Leigh syndrome transmitted by uniparental disomy of chromosome 9

EDITOR—Severe, isolated, and generalised deficiency of complex IV (cytochrome c oxidase, COX) can result in Leigh syndrome (LS) (MIM 256000), an early onset mitochondrial disorder characterised by rapidly progressive, symmetrical degeneration of the brain stem, diencephalon, and basal ganglia.1,2 SURF-1, a gene located on chromosome 9q34, has recently been identified as the gene responsible for numerous cases of LS.3-5

SURF-1 associated LS is usually inherited as an autosomal recessive trait. We report here a homozygous loss of function mutation of SURF-1 in two monozygotic LS female twins, owing to uniparental disomy of two almost identical maternal chromosomes 9.

The probands were born to non-consanguineous parents at 33 weeks of gestation by caesarean section. The mother was 46 years old. The pregnancy was uneventful until the 24th week, when persistent uterine contractions ensued. Two older sibs of the probands are alive and healthy. The female twins, owing to uniparental disomy of two almost identical maternal chromosomes 9q34, have mild to severe cognitive impairment, and psychomotor development was regular during the first 8 months of life. During the following months the patients developed a rapidly progressive clinical syndrome characterised by failure to thrive, psychomotor regression, hypotonia, ophthalmoplegia, mild bilateral optic atrophy, and ataxia. At 18 months both patients had mild lactic acidosis. MRI showed symmetrical paramedian lesions in the mesencephalon and brain stem, as typically found in LS. Both patients died of respiratory failure in the third year of life.

Needle muscle biopsies performed at 24 months of age showed a diffuse reduction of the histoenzymatic reaction to COX. Biochemically, COX activity in muscle homogenates was 12.1 nmol/min/mg in one patient and 3.6 nmol/min/mg in the second (normal values 68 ± 20), while the activities of the other respiratory complexes were all normal. The COX defect was also detected in cultured fibroblasts of one patient (0.4 nmol/min/mg, normal value 25 ± 11), but this assay was not performed in the second patient. Specific activities of the respiratory complexes in a muscle homogenate of the mother were all normal.

Automated sequence analysis of the nine exons of the SURF-1 gene in the probands showed the presence of a previously reported homozygous frameshift mutation (751C>T). This mutation destroys a BsuRI restriction site, which is present in the wild type gene. BsuRI RFLP analysis showed a heterozygous mutation in the mother, while no mutation was detected in the probands’ sister, or brother (fig 1). A de novo mutation in the paternal chromosome 9 identical to the mutation carried by the mother was considered unlikely. Non-paternity was excluded by linkage analysis with numerous microsatellite markers. To test the hypothesis of chromosome 9 specific paternal non-contribution, we then analysed three STSs (D9S1831, D9S1826, and D9S158), flanking the SURF-1 locus at 9q34. All three markers showed the presence of one maternal allele only, while the paternal allele was consistently absent. To verify whether the paternal non-contribution was the result of a microdeletion at 9q34, we sequenced P117B6, which contains the SURF-1 gene,3 was used as a probe in FISH experiments for metaphases from one proband. The probe detected two comparable signals on both chromosome 9 homologues (fig 2).

These results excluded the presence of a deletion in a paternal chromosome, suggesting instead a mechanism of uniparental disomy (UPD) of two maternal chromosomes. To test this hypothesis, additional microsatellites distributed along the whole of chromosome 9 were analysed for a total of 22 markers (fig 1). With the exception of two small regions (D9S288-D9S286, and D9S167-D9S283-D9S287, see fig 1) the alleles were all homozygous; in 15 instances the obligate contribution of the paternal allele was unequivocally missing. In particular, homozygosity was detected for 10/10 markers encompassing the SURF-1 locus, in the interval defined by markers D9S1831-D9S158. We conclude that loss of the contribution of a second normal SURF-1 allele has led to the manifestation of LS in our patients.

