\) and \(BRCA2\) genes. nh = no family history.

*Includes complete and partial ring. James et al\(^4\) suggest that pubic hair should be used for diagnostic purposes; 50% of all head hair samples show the ring in contrast to only 27% of pubic hair samples. This difference may arise from hair treatment among other factors.

†One woman supplied only head hair.

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![Figure 1 X-ray diffraction patterns from the pubic hair of women diagnosed with breast cancer. The left half represents the pattern with no ring, the right half shows the diffuse ring. The first strong meridional reflection (arrow 1) is used for normalising the patterns, arrow 2 shows the equatorial reflection, which gets intensified in cases when the diffuse ring appears.](image-url)
whether there was an association between the presence of the diffuse ring and breast cancer. There were 49 samples from women with breast cancer and 59 from unaffected women. A $\chi^2$ value of 0.86 was obtained. For 1% significance, a value of 6.65 and for 5% significance, a value of 3.84 is required. Thus, it can be concluded that there is no measurable association between the diffuse ring and breast cancer. The trace element (Zn, Cu, Fe, and S) analysis of intact hair showed no correlation with the ring structure in the diffraction pattern or with the subjects’ group. The women in the normal population group whose hair had shown the diffuse ring were examined and shown not to have breast cancer.

Our x-ray diffraction data do not support the recent claim that hair from breast cancer patients or those at high risk (BRCA1/BRCA2 mutation carriers) show a distinct diffuse ring. This conclusion for breast cancer diagnosis was also reached on a much smaller study of head hair only. In our study, diffraction patterns from 75% (37 of 49) of the breast cancer patients do not show this ring. Moreover, the $\chi^2$ test shows no association between the diffuse ring and breast cancer and, as such, the claim that x-ray diffraction of pubic hair can be used as a screening method for breast cancer or breast cancer predisposition is invalid.

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Mutation analysis of SMAD2, SMAD3, and SMAD4 genes in hereditary non-polyposis colorectal cancer

Editor—Transforming growth factor-β (TGF-β) family members are known to be involved in the regulation of cell proliferation, differentiation, and apoptosis. Members of the TGF-β family include TGF-βs, activins, and bone morphogenetic proteins (BMPs). Their signals are mediated to the cell nucleus by a network of transmembrane serine/threonine kinase receptors and their downstream effectors, the SMAD proteins. SMAD proteins play a key role in intracellular TGF-β signalling and inactivating mutations of SMADs, such as SMAD2, SMAD3, and SMAD4, provide resistance of cells to TGF-β induced growth inhibition.

To date, eight human SMADs have been identified. Two of them, SMAD2 and SMAD4, have been reported to be mutated in a subset of colorectal carcinomas. 1–6 Germline mutations of SMAD4 have been found in patients with juvenile polyposis, a condition predisposing to colorectal cancer. 7–10 SMAD3 mutations have not been reported in human cancers. In a recent study by Arii et al., 11 SMAD3 mutations were analysed in 35 sporadic colorectal and 15 HNPCC cancers and no mutations were found. Targeted disruption of the SMAD3 gene in mice has been reported to lead to development of colorectal cancer, 12 though other studies have not detected a clear association. 13–14 No genetic alterations in other SMADs have been reported in malignancy.

Hereditary non-polyposis colorectal cancer (HNPCC) is an autosomal dominantly inherited cancer susceptibility syndrome, associated with germline mutations in five DNA mismatch repair genes: MLH1, PMS1, PMS2, MSH2, and MSH6. 15–19 Inactivation of both alleles of a mismatch repair gene results in microsatellite instability (MSI) that is a hallmark of HNPCC tumours. 20–25 The genes responsible for microsatellite stable (MSS) HNPCC are still unknown.

Loss of growth inhibition by TGF-β is an important step in colon tumorigenesis and in HNPCC tumours with MSI this is mainly the result of frameshift mutations within a polyadenine sequence repeat in the TGF-β type II receptor (TGFβRII) gene. 26 It has been proposed that mutations in TGFβRII could underlie the cancer predisposition in MSS HNPCC, 27 and also that other genes involved in the TGF-β pathway are candidates for MSS HNPCC. 28 Chromosomal deletions are common genetic alterations in cancer and they are targeted at tumour suppressor loci. 27–28 Previous studies have shown that one copy of chromosome 18q is lost in over 70% of sporadic colorectal cancers. 26–32 The DCC (deleted in colorectal cancer) gene has been suggested as a candidate target gene in this region and loss of expression of DCC has also been reported in colorectal cancers. 33 However, mutations in the coding region of DCC seem to be rare 34 and the position of DCC as a candidate tumour suppressor is not clear. Two other candidate genes, SMAD4 and SMAD2, have recently been identified at the same 18q region 35 emphasising the possible role of the SMAD genes in colorectal tumorigenesis. The aim of the present study was to investigate whether germline mutations in SMAD2, SMAD3, and SMAD4 underlie microsatellite stable HNPCC.

Mutation screening was performed in 14 Finnish HNPCC kindreds from which lymphoblastoid cell lines were available. Based on genealogical evidence the families are unrelated, though the existence of early common ancestors cannot be excluded. One affected subject per family was included in the study. Of the kindreds, six fulfilled the Amsterdam criteria for HNPCC. 36 Other patients represent familial HNPCC-like colorectal cancer (CRC); the number of patients with CRC or endometrial cancer ranged from two to six per family (average three (Table 1). All kindreds selected for this study had previously been shown to be MLH1 and MSH2 mutation negative. 37 In three kindreds, DNA from tumour tissue had not been available. From 10 families one and in one family two colorectal cancer samples were available and no evidence of MSI had been detected (Table 1). The study

References

The forward (F) and reverse (R) primers were designed using the Primer3 server (http://www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi). Each gene was divided into five fragments, covering the whole coding region of the gene. The forward (F) and reverse (R) primers and size of each PCR product are listed in table 2.

The PCR reactions were carried out in a 50 µl reaction volume including 2 µl of cDNA, 1 × PCR reaction buffer (Perkin Elmer Applied Biosystems Division), 200 µmol/l of each dNTP (Finnzymes), 0.8 µmol/l of each primer, and 2 units of AmpliTaq GOLD polymerase (PE/ABI). The MgCl₂ concentration was 1.5 mmol/l for SMAD2 fragments 1 and 2, SMAD3 fragment 3, and all SMAD4 fragments. For all other fragments the MgCl₂ concentration was 2.5 mmol/l. SMAD2 fragment 2 reaction also included 10% of DMSO. The PCR conditions are available upon request.

After PCR, 5 µl of the PCR product was run on a 3% agarose (NuSieve) gel to verify the specificity of the PCR reaction. The rest of the PCR product was purified using QIAquick PCR purification Kit (Qiagen). Direct sequencing of the PCR products was performed using the ABI PRISM Dye Terminator or ABI PRISM dRhodamine cycle sequencing kits (PE/ABI). Cycle sequencing products were electrophoresed on 6% Long Ranger gels (FMC Bioproducts) and analysed on an Applied Biosystems model 373A or 377 DNA sequencer (PE/ABI).

The screen for the presence of a base substitution in SMAD3 controls, restriction enzyme digestion was performed. HpaI (New England BioLabs) digestion was used to detect A to G change in SMAD3 exon 3 at codon 170. New PCR primers for genomic exon 3 amplification were designed using the Primer3 server. The primers were: 5'-ATCGAACGTGACCGGACCTG (forward) and 5'-GCTGATCGACACTGAGCCACCTCT (reverse). The PCR reactions were carried out in a 50 µl reaction volume including 100 ng genomic DNA, 1 × PCR reaction buffer (PE/ABI), 200 µmol/l of each dNTP (Finnzymes), 0.8 µmol/l of each primer, and 2 units of AmpliTaq GOLD polymerase (PE/ABI), and 1.5 mmol/l of MgCl₂. The following PCR cycles were used for amplification: 10 minutes at 95°C, 40 cycles of 45 seconds at 95°C, 45 seconds at 56°C, one minute at 72°C, and final extension for 10 minutes at 72°C. HpaI cuts the PCR fragment (187 bp) that contains the substitution into two fragments (134 bp and 53 bp in size) whereas the wild type fragment lacks the restriction site and is not digested. The digestion was performed in 1 × NEBuffer (New England BioLabs) at 37°C overnight. After digestion, the PCR products were electrophoresed through a 3% agarose gel.