UPD is defined as the exceptional inheritance of a pair of chromosomes from one parent only, as the result of gamete complementation, chromosome loss in trisomy, or duplication in monosomy. In isodisomy, the uniparental pair is a duplicate of the same chromosome DNA template, and causes an increased risk of a recessive disorder by reduction to homozygosity.7 In our patients the presence of two small heterozygous regions can be explained as the result of two crossing over events in otherwise identical maternal chromosomes 9. These data indicate that the double maternal contribution was the result of a non-disjunction.
 comment: A case of Williams syndrome with a large, visible cytogenetic deletion

Editor—Williams syndrome (WS) is generally characterised by mental deficiency, gregarious personality, dysmorphic facies, supravalvular aortic stenosis (SVAS), and idio-pathic infantile hypercalcaemia. Patients with WS show allelic loss of STX1A, elastin (ELN), and LIMK1, with most exhibiting a submicroscopic deletion at 7q11.23, detectable by FISH. The common deletion size is about 1.5 Mb. Previous studies have shown that WS patients have consistent deletion sizes and share common proximal and distal breakpoints. Here we report a patient who has a large, atypical, visible chromosomal deletion of 7q11.2 and features consistent with, and in addition to, those typically seen in Williams syndrome.

The patient was originally referred to the genetics clinic at 5 months of age for evaluation of global developmental delay and dysmorphic features. She was delivered at 37 weeks’ gestation by caesarean section weighing 2350g (<5th centile). The initial course included a history of poor feeding in the newborn period. Clinical examination showed macrocephaly, cutaneous haemangioma, and craniofacial features consisting of a large anterior fontanelle, frontal bossing, depressed nasal bridge, cup shaped ears, hypertelorism, and prominent lips (fig 1A). Neurological examination showed generalised hypotonia with delayed and dysmorphic features. She was delivered at 37

UPD may also cause functional balance disruption of imprinted genes. The existence of imprinted genes on chromosome 9 is controversial, but it seems unlikely. Our patients did not show gross dysmorphic features or malformations apart from LS. With the limitations because of the brief survival and severe phenotype, this observation suggests that chromosome 9 does not contain maternally imprinted genes crucial for embryonic development.

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VALERIA TIRANTI
ELEONORA LAMANTEA
GRAZIELLA UZIEL
MASSIMO ZEVIANI

Divisione di Biochimica e Genetica, Istituto Nazionale Neurologico “Carlo Besta”, Via Celoria 11, 20133 Milano, Italy

Casa Sollevio della Sofferenza, S Giovanni Rotondo, Italy

PAOLO GASPARINI

Università Statale di Bari, Bari, Italy

ROSALIA MARZELLA
MARIANO ROCCHI

Imperial Cancer Research Fund, UK

MIKE FRIED

References

and very grey optic discs with surrounding peripapillary retinal pigment epithelial changes. Serum calcium levels were raised once (10.8 mg/dl, normal range 8.5-10.5 mg/dl), but have since been in the normal range. FISH analysis for the elastin locus on chromosome 7q11.23 showed a deletion consistent with Williams syndrome and repeat cytogenetic analysis showed a visible deletion in band 7q11.2 (46,XX,del(7)(q11.1q11.23)) (fig 2).

Follow up at 6½ years of age showed weight 19.8 kg (40th centile), height 107 cm (5th centile), and head circumference 52.5 cm (70th centile), with other notable findings that included prominent supraorbital ridging, periorbital fullness, stellate pattern to her irides, cup shaped ears in normal position, prominent, full lips, long philtrum, and a broad nose with anteverted nostrils (fig 1B). She had fifth finger clinodactyly and brachydactyly. Examination of her skin showed a haemangioma in the midline lumbosacral region, which had reportedly once extended from her occiput to her buttocks. She had a hoarse, raspy voice and frequent drooling.

Developmentally, she functioned in the severe mental retardation range. She showed significant delays in communication; expressive language was severely delayed with rare speech (a few words) and limited sign language and receptive language at <1 year of age. She had atypical behaviour including diminished interest in social interaction with others, self-injurious behaviour, intermittent stereotypic behaviour, and sleep disturbance.

The patient had a sister (aged 8 years) and a brother (aged 10 years) who were healthy with normal development. There were no other family members with mental retardation, short stature, or birth defects. The parents were non-consanguineous. Blood samples were obtained from both parents and the proband for additional molecular studies.

In order to identify a FISH probe for the gene encoding the \(\alpha\_\beta\) subunits of the L type voltage dependent skeletal muscle calcium channel (\(CACNL2A\)), a PCR primer set (exnCa-A: 5'-CGGTGAGTGCTAAGACCTGAATG-3', exnCa-B: 5'-CAGCCCTCATAGATGTCAGTAGG-3') was designed from exon sequence obtained from the EMBL database under accession number Z28599. Primers were used at a final concentration of 1.5 µmol/l in a 20 µl reaction. The amplification was performed with an annealing temperature of 60°C for 30 cycles. Total human DNA (25 ng) was used as a template. The resulting 311 bp product was electrophoresed on a 1% low melting point agarose gel. The gel fragment was excised and diluted 1:3 with sterile water and was labelled with \(^{32}\)P-dCTP by standard methodology. The probe was hybridised to high density filters arrayed with clones from a human total genomic P1 library. Four positive coordinates were