In this work we analysed SMAD2, SMAD3, and SMAD4 mutations in 14 familial colon cancer kindreds, 11 of these displaying at least one MSS tumour. The microsatellite analysis data derived typically from one single tumour per family suggest that these kindreds do not segregate DNA mismatch repair gene mutations, but does not exclude this possibility. Previous studies had evaluated MLH1 and
SMAD mutations in the series with negative results. SMAD gene mutation analysis was performed by automated sequencing covering the translated region of the genes. Genetic alterations were not detected in SMAD2 or SMAD4 in any of these patients. In SMAD3, three discrepancies were detected between GenBank sequence (U76622) and sequences from our patients, firstly the A to G change at the third position of codon 103 (exon 2). Homozygous A to G change was seen in 11 of our 14 patients and in three of them the substitution was heterozygous. This discrepancy has been reported earlier and the variant does not cause any amino acid change. A second, silent change detected was a C to T transition at nucleotide 907 (exon 6). This change was homozygous and it was present in one of our 14 HNPPC patients (in family 31). The frequency of these variants in the normal population was not analysed, as the changes were silent. The third change was an adenine to guanine transition at nucleotide 545, which is predicted to convert isoleucine to valine at amino acid 170 (fig 1). This change was detected in two patients (in families 65 and 75). For this variant, 110 Finnish controls were analysed by restriction enzyme digestion (HpaI). Seven out of 110 controls displayed the change (6.4%). To compare further the frequency of this polymorphism in colon cancer patients and controls, 132 patients were included in the analysis. Taken together, in the 14 HNPPC patients and 132 colon cancer patients the frequency of this polymorphism was 8.9% (13/146). From those 13 cancer patients who had valine instead of isoleucine at codon 170, four turned out to be familial. Segregation of the polymorphism was analysed in two of these families where DNA from multiple family members was available and the polymorphism did not segregate with cancer in these families.

SMAD2, SMAD3, or SMAD4 mutations were not found in any of our patients using a cDNA based mutation analysis. It should be noted that like all other mutation detection methods, this method may miss a subset of mutations. Also, the potential existence of founder mutations in the Finnish population may have hampered our efforts to detect SMAD gene defects in HNPPC. However, it is likely that defects of SMAD2, SMAD3, or SMAD4 may not be a common cause of familial colon cancer. Further work is necessary to unravel the molecular background of MSS HNPPC.

We thank Siv Lindroos, Liisa Suksi, and Päivi Laibo for technical assistance.

Novel mutation in the MYOC gene in primary open angle glaucoma patients

EDITOR—Glaucoma is the world’s leading cause of irreversible blindness and is characterised by progressive optic disc cupping with corresponding visual field loss. Both intraocular pressure (IOP) and positive family history are risk factors for the development of the disease. Juvenile open angle glaucoma (JOAG) is a subtype of open angle glaucoma characterised by an early onset (10 to 35 years of age) and autosomal dominant inheritance with high penetrance, a characteristic which has led several authors to investigate affected families in an attempt to identify a gene or genes associated with this condition. With the use of genetic linkage analysis in families with JOAG, a genetic locus (GLC1A) was recognised on chromosome 1q21-q31. The gene associated with GLC1A has been identified and it codifies a 57 kDa protein named trabecular meshwork induced glucocorticoid response protein (TIGR), also known as myocilin (MYOC). The MYOC gene is composed of three exons of 604, 126, and 785 bp, respectively. During screening for mutations in the MYOC gene in 25 unrelated Brazilian patients with JOAG, an unreported mutation (Cys433Arg) was detected, present in seven of them.

Patients were followed at the Glaucoma Service of the State University of Campinas, Brazil. They underwent an ocular examination, including gonioscopy by Posner lens, applanation tonometry, slit lamp biomicroscopy, optic nerve evaluation, and automated perimetry (Humphrey 630, program 30-2). JOAG was defined as the presence of characteristic bilateral optic nerve damage and visual field loss in the presence of an open angle in subjects younger than 36 years of age. Each patient included in this study came from different families according to interview data. The study was approved by the Ethics Committee of the State University of Campinas. At the time of the ocular examination, the mean age of JOAG patients was 25.52 years (SD 6.99), ranging from 10 to 35 years, and the mean IOP was 29.96 mm Hg (SD 13.00). Thirteen patients (52%) were male and 12 (48%) female; 13 (52%) were white, 11 (44%) black, and one (4%) was Asian. Some of the patients (48%) were female; 13 (52%) were white, 11 (44%) black, and one (4%) was Asian. Six patients (85%) of those with the mutation had a positive familial history of glaucoma. The mean age of patients harbouring this mutation was 27.00 years (SD 6.02), ranging from 15 to 35 years and the mean IOP was 39.13 mm Hg (SD 12.62). In contrast, JOAG patients without the mutation had a mean age of 24.02 (SD 7.46) and a mean IOP of 25.65 mm Hg (SD 11.68) (p>0.05). In another patient, a previous report mutation (Pro370Leu) was identified. One of the patients who showed the Cys433Arg mutation had the family investigated for its presence. Nine subjects were studied and four harboured the Cys433Arg mutation (fig 3). Three of them had glaucoma and one had ocular hypertension without optic nerve or visual field damage. The other members who did not have the disease were not affected with the Cys433Arg mutation.

In order to discriminate between a founder effect and de novo recurrence, haplotype analysis was performed in the six patients with a positive family history who had the new mutation and in one family using four microsatellite markers, mapped at band 1q21-25, closely linked to the GLC1A locus, D1S210, D1S2790, D1S1619, and NGA19. Polymerase chain reaction (PCR) was carried out following standard procedures and primer sequences were obtained from the Genome Data Bank. For allele scoring, PCR products were size fractionated on a 6% polyacrylamide-urea gel and autoradiographed. The analysis of four microsatellite markers showed that the Cys433Arg mutation is associated with a common haplotype, suggesting that these patients inherited their mutation from a common ancestor. A pedigree of the family analysed can be seen in fig 3, depicting a potential disease haplotype.
Figure 2  Direct sequencing of the PCR product showing a T-C substitution at codon 433 of the MYOC gene, which changes the amino acid Cys (TGT) to Arg (CGT). The arrow indicates the exact location of the mutation.

Figure 3  Pedigree of a JOAG patient's family (the proband is indicated with an arrow). Solid symbols indicate affected subjects, all harbouring the Cys433Arg mutation. II.3, indicated with a dotted symbol, has not developed glaucoma, but has very high IOP levels and also shows the Cys433Arg mutation. Four microsatellite markers, located in the vicinity of the GLC1A locus, were used for haplotype analysis. The pedigree shows the genotypes at polymorphic microsatellite loci as well as a potential disease haplotype shown in the boxes.
Since the first description of the MYOC gene (then called the TIGR gene) by Stone et al.1 as one of the genes related to open angle glaucoma at the GLC1A locus, several mutations have been described among patients with open angle glaucoma.10–14

During the screening of exon 3 of the MYOC gene in our JOAG patients, we identified a mutation at amino acid 433 (exon 3) which encodes for an arginine instead of a cysteine in 28% of the patients. The mutation is located in a highly conserved amino acid sequence, the olfactomedin (OLFm)-like domain, a region where most of the mutations have been identified.11 In fact, the cysteine residue 433 is of particular interest, as it is located within the most conserved region between species, from C elegans to humans. As in other olfactomedins, it is likely that this cysteine residue is involved in protein oligomerisation by disulphide linked polymer formation.12,13 According to Nguyen et al.,16 oligomerisation of the MYOC protein could be an important feature in the obstruction of the trabecular meshwork. It is possible that MYOC dimers or polymers are linked to form a higher molecular mass structure via a cysteine-cysteine formation, similar to that predicted in olfactomedin by Yokoe and Anholt.15 Therefore, mutations in this domain may alter protein oligomerization and lead to IOP elevation.17

Clinically, the Cys433Arg mutation seems to be closely related to glaucoma; it was found in three glaucomatous relatives of one patient and in a relative with ocular hypertension. This change was not found in our control group of 130 unrelated subjects or in any healthy subject studied, indicating that it is a probable disease causing mutation, which, to our knowledge, has not yet been described. Affected patients tend to present with the disease during the third decade, with very high IOPs (high 30s). Hence, the phenotype-genotype correlation is closer to that which has been reported for the Pro370Leu mutation,18 which also determines a severe disease with an early onset, in contrast with the Gin368Stop mutation, which is associated with later onset of glaucoma.19

Haplotype analysis showed that the six patients with a positive familial history who harboured the mutation had the same disease associated haplotype, indicating that this mutation has probably arisen from a common ancestor, as shown for the Asn480Lys mutation17 and for the 1177GACA→T mutation.18

Although the mechanisms involved in the association of the MYOC gene, POAG, and JOAG are not completely understood,11 it is not unreasonable to expect that the pathophysiology of these diseases will be elucidated, leading to better treatments. Furthermore, it may be used as a screening test to identify susceptible subjects long before the development of optic nerve damage, allowing early treatment and possibly avoiding the disease related visual impairment. Finally, it may be possible to modify the MYOC gene in order to inhibit phenotypic changes induced by mutations, thereby ultimately halting the development of glaucoma.

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Three novel SALL1 mutations extend the mutational spectrum in Townes-Brocks syndrome

EDITOR—Townes-Brocks syndrome (TBS, MIM 107480) was first described by Townes and Brocks1 in 1972 as an association of imperforate anus, supernumerary thumbs, malformed ears, preauricular tags, and sensorineural hearing loss. Several additional familial as well as isolated cases have been reported.2 TBS is caused by mutations of the putative zinc finger transcription factor gene SALL1.3 All SALL1 mutations identified to date in TBS patients are located 5' of the first double zinc finger encoding region.4 Three of these are nonsense mutations at two different positions. The mutation 826C>T was found in three unrelated sporadic cases, and at position 1115 one patient carried an adenine (1115C>A) and another a guanine (1115C>G) instead of a cytosine. All seven other reported mutations are short frameshift deletions of 1, 2, 7, or 10 base pairs.4
SALL1 encodes four double zinc finger domains which are characteristically distributed over the entire protein. All known mutations have been predicted, if the mutated transcripts are indeed translated, to result in prematurely truncated proteins lacking all double zinc finger domains presumed to be essential for SALL1 gene function. Since no mutations were found 3' of the most 5' located double zinc finger encoding region, it was assumed that only those mutations which remove all double zinc fingers could cause TBS, whereas mutations located further 3' in SALL1 could result in a different phenotype or no abnormal phenotype at all. Here we describe three novel mutations in three independent families illustrating that truncating mutations positioned further 3' of the previously described hotspot region in SALL1 also result in TBS.

SALL1 mutation analysis in family 1 (patient 1) showed a heterozygous mutation 840delC which is located 5' of the region encoding the first double zinc finger (fig 2A, fig 3). This mutation was also detected in her affected brother. However, neither parent showed the mutation in their peripheral lymphocytes. Paternity was confirmed in this family (data not shown). In family 2, we found a heterozygous nonsense mutation 1509C>A (Y503X) in the affected girl (patient 2, fig 2C, fig 3). This mutation was also detected in her affected newborn brother. However, neither parent showed the mutation in their peripheral lymphocytes. Paternity was confirmed in this family (data not shown). In family 3, molecular analysis was performed on L1 (patient 4, fig 1A), and weight <3rd centile), probably secondary to chronic renal insufficiency. At the age of 6 haemodialysis was begun because of severe renal insufficiency. Intelligence is normal.
II.1, II.2 (patient 5, fig 1A), III.1, and III.2 (patient 3, fig 1A). No mutation was found in the whole SALL1 coding region. However, within the intron 2 sequence, a heterozygous transition IVS2-19T>A (fig 1B) was found in III.2, and subsequently in I.1 and II.2, but not in the unaffected family members. This mutation was predicted to create an aberrant splice acceptor site. By comparing the surrounding sequences of the aberrant and the normal intron 2 splice acceptor site to consensus sequences, it was estimated that the aberrant splice site was as likely to be functional as the normal site. The mutation was excluded in 200 control alleles.

In order to test if the mutation indeed created a functional splice site, lymphoblastoid cell lines of patients II.2 and III.2 were examined by RT-PCR. In both patients, direct sequencing of RT-PCR products showed an identical pattern of two different overlapping sequences indicating that both the mutated and the normal transcript were present in similar amounts. Sequencing of the subcloned RT-PCR fragments showed the wild type allele (fig 1C) and
a mutated allele (fig 1D) carrying an insertion of 17 bp derived from intron 2 sequence between the aberrant and the normal splice acceptor sites. It is placed within the coding region for the most carboxy-terminal double zinc finger between exon 2 and exon 3 sequences (fig 1B-D fig 3). The frameshift resulting from the insertion is further predicted to cause premature termination of the SALL1 protein (1208 amino acids instead of 1324 in the wild type).

In addition to the mutations reported here, the following polymorphisms were detected in SALL1: IVS1+119G>A, IVS1+118C>G, IVS1+36delAC (all intron 1), 2574T>C, 3456C>T (both exon 2), IVS2-31delCT (intron 2), 3872A>G (N1291S), and 3915C>T (exon 3). The intronic polymorphisms occurred in more than 10% of all subjects (affected and unaffected) analysed for SALL1 mutations by our group. The exonic mutation N1291S is thought to be silent since it was found in two unaffected persons. The other exonic variations do not affect translation and are not segregating with the phenotype. Since the exonic sequence variations have only rarely been found, it is as yet unclear if they represent true polymorphisms or rare sequence variants.

All SALL1 mutations previously reported in TBS reside in exon 2, 5' of the coding region for the first double zinc finger domain (fig 3), and are predicted to result in SALL1 haploinsufficiency. Nonsense mutations seem to occur less frequently than small deletions, and both known nonsense mutations were found independently in two and three families indicating the existence of two hotspots at nucleotides 826 (mutated in three families) and 1115 (mutated in two families). In contrast, SALL1 small deletions as a group occur more often but they seem to represent private mutations only. 840delC is yet another short deletion located 5' of the coding region for the first double zinc finger domain (fig 3).

The phenotype of the patient carrying this mutation is typical for TBS, that is, he shows anal, ear, and thumb malformations. Interestingly, this man also shows acute optic neuropathy. While this has not been reported so far in TBS, this might represent another rare feature of the syndrome.

The two other mutations described in this report are the first SALL1 mutations located 3' of the region where all previously known mutations cluster. The 1509C>A mutation is neighbouring the 3' end of the double zinc finger 1 coding region (fig 3). While this mutation could result in a prematurely terminated SALL1 protein lacking double zinc finger domains 2-4, it is still unclear if the mutated transcript remains stable and the corresponding protein is indeed expressed. Therefore, this mutation could well result in haploinsufficiency if the mutated transcript is readily degraded. This mutation is the third nonsense mutation detected so far in SALL1, and it is the first one to be found in a family with dominant transmission since all other nonsense mutations known so far have been detected as de novo mutations in patients with severe features of TBS. Interestingly, one of the parents carries the mutation in the germline but not in lymphocytes. Yet the parental origin of the mutation needs to be determined in order to explain if the anteriorly placed anus seen in the mother could also reflect the presence of the mutation in other tissues. However, it is clear that the preaxial polydactyly reported in the father's family cannot be related to the mutation which caused TBS in his children.

The most interesting mutation shown here is IVS2-19T>A (fig 1B-D). We were able to show that the predicted transcript resulting from aberrant splicing is indeed expressed. While quantitative PCR has not been performed, direct sequencing of the RT-PCR products indicates that the aberrant transcript is as abundant as the normal one. It seems therefore that splicing of the mutated
primary transcript occurs preferentially if not completely at the aberrant splice site. The predicted protein encoded by the mutated transcript contains intact coding sequences for all double zinc finger domains except for the double zinc finger 4 in which the carboxy-terminal zinc finger motif is interrupted. How this mutation might lead to the phenotype remains to be elucidated. It has previously been shown in the Drosophila transcription factor Krüppel that a missense mutation replacing one of the conserved cysteine residues within the second of five tandemly arranged finger motifs results in a null allele. Therefore, the splice mutation reported here is likely to result in loss of biological function of the most carboxy-terminal double zinc finger domain. It remains unclear if this is sufficient to result in SALL1 haploinsufficiency causing TBS. The predicted mutant protein is 116 amino acids shorter than the wild type protein and contains different carboxy-terminal amino acids because of the frameshift. An alternative explanation for the effect of the mutation could therefore be that the changed three dimensional structure of the mutated protein results in a non-functional SALL1 protein which is unstable or not able to bind to its target sequences.

The phenotype of the severely affected family members reported here is not significantly different from other TBS cases in which classical truncating mutations were found. Therefore, we assume that all mutations shown in this report will lead to haploinsufficiency for SALL1, as suggested to be the common result of all mutations previously reported. 1

Data access GenBank: http://www.ncbi.nlm.nih.gov/. Accession numbers: Y18264 (SALL1 exon 1 and intron 1 genomic sequence (partial)), Y18265 (full SALL1 coding sequence), X98833 (SALL1 genomic sequence of intron 1 (partial), exons 2 and 3 and intron 2). Mutation accession numbers (Human Genetic Online Mutation Data Submission): H971415 (840delC), H971417 (IVS2-1G→T), exons 2 and 3 and intron 2). Mutation accession numbers (Human Genet- ics Online Mutation Data Submission): H971415 (840delC), H971417 (IVS2- 1G→T), exons 2 and 3 and intron 2).