Figure 1  Front view of the patient at 22 months (A) and 6½ years of age (B). The child has characteristic Williams syndrome facies including frontal bossing, prominent supraorbital ridging, periorbital fullness, stellate pattern to her irides, cup shaped ears in normal position, prominent, full lips, long philtrum, and a broad nose with anteverted nostrils.
submitted to the Baylor College of Medicine YAC core and streaks, representing 12 P1 clones per coordinate, were received. For each, single colonies were tested by PCR using the exnCa primer pair. Clones from coordinate 101F1 were found to be positive for the primer sequence. The positive clone was grown and DNA was prepared using the Qiagen Plasmid Midi Kit following the amended instructions for P1 clones distributed by Qiagen. A cosmid size FISH probe was made by subcloning the P1 clone using the SuperCos 1 Cosmid Vector Kit available from Stratagene. A clone (CaE-1) specific to the exnCa primer pair was isolated by testing subclones by PCR as described above.

A cosmid containing the D7S849 locus, known to be linked to the CACNL2A locus, but not contained in the previous P1 clone, was subcloned from a yeast artificial chromosome (YAC) isolated from the CEPH Mark I YAC library by the Baylor College of Medicine YAC core using the D7S849 primer set. YAC DNA was prepared by a standard caesium chloride protocol and subcloned using the SuperCos I Cosmid Vector Kit. Human clones were identified by hybridisation of colony lifts with 25 ng of total human DNA radiolabelled with $^{32}$P. Human clones were then screened by PCR with D7S849. A single clone, positive for D7S849, was identified (CaE-2) and DNA was isolated using a Qiagen Plasmid Midi Kit and was used (20 ng/µl) as a FISH probe against patient metaphase chromosomes.

Additional probes used in the FISH analyses included a cosmid containing the 5' end of the elastin gene (cELN27), a cosmid containing the full sequence of LIMK1, and a bacterial artificial chromosome clone (BAC) containing the STX1A gene (BAC 137N23; Research Genetics, Huntsville, AL).

All FISH probes were labelled by nick translation with digoxigenin-dUTP and detected with anti-digoxigenin conjugated to rhodamine. Either a biotin labelled chromosome 7 alpha satellite centromere probe or a digoxigenin labelled chromosome 7q telomere probe (Oncor, Inc., Gaithersburg, MD) was used as a control to identify the chromosomes 7. The centromere probe was detected using avidin conjugated to fluorescein isothiocyanate (FITC). Slides were counterstained with DAPI. FISH analyses were performed as recently described.

This patient was deleted for all the FISH probes tested, including the CACNL2A gene and the locus D7S849 (fig 3).

DNA was extracted from peripheral blood from the patient and each parent using standard methodology. Polymorphic dinucleotide repeat markers were used to detect deletions and determine the parental origin of the deletion as previously described. A deletion was evident when the proband failed to inherit an allele from one of the parents. The following loci were examined (listed centromeric to telomeric): D7S572, D7S1870, D7S489U, D7S2476, ELN, LIMK1, D7S613, D7S2472, D7S1870, D7S489L, D7S849, D7S675, D7S699, D7S440, and D7S634.

The patient was deleted for markers D7S489U (centromeric) to D7S440 (telomeric) and uninformative for D7S634. The centromeric breakpoint was the same as seen in classical WS patients. The patient's distal deletion breakpoint was telomeric to the classical breakpoint (D7S1870), beyond the marker D7S440, with the exact distal breakpoint undetermined.

WS presents as a remarkable collection of features with significant phenotypic variability among patients. Variability in the phenotype could be the result of different sized deletions around ELN or the variation in gene content or gene activity of the hemizygous alleles on the non-deleted chromosome. Our previous studies have shown the size of the deletions in the majority of WS patients studied to be consistent between the markers D7S489U and D7S1870. The current patient represents a rare exception.