Genotype-phenotype correlation in three homozygotes and nine compound heterozygotes for the cystic fibrosis mutation 2183AA→G shows a severe phenotype

Editor—Cystic fibrosis (CF) is the most common lethal childhood disorder in white populations and occurs at a frequency of about 1/2500 with regional variations. Over 1000 mutations in the CF transmembrane conductance regulator (CFTR) gene accounting for the disease have been identified so far and the most common gene mutation is ΔF508. 1 The frameshift mutation 2183AA→G in exon 13 was first described in three Canadian CF patients 2 and later was shown to have a significant frequency in patients from mid and southern Europe. The frequency among CF patients is 9.3% in north east Italy, 3 2.4% in the Tyrol, 4 1-2.1% in Belgium, 5 1.8% in Greece, 6 1% in Bavaria, Bulgaria, and France, 7 and 0.4% in mid and northern Germany. 8 We identified three homozygotes among 120 Turkish patients (2.5%), two born to first cousin parents, three compound heterozygotes among 185 Bulgarian patients (0.8%), and seven compound heterozygotes among 650 Spanish patients (0.5%). The mutation was detected by denaturing gradient gel electrophoresis or single strand conformational analysis followed by DNA sequence analysis. We report here the genotype-phenotype correlation in 12 patients with CF with the mutation 2183AA→G (three homozygous and nine compound heterozygous for 2183AA→G and other mutations). The anamnestic, clinical, and laboratory data are summarised in table 1. Pancreatic insufficiency (PI) was assessed by the fat content of stools and requirement of pancreatic enzyme replacement therapy. Gastrointestinal pseudo-obstruction (GI) are abdominal cramps and pain and frequent passage of foul and fatty faeces. The presence of pulmonary symptoms was defined as having at least one of the following clinical findings: increased rate of breathing, wheezing, dark coloured/profuse sputum, and recurrent attacks of coughing. Dehydration includes at least one of the following: decreased skin turgor and turgor, decreased output of urine, and sudden weight loss. The presence of bronchiectasis was evaluated by chest x rays and thin section computerised chest tomography.

Patient 1 was homozygous for 2183AA→G. She was admitted to hospital at 2 months of age and died within a week. Clinical findings were clearly of CF with pancreatic insufficiency. The second homozygous patient (patient 2) was examined for CF because all his four sibs had died of the disease before the age of 1 year. He had pulmonary insufficiency at 15 days. He had fatty and foul stools, bronchial hyperactivity, and early Pseudomonas colonisation. As a result of medical treatment, he no longer has steatorrhoea.
Table 1 Anamnestic, clinical, and laboratory data for CF patients carrying the mutation 2183AA→G

<table>
<thead>
<tr>
<th>Patient No</th>
<th>Nationality</th>
<th>Second CF mutation</th>
<th>Sex</th>
<th>Onset of symptoms</th>
<th>Meconium ileus</th>
<th>No of affected sibs</th>
<th>Disease progression for CF sibs</th>
<th>Age (mo)</th>
<th>Data at latest visit</th>
<th>Lung colonisation with bacterial pathogens</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Turkish</td>
<td>2183AA→G</td>
<td>F</td>
<td>25 d</td>
<td>No</td>
<td>0</td>
<td>All died &lt;1 y</td>
<td>7.5 y</td>
<td>N</td>
<td>Pseudomonas, Staphylococcus aureus</td>
</tr>
<tr>
<td>2</td>
<td>Turkish</td>
<td>2183AA→G</td>
<td>F</td>
<td>15 d</td>
<td>No</td>
<td>4</td>
<td>All died 1 y</td>
<td>2 y</td>
<td>N</td>
<td>Pseudomonas, Staphylococcus aureus</td>
</tr>
<tr>
<td>3</td>
<td>Turkish</td>
<td>2183AA→G</td>
<td>M</td>
<td>2 mth</td>
<td>No</td>
<td>1</td>
<td>All died 1 y</td>
<td>6 y</td>
<td>N</td>
<td>Pseudomonas, Staphylococcus aureus</td>
</tr>
<tr>
<td>4</td>
<td>Bulgarian</td>
<td>2183AA→G</td>
<td>M</td>
<td>At birth</td>
<td>Yes</td>
<td>0</td>
<td>All died 1 y</td>
<td>3 y</td>
<td>N</td>
<td>Pseudomonas, Staphylococcus aureus</td>
</tr>
<tr>
<td>5</td>
<td>Spanish</td>
<td>2183AA→G</td>
<td>F</td>
<td>3 mth</td>
<td>Yes</td>
<td>0</td>
<td>All died 1 y</td>
<td>3 y</td>
<td>N</td>
<td>Pseudomonas, Staphylococcus aureus</td>
</tr>
<tr>
<td>6</td>
<td>Spanish</td>
<td>2183AA→G</td>
<td>M</td>
<td>1 mth</td>
<td>Yes</td>
<td>1 (11 y)</td>
<td>All died 1 y</td>
<td>8 y</td>
<td>N</td>
<td>Pseudomonas, Staphylococcus aureus</td>
</tr>
<tr>
<td>7</td>
<td>Spanish</td>
<td>2183AA→G</td>
<td>F</td>
<td>At birth</td>
<td>Yes</td>
<td>0</td>
<td>All died 1 y</td>
<td>2 y</td>
<td>N</td>
<td>Pseudomonas, Staphylococcus aureus</td>
</tr>
<tr>
<td>8</td>
<td>Spanish</td>
<td>2183AA→G</td>
<td>M</td>
<td>2 mth</td>
<td>Yes</td>
<td>0</td>
<td>All died 1 y</td>
<td>2 y</td>
<td>N</td>
<td>Pseudomonas, Staphylococcus aureus</td>
</tr>
<tr>
<td>9</td>
<td>Bulgarian</td>
<td>2183AA→G</td>
<td>M</td>
<td>ND</td>
<td>No</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>10</td>
<td>Spanish</td>
<td>2183AA→G</td>
<td>F</td>
<td>ND</td>
<td>No</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>11</td>
<td>Bulgarian</td>
<td>2183AA→G</td>
<td>M</td>
<td>ND</td>
<td>No</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>12</td>
<td>Bulgarian</td>
<td>2183AA→G</td>
<td>F</td>
<td>ND</td>
<td>No</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
</tbody>
</table>

The phenotype of the mutation 2183AA→G was assessed to be severe with pancreatic involvement, failure to thrive, and variable lung involvement (9/12 patients). In 5/10, colonisation with bacterial pathogens was observed. Two patients died too young (1-2 months) for bacterial colonisation to be assessed. Two of the ΔF508/2183AA→G patients had meconium ileus. The mutation may cause various other complications, with two patients exhibiting hepatic involvement and two bronchiectasis. All patients studied were diagnosed very early. Grouping the patients and their sibs together, six homozygotes died within the first year of life and two compound heterozygotes died at the ages of 1 month and 12 years.

In most of our heterozygous patients, the CFTR gene was only partially screened for mutations using either DGGE or SSCP. Thus, it is possible but unlikely that some
Alkaptonuria in Italy: polymorphic haplotype background, mutational profile, and description of four novel mutations in the homogentisate 1,2-dioxygenase gene

Alkaptonuria (AKU, OMIM 203500) is a rare disorder caused by the deficiency of homogentisate 1,2-dioxygenase (HGO, EC 1.13.11.5). HGO catalyses the conversion of homogentisate (HGA) to maleylacetoacetate in the phenylalanine/tyrosine catabolic pathway. As a consequence, affected subjects excrete HGO in their urine, which becomes dark upon exposure to air. The medical interest in this condition stems from its association with ochronosis, or the deposition of a brownish pigment in connective tissues including cartilage, where its accumulation can produce a debilitating degenerative joint disease.

AKU occupies a unique place in the history of human genetics because it was the first disorder to be described as a Mendelian recessive trait. Recent advances in the understanding of the molecular basis of AKU have verified that loss of function mutations in the HGO gene are responsible for the disease. A few mutations have been repeatedly detected in patients from different European countries. Since these mutations segregated with specific haplotypes, they should be considered to be old mutations that have spread throughout western Europe with migration. However, allelic heterogeneity is the main feature emerging from the above and other studies.

To determine the extent of allelic heterogeneity in Italian patients, we started a systematic search for AKU mutations. To find the mutations, we employed a series of approaches: allelespecific PCR, sequencing of all exons of the AKU gene in Italian patients and in 63 control chromosomes, linkage analyses, and linkage disequilibrium studies.

The authors thank the European Community Concerted Action for the Coordination of Cystic Fibrosis Research and Therapy for providing the DGGE and the mutation screening in Italian AKU patients and carrier identification by DNA typing. The authors also thank the authors of the following studies for making their data available:

- Nutrition and Metabolic Disorders Division, Istanbul University Medical School, Istanbul, Turkey
- **Pediatrics, Akoje University Medical School, Izmir, Turkey
- ††Cystic Fibrosis Unit, Pediatrics Service, Hospital S Juan Des, Barcelona, Spain
- **Pediatric Service, Hospital General, Santiago Compostela, Spain
- **Pediatric Service, Hospital Central, Oviedo, Spain
- **Gastroenterology Service, Hospital La Fe, Valencia, Spain
- **Pediatric Service, Hospital Clinico, Valladolid, Spain
- †††Centro Bioquimica Espinardo, Murcia, Spain
- **Laboratory of Molecular Pathology, Medical University, Sofia, Bulgaria

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1 Cystic Fibrosis Genetic Analysis Consortium. www.genet.sickkids.on.ca
5 Tzetis M, Kanavakis E, Antoniadi T, et al. Characterization of more than 85% of cystic fibrosis alleles in the Greek population, including five novel mutations. Hum Genet 1997;101:121-5.
6 Dörk T, Mekus F, Schmidt K, et al. Detection of more than 50 different CFTR mutations in a large group of German cystic fibrosis patients. Hum Genet 1994;94:533-42.
cases were diagnosed in adulthood on the basis of clinical and radiological examination. Seventeen normal relatives were also investigated. Both genomic DNA and HGO cDNA were obtained from peripheral blood by standard methods.

SSCP was extracted from peripheral blood lymphocytes by the guanidinium thiocyanate-phenol-chloroform method. cDNA synthesis was performed using oligo dT and specific primer mapping in the 3' UTR of the HGO gene. From the complete sequence of a human HGO cDNA (AF045167), primers were designed to obtain overlapping amplicons spanning the entire coding sequence of cDNA (AF045167), primers were designed to obtain overlapping amplicons spanning the entire coding sequence of HGO by nested PCR, as described previously. Primers HTEL and HTER were used in the first PCR, whereas each of the primer pairs HS1L/HS9, HS4/HS7, HS6/HS3F, HS8/HS12, HS11F/HS10, HS13/HS5 were used in the second PCR. The primer sequences and the expected lengths of the PCR products are shown in table 1. PCR products were heat denatured and subjected to electrophoresis on a non-denaturing 6-8% polyacrylamide gels and the alleles were visualised by silver staining. The alleles were numbered consistently with intron primers. PCR products were purified by column filtration and sequenced directly with a dye terminator cycle sequencing kit (ABI PRISM Perkin Elmer, Norwalk, USA) using the ABI 377 automated sequencer (Applied Biosystems, Foster City, USA) and its associated analysis software.

Three intragenic STRs, HGO-1 (D3S4496, intron 4), HGO-2 (D3S4497, intron 13), and HGO-3 (D3S4556, intron 4), have been described previously and were analysed by PCR with modifications to comply with non-isotopic detection. The PCR products were run on denaturing 6-8% polyacrylamide gels and the alleles were visualised by silver staining. The alleles were numbered consecutively and sized by comparison with known samples. Four SNPs, IVS9+56G/A, IVS5+25T/C, IVS6+46C/A, and c1245G/C, have also been described and were studied by SSCP on non-denaturing 6% polyacrylamide gel electrophoresis followed by silver staining. Genotype assignment was made possible by comparison with known samples. Familial segregation provided unequivocal derivation of the haplotypes present on the AKU chromosomes.

Five additional unrelated AKU families were analysed for mutations and polymorphisms in the HGO gene. The IVS9-56G→A and IVS9-17G→A HGO mutations in one Italian patient have already been described. Therefore, the mutations found in 12 AKU chromosomes of Italian ancestry are presented here (table 2). Since consanguineous marriage occurred in three families, only nine chromosomes may be considered to be independent in origin. In fact, patients from these families were homozygous for the AKU mutations G1526 (c621insG), G270R (c975G→A), and G360R (c1245G→C), respectively. The AKU patients in another family were compound heterozygotes for K248R (c909A→G) and IVS7+5G→A (c636+5G→A). Finally, in family VRN, the AKU patient is most likely a compound heterozygote for G360R and an as yet unknown HGO mutation. Therefore, as many as eight different HGO mutations were found in these families, four of which were novel. We also anticipate that the AKU mutation that remains to be identified will be novel (table 2) because we know that it is different from all previously characterised AKU mutations. We provisionally denoted this mutation as VRN. Three of the four novel mutations (K248R, G270R, and G360R) are missense mutations that affect HGO amino acid residues that are conserved in different species and are likely to be loss of function mutations. K248R is the consequence of an A to G transition at position c909 in exon 10, G270R results from a G to A transition at position c975 in exon 11, and G360R is caused by a G to C transversion at position c1245 in exon 13. This latter mutation was found twice in two unrelated patients. The other novel AKU mutation (IVS7+5G→A) is a G to A transition in the fifth nucleotide position of the donor (5') splice site sequence of intron 7, which most likely causes aberrant splicing of HGO. None of these four novel AKU mutations were observed, using SSCP screening, in a sample of 100 control chromosomes. Finally, the mutation G1526 originated from a one base insertion at position c621, which determined a frameshift eventually leading to premature arrest of the protein synthesis. This same mutation was described in two Slovak families. Although the loss of function nature of all these HGO mutations was not formally proven, SSCP and sequence analysis of the relevant DNA fragment in family members confirmed in all cases that the pattern of inheritance of AKU was compatible with the segregation of the HGO mutations.

### Table 1: PCR primers for nested PCR analysis of HGO cDNA from blood lymphocytes

<table>
<thead>
<tr>
<th>Forward primer</th>
<th>Reverse primer</th>
<th>PCR product (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HTEL</td>
<td>HTER</td>
<td>1556</td>
</tr>
<tr>
<td>HS1L</td>
<td>HS9</td>
<td>258</td>
</tr>
<tr>
<td>HS4</td>
<td>HS5</td>
<td>290</td>
</tr>
<tr>
<td>HS6</td>
<td>HS1F</td>
<td>278</td>
</tr>
<tr>
<td>HS8</td>
<td>HS10</td>
<td>291</td>
</tr>
<tr>
<td>HS11F</td>
<td>HS10</td>
<td>288</td>
</tr>
<tr>
<td>HS13</td>
<td>HS5</td>
<td>314</td>
</tr>
</tbody>
</table>

### Table 2: HGO mutations and haplotypes identified in Italian AKU patients

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Type</th>
<th>Nucleotide change*</th>
<th>Associated polymorphism</th>
<th>No</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>G1526</td>
<td>Frameshift</td>
<td>c621insG</td>
<td>T T 191 161 T C 187</td>
<td>1</td>
<td>10</td>
</tr>
<tr>
<td>IVS7+5G→A</td>
<td>Intron change</td>
<td>c636+5G→A</td>
<td>A T 199 161 T C 181</td>
<td>1</td>
<td>This study</td>
</tr>
<tr>
<td>IVS9-56G→A</td>
<td>Intron change</td>
<td>c817-56G→A</td>
<td>A T 195 161 T C 181</td>
<td>1</td>
<td>9</td>
</tr>
<tr>
<td>IVS9-17G→A</td>
<td>Intron change</td>
<td>c817-17G→A</td>
<td>A T 189 161 T C 191</td>
<td>1</td>
<td>9</td>
</tr>
<tr>
<td>K248R</td>
<td>Missense</td>
<td>c909A→G</td>
<td>A T 197 161 T A 171</td>
<td>1</td>
<td>This study</td>
</tr>
<tr>
<td>G360R</td>
<td>Missense</td>
<td>c975G→A</td>
<td>A T 195 161 T C 187</td>
<td>1</td>
<td>This study</td>
</tr>
<tr>
<td>VRN</td>
<td>Missense</td>
<td>c1245G→C</td>
<td>A A 193 163 C T 197</td>
<td>2</td>
<td>This study</td>
</tr>
</tbody>
</table>

*Positions of nucleotide changes are from the transcription start site (AF045167).
†The alphanumerical strings represent the haplotypes formed by the following HGO intragenic markers: IVS2+35T/A, c407T/A, HGO-3, HGO-1, IVS5+25T/C, IVS6+46C/A, HGO-2.
We managed to perform SSCP analysis of cDNA fragments from two families, one where the G360R mutation was segregating and the other where the patients were compound heterozygotes for the K248R and the IVS+5G→A mutations. It is interesting to note that this latter supposedly splice site mutation did not affect the SSCP pattern of the cDNA amplicon defined by primer pair HS6/HS3F spanning exons 7 to 9. Furthermore, IVS+5G→A seemed to have no influence on HGO mRNA stability, as judged by the presence of both wild type and mutant bands in the cDNA amplicon defined by primer pair HS8/HS12 containing the K248R site.

In the light of the recent report of a preferential occurrence of HGO mutations in the CCC/GGG sequence motif,9 we analysed the sequence context of the four novel mutations found in the present work. It could not be coincidental that G270R and G360R mutations take place in tri- and penta-G runs, respectively. Moreover, the G152fs mutation previously described in two Slovak families10 occurs in a tetra-G run. Whether the G152fs mutation we found in an Italian family has an independent origin remains to be determined. Haplotyping of the Slovak pedigrees as well as comparison with the Italian one could provide strong evidence that the CCC/GGG motif is a mutational hot spot in HGO.

Table 2 also shows the haplotypes at the HGO intragenic markers IVS2+35T/A, c407T/A, HGO-3, HGO-1, IVS5+25T/C, IVS6+46C/A and IVS6-24A/G are associated with each AKU chromosome. Analysis of the HGO haplotypes harbouring the purported causative AKU mutations showed that the three intronic mutations were found in a common haplotypic background composed of the very same alleles at four SNPs as well as at HGO-1. Beltrán-Valero de Bernabé et al.10 referred to this as haplotype A, the most frequent in European populations. Two other mutations, G152fs and G270R, were detected in a gametic association, haplotype D, which is derived from haplotype A by variation at the SNP IVS2+35T/A. Closely related to haplotype A is also that derived from haplotype A by variation at the SNP IVS2+35T/A and IVS6+46C/A, respectively. On the other hand, the mutation VRN was probably within the so-called haplotype E.9 It has been postulated that haplotype E has a North African origin, an ethnic component that is known to have contributed to the modern Italian population. Whether the VRN mutation has originated in Italy or has been introduced into this country with the different migrations is at present unknown.