The gene encoding the $\alpha_2\beta$ subunits of the L type voltage dependent skeletal muscle calcium channel (CACNL2A) was mapped to 7q21-q22. In addition, a form of malignant hyperthermia susceptibility (MHS) has been linked to CACNL2A by analysis of a (CA), repeat polymorphism, D7S849, mapping to 7q11.23-q21.1. The occurrence of hypercalcaemia and the reports of masseter spasm and sudden death during surgical procedures in WS patients and the mapping of CACNL2A near the WS critical region on chromosome 7, Mammi et
The authors thank the family for their participation, Dr M Keating (University of Utah) for the elastin-containing cosmid, and Dr Tassabehji (St Mary's Hospital, UK) for the LIMK1 containing cosmid. This research was supported in part by an American Heart Association grant in aid (LGS) and NIH grant RO3 HD 35112 (LGS).
First molecular evidence for a de novo mutation in RS1 (XLRS1) associated with X linked juvenile retinoschisis

EDITOR—Juvenile retinoschisis (RS, OMIM 312700) is an X linked recessive vitreoretinal disorder that variably affects visual acuity because of microcystic degeneration of the central retina.1 2 In approximately 50% of affected males, peripheral scissia may also occur. Major sight threatening complications include vitreal haemorrhages, retinal detachment, and neovascular glaucoma.1

Recently, the gene underlying RS, designated RS1 (also called XLRS1), was positionally cloned1 and more than 80 different mutations covering a wide mutational spectrum, including intragenic deletions, splice site, frameshift, nonsense, and missense mutations, were identified.4 7 Interestingly, missense mutations mainly cluster in exons 4 to 6 of the RS1 gene known to encode a highly conserved discoi- din domain thought to be involved in cell-cell interactions on membrane surfaces.9

The high recurrence rate of some of the RS1 mutations (for example, Glu72Lys in more than 34 patients from different ethnic backgrounds) suggests a significant de novo mutation rate in RS.5 In this report, we provide the first molecular evidence of a de novo RS1 mutation (c.203Leu) in a Greek family. The Pro203Leu mutation is present in two brothers diagnosed with severe features of RS at the ages of 9 and 5 years, respectively. We show that the mother is a heterozygous carrier while neither of the maternal grandparents carry the Pro203Leu mutation. The Pro203Leu mutation was recently detected in two brothers III.1 and III.2 (fig 1 and data not shown).

Table 1  Polyomorph microsatellite markers used in the study

<table>
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<tr>
<th>Name</th>
<th>Locus</th>
<th>Primer sequence 1 (5′–3′)</th>
<th>Primer sequence 2 (5′–3′)</th>
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<td>AATTGACGCCCCTAGGAGGAG</td>
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<td>GAGTGCCCCCTTATTGAAGTGG</td>
<td>This study</td>
</tr>
</tbody>
</table>

†GenBank Acc No U828282


In the younger brother (III.2), bullous cyst-like retinal changes in both eyes had been diagnosed at the age of 1 year. Four years later fundoscopy showed a bullous retinal detachment in the inferotemporal retina of the RE including the macula with some cystic changes in the area of the inferior temporal vascular arcade. In the LE, only pigmentary abnormalities and whitish subretinal deposits consistent with a collapsed schisis could be seen. Best corrected visual acuity was light perception RE and 2/100 LE. Because of severe nystagmus and reduced compliance, the ERG was not recorded.

Fundus examination and ERG were normal in the mother (II.1) and maternal grandfather (I.2).

Genomic DNA from the members of the Greek family was extracted using standard techniques. Haplotyping was done using microsatellite markers 207F/R (DXS207), 389gt, 418F/R (DXS418), and RX324 (DXS443) closely flanking the RS locus (table 1).4 7 Microsatellite marker 389gt was identified in PAC clone dJ389A20 as a (CA)30 dinucleotide repeat derived from PAC clone dJ389A20 (http://www.sanger.ac.uk).

135, a phosphorylation target of BTK.

The repeat sequences were PCR amplified in the presence of 3P-dCTP (3000 Ci/mmol) using flanking oligonucleotide primers and conditions as given in the references (table 1). To confirm paternity, an additional two highly polymorphic microsatellite markers at the ATM locus on 11q23 and the BRCA1 locus on 17q21 (D17S855) were used (table 1).

For mutational analysis, the six exons of the RS1 gene were PCR amplified from genomic DNA of patients III.1 and III.2 with intronic oligonucleotide primers flanking the respective coding exons and amplification conditions as described previously.7 Mutation detection was done by single stranded conformational analysis (SSCA). Amplification of the coding exons was carried out with Taq polymerase (Gibco BRL) in a 25 µl volume in 1 × PCR buffer supplied by the manufacturer. PCR products were electrophoretically separated on a 6% non-denaturing polyacrylamide gel with or without 5% glycerol at 4°C. DNA fragments showing aberrant mobility shifts as well as the corresponding maternal and grandparental PCR products were directly sequenced using the Thermosequenase radiolabelled terminator cycle sequencing kit (Amersham, Life Science).