Only two of the AKU mutations found in Italians (G152fs and IVS9-56G→A) have been encountered in patients from other European countries. One of them, as indicated before, is the G152fs mutation that was identified in two Slovak AKU pedigrees.10 It would be interesting to determine whether the G152fs mutation has an eastern European origin and appeared in Italy by migration. The IVS9-56G→A AKU mutation was also identified earlier in an AKU chromosome of a French patient.9 Interestingly the IVS9-56G→A mutation in the Italian and the French patients are associated with the same HGO haplotype. In this case, we postulate an Italian origin for this mutation since the French IVS9-56G→A carrier patient has Italian ancestors.

It is important to note that the mutations P230S, V300G, and M368V, which are relatively common mutations,7 12 15 19 were absent in our patients. P230S and V300G are typically associated with haplotype E and are thought to be North African in origin.7 The M368V mutation is widely distributed throughout Europe and is associated with haplotype A. It is also interesting that the mutation G360R was found twice within the same haplotype in two families from different ends of the Italian peninsula; patient VRN was from Calabria (southern Italy), whereas the affected sons of a consanguineous marriage were from South Tyrol, a German speaking region on the Austrian border. Additional HGO mutational and polymorphism analyses of AKU patients from many more different countries would be necessary to understand the population genetics of AKU and the migration of the different AKU alleles.

In conclusion, we report here an extensive description of the spectrum of AKU mutations in Italy, including the characterisation of their associated intragenic HGO polymorphisms. Four novel mutations were found, which include both missense mutations and subtle intronic changes. The Italian AKU sample confirms the high degree of allelic heterogeneity of the HGO gene and illustrates the complications of mutation screening in AKU patients. These data should facilitate the future identification of these AKU alleles in this and other populations.

Note added in proof

The mutation G270R has recently been described by Müller et al. (Eur J Hum Genet 1999;7:645–51).

We thank Pier Luigi Mattiuz and Umberto Serni for encouragement and suggestions. We are also grateful to Alfredo Brusco and to Claudio Castellan for helping us to identify AKU patients and families. This work was supported in part by a grant from the University of Florence, MURST ex 60% funds, by the Fundación José Antonio de Castro, the Spanish Comisión Interministerial de Ciencia y Tecnología (SAF96/0053, SAF97/1789E), and the Comunidad de Madrid (08/60015/1997). In addition, this study is based on work supported by the Fundación Conchita Rábago de Jiménez Díaz under a grant awarded to DB-VdeB.

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Rough skin, brittle hair, and photosensitivity: a mild phenotypic variant of trichothiodystrophy

EDITOR—The trichothiodystrophies (TTD) are named primarily for the hair sulphur deficiency which is their most specific feature and which leads to brittleness of the hair. Other ectodermal tissues may be affected and typically the skin is ichthyotic and the nails dystrophic. Additionally, there may be a distinctive facies and physical and developmental retardation of varying degree of severity. Inheritance is autosomal recessive and at least three loci exist, of which two are known, the excision repair/transcription factor genes XPD/ERCC-2 and XPB/ERCC-3. We describe an 8 year old girl in whom the diagnosis of a mild and in some respects atypical form of TTD was made on the synthesis of clinical, pathological, and biochemical data. The genotypic basis of this clinical phenotype has yet to be established.

The patient was the second child of a dizygous twin pregnancy born to unrelated, healthy, white parents by emergency caesarean section at 32 weeks because of pre-eclampsia. The family history was unremarkable and her male co-twin was healthy. Birth weight was 2100 g (90th centile for this gestation). Birth length and head circumference were 51.5 cm and 32.5 cm respectively. The skin was dry and flaky from birth (but never “collodion”), and in using a towel her mother had to pat her dry, rather than to rub. Thickening of the palms and soles developed in the first year of life. The nails were brittle from birth. Hair growth has always been slow and she has never had a proper haircut, only trims. Desquamated cells from the external auditory canal failed to clear and she has required periodic syringing.

She was referred to our service at 5 years of age because of concerns related to persistent dermatitis, dermal photosensitivity suggested by easy burning in the sun, mild developmental delay, and distinctive facial appearance. We noted the following features: hair that was “wiry” in texture, fragile, and easy to extract; abnormal scalp hair distribution with temporal recession; prominent forehead with sparse eyebrows (fig 1); a generalised dryness of the skin with areas of keratoderma; and brittle, spoon shaped fingernails and toenails. The keratoderma was particularly marked on the soles and palms (fig 2) and at the popliteal and antecubital flexures. Apart from congenital absence of the second premolars, the teeth were normal. Her weight was 27 kg (90th centile), height 128 cm (97th centile), and head circumference 54 cm (98th centile). These measurements are consonant with the parental heights and weights, which were in the 90th-97th centile range. She was attending a normal school and was in the appropriate class for

We used this occasion to test the robustness of buccal smears for diagnostic purposes. We had previously used buccal smears successfully for the diagnosis of xeroderma pigmentosum complementation group A (XPA) patients (J E Cleaver, M McDowell, unpublished data), but we expected that the XPD gene, being larger than XPA, and with more introns, might prove even more difficult. Buccal smears were taken from the patient and her co-twin and sent by express mail from Melbourne to San Francisco. Samples were then solubilised in alkali extraction buffer and subjected to genomic amplification by PCR, using primers that flank those genomic regions in which mutations noted above had previously been identified. The PCR products were subcloned into a cloning vector and individual inserts sequenced. The unaffected co-twin had no causative mutations in the regions investigated, although there were two common neutral polymorphisms (c687G>A, c711C>T). The index case had neither of these polymorphisms and neither was the c1381C>G, c2146del45 null allele identified. We sequenced about 300 nucleotides around the region of the causative mutation (c2173G>C) and found only wild type sequences.

This child presents a mild phenotypic form of trichothiodystrophy (TTD). The scalp hair was abnormal in its texture, strength, and distribution, and the electron microscopic (but not light microscopic) picture was similar to that of the classical form of TTD. Hair cysteine content was reduced and the A layer of the cuticle cells defective, substantiating the diagnosis. Other clinical observations included keratoderma, nail dystrophy, and mild developmental delay. Linear growth was unaffected.

TTD can present with a notably wide clinical range. In its mildest form, the disorder may be confined clinically to an abnormality of the hair. The “tiger tail” hair sign is typical but not universal, as indeed our case exemplifies. A further grade of affection is illustrated in our patient, with mild to moderate involvement of the ectoderm and certain of its appendages, as well as (if indeed this is causally related) a minor cognitive component. At the other end of the spectrum, TTD is a seriously disabling disease, with a severe skin affliction and mental defect and growth retardation.

The TTDs comprise one of a group of related disorders resulting from abnormalities in components of the nucleotide excision repair (NER) system, these factors having a second role as subunits of the basal transcription factor TFIIH. Three TTD complementation groups exist, corresponding to the genes XPD/ERCC-3, XPD/ERCC-2, and an uncloned gene TTDA. Xeroderma pigmentosum (XP) and a form of Cockayne syndrome (CS) with XP-like symptoms are also the result of defects.
in the NER/TFIHH system, and the three conditions XP, CS, and TTD overlap at a clinical and molecular level. The phenotype in XP includes photosensitivity, pigmented abnormalities, neurodegeneration, and (unlike TTD) a predisposition to skin cancer; CS is characterised by neurodysemelination, photosensitivity, and physical and mental retardation.

Mutations in one particular NER/TFIHH subunit, XPD/ERCC-2, account for the great majority of photosensitive TTD patients, and are seen in patients with XP complementation group D (XPD), and in patients with combined clinical features of XP and Cockayne syndrome. In vitro insertion of XPD/ERCC-2 in cells of the three conditions corrects the UV induced DNA damage in cells, showing a locus homogeneity with allelic heterogeneity in the three clinical phenotypes. The gene has yet to be identified in a second TTD complementation group, in which the phenotype is severe. Mutations in the gene XPB/ERCC-3, which codes for another NER/TFIHH subunit, have recently been identified in the third complementation group of TTD, characterised by a mild phenotype, and so far represented only by two sibs; the Cockayne/XP syndrome has also been associated with this locus. The two reported XPB/ERCC-3 sibs displayed a dermatological phenotype of “collodion baby”, proceeding to a residual mild ichthyosis of the trunk and a mild photosensitivity. Hair microscopy showed a “tiger tail” pattern. They were noted to be of normal intelligence and of normal weight and height, although a “mild learning disability” was recorded in one, and this child also had growth indices.

We have not been able to find an XPB/ERCC-2 mutation in our patient, although this possibility is by no means excluded. The mildness of the phenotype may suggest an equivalence to the XPB/ERCC-3 sibs in Weeda et al, but there is a difference in that she had not presented as a colobion baby, her linear growth is not compromised, her keratoderma is more marked, and light microscopy did not show “tiger tailing”. Which, if either, locus underlies her case remains open to question.

We thank Dr Richard McNeill who referred the patient, Dr C W Chow and Professor J D Dowling who performed hair electron microscopy, Dr C Baker who did the skin light testing, and Mr Gary Corino of the Commonwealth Sci-

The first description of lethal pterygium syndrome with facial clefting (Bartoscas-Papas syndrome) in 1600

Editor—A recently reviewed 12 page pamphlet dated 1600, housed at the Bodleian Library, Oxford, contains a detailed account of a severely malformed infant born in Herefordshire in January 1600. The child, whose gender was uncertain to the observers, was born to first cousins. “A most strange, and true discourse, of the wonderfull judgement of God. Of a monstrous deformed infant, begotten by incestuous copulation, betwenee the brother’s sonne and the sister’s daughter, being both vnmarried persons”. Adhering closely to the language of the day the infant is described thus.

Head longer than ordinary children with no hair on the head or eyebrows.

Both eyes standing far out of the head, unequal to each other - right eye very small, like a black sloe stucked half out in the flat face - no eyelid or eyepit - “as it were a bullet stucking in a plain wall”; the left eye was very big and emient, sticking out like the other but with eyelids which were drawn the upper up and the lower down as if inside out.

Nose depressoed flat to face - no nostrils - at lower end a round botten of fleshy substance the size of a nut. On either side, higher than the nose the upper lip was slitt or hare-thorne from which two slits thro’ the pallet or roof of the mouth there passed two hoolow trenches, almost two fingers deep - to the gullet, which seemed to be the passage of the nostrils - the lower part of the mouth on either side of the tongue like a deep trench.

Mouth smaller than normal - no gums, jawbones or lips. Face more wrinkled than most - grim to behold.

No thumbs or any outward partition of fingers - fingers covered all with one skin, “as with a mitten”, but with joints.

Finger of left hand (digitus annularis/ring finger) had nail and was separated towards the end.
Sex reversal and diaphragmatic hernia in phenotypically female sibs with normal XY chromosomes

Editor—True agonism, characterized by the absence of gonads in both XY and XX patients, is a rare, mostly sporadic, and isolated condition. Its association with diaphragmatic hernia seems to be extremely rare and has always been described associated with multiple congenital malformation (MCA) syndromes of unknown origin. Sex reversal and diaphragmatic hernia have been described once with a heterozygous \( \text{WT1} \) mutation in a sporadic case. The association of normal feminisation, absent gonads, and diaphragmatic hernia in two XY sibs without any other malformation suggested other diagnostic possibilities. Since further investigations did not find any chromosomal or known genetic cause for this familial sex reversal syndrome, we suggest that these cases could represent a new sex reversal syndrome, which could be either autosomal recessive or X linked, and may result from either unreported mutations of \( \text{WT1} \) or anomalies of other developmental genes. The proband (fig 1, II.4) is the fourth child of non-consanguineous, healthy parents with an unremarkable family history. Their first child (II.1), a girl born at term in 1989, died of severe respiratory distress at 2 days of age after surgery for a left diaphragmatic hernia. She was of normal size (weight 3200 g, 50th centile) and according to the paediatricians not dysmorphic. No additional malformation was found at necropsy apart from the large left diaphragmatic hernia and a single umbilical artery. Chromosomal analysis was not performed. Two subsequent pregnancies resulted in normal, healthy, male children (II.2, II.3).

At 34 weeks’ gestation of the fourth pregnancy, ultrasonography detected dextrocardia owing to a left diaphragmatic hernia involving the stomach, left lobe of the liver, and numerous intestinal loops. Chromosomal analyses were performed on both lymphocytes from fetal blood and fibroblasts from amniotic fluid. They were normal male: 46,XY. Delivery was spontaneous at 37 weeks’ gestation. Neonatal measurements were within normal limits (weight 2370 g, 10th centile, OFC 31 cm, 10th centile).

Figure 1 Family pedigree.

Intubation was performed immediately after birth and the infant was transferred to the intensive care unit. HFO and NO treatments were given. Apart from the respiratory distress syndrome, the clinically female infant was normal except for bilateral membranous syndactyly of the second and third toes. This was absent in all three sibs but present to a lesser degree in her father. Cardiac and abdominal ultrasonography were normal. The diaphragmatic hernia was surgically repaired at 2 weeks of age, when an almost total absence of the left diaphragm was noted. This required the fitting of a Goretex® plate. The subsequent course was favourable and ventilatory support was discontinued at 1 month of age. At 9 months the patient was in good health; weight was 6 kg (−2 SD), height 66 cm (−1 SD), OFC 43 cm (−1 SD), and neuromotor development was normal.

Further investigations were performed in the proband who had completely feminised external genitalia, a normal male karyotype, severe diaphragmatic hernia, and whose sister had died of diaphragmatic hernia. Cholesterol and 7OH cholesterol were normal so that Smith-Lemli-Opitz syndrome (MIM 270400) could be excluded. Skeletal x rays showed somewhat curved clavicles but no anomaly that could indicate campomelic dysplasia (MIM 114290). Hormonal profile in the neonatal period showed very low testosterone (0.21 ng/ml, normal 2-4 ng/ml) and dehydrotestosterone (0.04 ng/ml), with normal FSH (1.8 IU/l) and LH (1.1 IU/l) levels, as seen in both complete XY gonadal dysgenesis and agonadism. Ultrasonography of the visceral organs showed the presence of an apparently normal uterus. Pelvic endoscopy was performed at 6 months of age and confirmed the absence of a normal uterus and fallopian tubes; however, no gonads were found, not even in an ectopic position. High resolution G banding chromosome analysis confirmed the normal male karyotype; in particular no anomalies were observed in the regions of localised or putative sex determining genes, such as Yp11.3 (SOX9), Xp21.3 (DSS/DAX-1), 11p13 (WTT1), 17q24 (SOX9), 9p, 1 or 10q. SRY was present and PCR analyses of both the promoter and the unique exon showed that they were present and of normal size. Furthermore, fluorescent in situ hybridisation (FISH) of the Y chromosome performed on paraffin preserved tissue from the dead sib detected retrospectively the presence of a Y chromosome. SRY analyses could not be performed because of the small amount of tissue preserved, and it was not possible to study retrospectively the internal genitalia of this normally feminised infant.

As diaphragmatic hernia has been described in one case of Denys-Drash syndrome (DDS, MIM 194080), renal function was carefully investigated in the proband whose renal ultrasonography was normal) and was found to be normal. Moreover, renal tissue of the dead sister was re-examined and found to be normal. Finally, in the proband no anomaly was found in exons 7, 8, or 9 of the WT1 gene, which is responsible for DDS and Frasier syndrome (FS, MIM 136680).

Here we report two sibs with a normal male karyotype and diaphragmatic hernia. Clinical and laboratory investigations of sex reversal established the diagnosis of true agonadism, which is a rare, mostly sporadic condition characterised by the absence of gonadal structure. Agonadism has almost always been diagnosed in cases with a normal male (XY) karyotype, female external genitalia, and absence of extragenital anomalies. However, the condition could have been overlooked in karyotypically female patients because of the absence of sex reversal. In XY patients, agonadism has to be differentiated from XY pure gonadal dysgenesis (Swyer syndrome resulting from SRY mutations (MIM 306100)), in which the gonads are...
reduced to streaks but are present, and both external and internal genitalia are normal female. In XY patients, agonadism was termed embryonic testicular regression syndrome because, from an embryological point of view, it may be the result of secondary precocious regression rather than true agenesis of the primary undifferentiated gonads. Thus, early testicular tissue action (anti-Müllerian hormone (AMH) and testosterone) could explain the range of virilisation in some agonal XY patients. Because of the few familial cases of XY embryonic testicular regression syndrome, genetic determinism has been suggested.

Agonadism has seldom been observed with an XX chromosomal constitution in either sporadic (n=1) or familial cases (both XY and XX affected sibs of consanguineous parents). Externally normal female in all five patients, but Müllerian ducts were either absent, hypoplastic, or normal, whereas no transient testicular anti-Müllerian effect can have acted in these XX patients. Thus, the question is raised of the involvement of autosomal genetic factors maintaining both gonads and Müllerian ducts (the latter independently of AMH action).

On the other hand, agonadism has also been described associated with variable extragenital anomalies in both sporadic and familial cases (table 1), of which one sporadic and one familial cases were also associated with diaphragmatic hernia. However, the remaining features in these patients are sufficiently different from those we describe to exclude comparison. In the present study, described by Oyer et al, Müllerian derivative defects and bicuspid aortic valve were observed. In theibs born to unrelated parents described by Sorgo et al and Kennerknecht et al, Müllerian ducts were present although rudimentary, and diaphragmatic hernia was associated with a heart defect in a patient with an XY chromosomal constitution, whose XX sib presented with omphalocele, heart defect, and cleft palate.

Diaphragmatic hernia and sex reversal has been described associated with multiple malformations in three unrelated phenotypic girls with a normal XY karyotype. However, the multiple associated malformations, cyanotic complex heart defect (n=2), hypoplastic left ventricle, ectopic spleen, and horseshoe kidney (n=1), and above all the presence of testis tissue are sufficiently different from our observations to distinguish these conditions.

We also looked for WT1 mutations (which were first described in patients with Wilms tumour, then in DDS syndrome, and more recently in Frasier syndrome), because of the description of a WT1 point mutation (arg 366 his) in a phenotypic girl with a normal male karyotype, a large left postero lateral diaphragmatic hernia, and features of DDS (dysgenetic ovaries, double uterus, double vagina, and severe glomerulopathy), who died at 5 hours of age from respiratory distress. Furthermore, transgenic mice with a homozygous WT1 deletion consistently have diaphragmatic hernia and heart defects besides their urogenital malformations, although no WT1 mutation has been found in patients with isolated diaphragmatic hernia. WT1 is expressed in abdominal and lung mesothelium and encodes four isoforms of zinc finger transcriptional factors that could regulate several genes involved in the development of the diaphragm as well as those implicated in sex determination and differentiation, such as SRY, AMH, and the androgen receptor genes. Our patient did not fit all the diagnostic criteria for either DDS or FS; she had agonadism rather than gonadal dysgenesis, her Müllerian structures were normally developed while they are often hypoplastic or absent in DDS or FS, she has not presented any renal anomalies up to the age of 1 year, and no mutation has been found in WT1 exons 7, 8, or 9. However, the absence of identified gonads could be an extreme form of gonadal dysgenesis, testicular regression could have been precocious enough to prevent AMH secretion, and renal dysfunction owing to WT1 mutations could appear later (as seen in FS). Since, to our knowledge, no other familial cases of true agonadism associated with diaphragmatic hernia have been published, and since we did not find WT1 mutations known to be implicated in DDS and FS syndromes in our patient, we suggest that such cases could represent a new sex reversal syndrome that could be either autosomal recessive or X linked, and result from either unreported mutations of WT1 or anomalies of other developmental genes.


**Letters**


Letters

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Clinical variability of Stickler syndrome with a \textit{COL2A1} haploinsufficiency mutation: implications for genetic counselling

Editor—Snead and Yates\(^1\) have recently reviewed clinical and molecular findings in Stickler syndrome, the autosomal dominant connective tissue disorder characterised by ocular manifestations, facial abnormalities, cleft palate, sensorineural hearing loss, and degeneration of epiphyseal and articular cartilage (hereditary progressive arthro-ophthalmopathy).\(^2\)\(^-\)\(^4\) Mutations in the structural genes for collagen II (\textit{COL2A1}) and collagen XI (\textit{COL11A1}, \textit{COL11A2}) have been identified in patients with a Stickler syndrome phenotype.\(^5\)\(^-\)\(^13\) Based on locus heterogeneity, a subclassification of \textit{COL2A1} associated Stickler syndrome type I, \textit{COL11A1} associated Stickler syndrome type II, and \textit{COL11A2} associated Stickler syndrome type II was established (OMIM 108300, 120280, and 184840). A clinical subclassification based on the presence or absence of an ocular phenotype, and on the

\begin{figure}[h]
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\includegraphics[width=0.8\textwidth]{figure1}
\caption{The proband in the newborn period (note midface hypoplasia, micrognathia, apparent exophthalmos, and deep set ears) and at 5 years of age. The face is slightly flat with maxillary hypoplasia and retrognathia. Her height is on the 90th centile; note also mild neck webbing and flat feet. (All photographs reproduced with permission.)}
\end{figure}
features of the ocular phenotype, correlates reasonably well with the genotype.\textsuperscript{19}

Clinical variability in Stickler syndrome is well known,\textsuperscript{4,13,15} but correlations with specific mutations are scarce. We report a novel COL2A1 gene mutation found in a patient with flat face, cleft palate, myopia, and hearing loss (Stickler syndrome) and unexpectedly also in her father and her paternal grandmother who were considered to be healthy. The patient is the first child of healthy, non-consanguineous Swiss parents. The pregnancy was uneventful and she was delivered at term by caesarean section because of breech position. Birth weight was 3890 g (90th centile), birth length 50 cm (50th centile), and head circumference 37 cm (>97th centile). Macrocephaly and facial dysmorphism were noted in the neonatal period, including a flat midface, deep set ears, exophthalmos, palpebral oedema with telangiectasia, micrognathia, and median clefing of the soft and part of the hard palate (fig 1). No other abnormalities were recognised at that time. At the age of 5 years, midface hypoplasia and micrognathia were still evident. In addition, she presented with mild bilateral hypoacusis, bilateral myopia (4 dioptres), slight webbing of the neck, minimal pectus carinatum, and flat feet (fig 1). Her growth was on the 90th centile. The clinical signs and symptoms as well as radiological findings of mild spondyloepiphyseal dysplasia suggested the diagnosis of Stickler syndrome.

All 54 exons of the COL2A1 gene, including the flanking splice sites, were amplified and screened by SSCP analysis. Exon 12 gave an abnormal pattern and was subcloned and sequenced, showing a deletion of 2 bp (nt 697-698), for which the patient was heterozygous. The mutation predicts a downstream premature TGA-stop codon in exon 13 (fig 2). The father’s DNA gave a similar heteroduplex pattern, and direct sequencing confirmed his heterozygous mutation carrier status. He had been regarded as unaffected, but re-evaluation showed some features consistent with Stickler syndrome including mild bilateral myopia (2 dioptres), a high arched palate, and a partially split uvula. His body habitus showed no distinctive features except for his height of 190 cm (>97th centile) (fig 3); hearing was normal and there was no history of arthrogryposis. Childhood photographs were reviewed and found to be unremarkable. We subsequently investigated the paternal grandparents and found that the grandmother carried the same COL2A1 gene mutation in the heterozygous state in her blood leucocytes. She considered herself healthy and declined further investigations. Her physician observed no features of Stickler syndrome. To rule out the presence of a second COL2A1 mutation in the proband leading to a more severe clinical phenotype, all 54 exons and the flanking intron splice site sequences were analysed by direct sequencing in the proband as well as in her father and grandmother. Except for a few already known common polymorphisms, no additional sequence abnormality was observed.

The 2 bp deletion in exon 12 of the COL2A1 gene identified in this family leads to a frameshift with a premature stop codon in exon 13. This causes the synthesis of truncated procollagen α1(II) chains, which are unable to participate in collagen II triple helix formation, without exerting other negative effects (haploinsufficiency). (B) Heteroduplex analysis of the exon 12 amplicon in the patient (Pt), her mother (Mo) and father (Fa), the paternal grandmother (Gm) and grandfather (Gf), as well as three controls (C1, C2, C3). Blood leucocyte DNA was used as template. The figure shows the presence of heteroduplex PCR products as well as three controls (C1, C2, C3). Blood leucocyte DNA was used as template. The figure shows the presence of heteroduplex PCR products as well as three controls (C1, C2, C3).
side, counselling must take into account the possibility that inheritance of such a mutation may have only minimal clinical consequences or remain silent, but it can be difficult for prospective parents to make use of information with this degree of uncertainty.

Some indications for future research may be derived. First, the question might be asked of whether variability is more frequent in COL2A1 haploinsufficiency mutations than in the other COL11A1 and COL11A2 mutations associated with Stickler syndrome. Second, a systematic ascertainment of families segregating such COL2A1 haploinsufficiency mutations might allow the penetrance of single clinical traits, such as cleft palate or severe myopia, to be determined. It cannot be excluded at present that among carriers of such mutations, subjects with the full blown Stickler phenotype are the exception rather than the rule; this remains to be investigated. Such insight would be helpful for counselling and parental decision making.

We are grateful to our young patient and her parents for cooperation and for permission to publish their photographs; to her grandparents and Dr Z Schneider for clinical information; and to Pia Herrmann, Jutta Busch, and Sabine Fleig for prospective parents to make use of information. We are grateful to Andreas Superti-Furga and from the Deutsche Forschungsgemeinschaft to Andreas Superti-Furga, and to Anna Pia Hermanns, Jutta Busch, and Sabine Fleig for clinical information; and to Pia Hermanns, Jutta Busch, and Sabine Fleig for prospective parents to make use of information.

Figure 3 The patient's father at 41 years of age. He is 190 cm tall and thus on the 97th centile for the Swiss population. He has mild myopia (2 dioptres), a compatible but non-specific finding. Little in his physical appearance suggests a collagen disorder; the only telltale finding was a partially bifid uvula.


Figure 3 The patient's father at 41 years of age. He is 190 cm tall and thus on the 97th centile for the Swiss population. He has mild myopia (2 dioptres), a compatible but non-specific finding. Little in his physical appearance suggests a collagen disorder; the only telltale finding was a partially bifid uvula.

Can hair be used to screen for breast cancer?

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