Prescreening by SSCA of the six coding exons of the RS1 gene showed a similar aberrant band shift in exon 6 in the two brothers III.1 and III.2 (fig 1 and data not shown). Direct sequencing of PCR products identified a C to T transition at nucleotide position 608 of the cDNA. This is predicted to result in a proline to leucine substitution at codon 203 (fig 1). Subsequently, sequencing of RS1 exon 6 was performed in the mother, II.1, as well as in both mater-
BRCA1, ATM/in45 and D17S855 localised within the type in the two Greek brothers. Therefore should be responsible for the RS phenotypic markers closely flanking the RS1 gene on Xp22.2. The order of markers is from telomere to centromere. Haplotypes with Pro203Leu mutation in exon 6 of the RS1 gene are boxed. Note that the grandfather, I.2, shares the disease associated haplotype with his two grandsons III.1 and III.2 but does not carry the Pro203Leu mutation.

Figure 1 Analysis of a three generation Greek family with two cases of X linked juvenile retinoschisis (III.1 and III.2). Polymorphic markers at the ATM and the BRCA1 locus (D17S855) were used to confirm paternity. Haplotype analysis was performed using microsatellite markers DXS207, 389gt, DXS418, and DXS443 that closely flank the RS1 gene on Xp22.2. The order of markers is from telomere to centromere. Haplotypes associated with the Pro203Leu mutation in exon 6 of the RS1 gene are boxed. Note that the grandfather, I.2, shares the disease associated haplotype with his two grandsons III.1 and III.2 but does not carry the Pro203Leu mutation.

Haplotype analysis has shown that the maternal grandfather of the two Greek RS patients carries the haplotype that becomes disease associated in his daughter and his two grandsons. This provides strong evidence that the Pro203Leu mutation is in fact a de novo event. It should be pointed out that the Pro203Leu mutation occurred at a CpG dinucleotide (codon 203: CCG to CTG) which, if methylated at the genomic level, is known to be frequently involved in C→T transitions. We cannot exclude that the unaffected grandfather is a mosaic for the Pro203Leu mutation with the mutant genotype being present in one or more tissues, excluding the ocular tissues but including a precursor of the germ cells. Assuming such a situation in the grandfather, the mutation could be transferred to his daughter and would then be perceived as a de novo germinal mutation.

Besides the Greek family, we were able to analyse the segregation of RS1 mutations in another four pedigrees where RS occurred in a single generation of large families. There was no further evidence of de novo events in the extended families. However, considering the small number of families tested, the present study supports an earlier notion that the new mutation rate in RS may be significant. Further segregation analyses in multigeneration families with “sporadic” or only a few cases of RS will be required to estimate more accurately the frequency of de novo mutations in X linked juvenile retinoschisis.

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ANDREA GEHRIG
BERNHARD H F WEBER
Institut für Humangenetik, Biozentrum, Universität Würzburg, Am Hubland, 97074 Würzburg, Germany

MONIKA ANDRASSI
MONIKA ANDRASSI
Abteilung für Kinderophthalmologie, Strabismologie und Ophthalmogenetik, Klinikum der Universität, 93042 Regensburg, Germany
Correspondence to: Dr Weber
Pathogenicity of homoplasmic mitochondrial DNA mutation and nuclear gene involvement

Editor—Seneca et al reported a homoplasmic deletion of a T nucleotide in a 5T stretch (15 940-15 944 base pairs (bp)) of mitochondrial DNA (mtDNA) in two families associated with clinical and pathological findings of mt cytopathy. Although this deletion was homoplasmic and did not fulfil the classical criteria of pathological mutation, Seneca et al suggested that it was pathological, as they could not identify any other heteroplasmatic mutations, deletions, or duplications in tRNA genes of mtDNA in these patients. However, this mutation was present not only in affected patients but also in asymptomatic relatives in both families. Therefore, this mutation does not cosegregate with the disease. It is difficult to confirm whether homoplasmic mutations are pathological, as was recently indicated by Chinnery et al.1 There are currently no concrete criteria to determine what kind of homoplasmic mtDNA abnormalities are pathological. Maternal inheritance is an important characteristic to confirm their pathogenicity, which, however, was not significant in these two families. The mode of inheritance of this deletion is difficult to confirm, as it is currently unknown whether the single nucleotide deletion is inherited maternally like mtDNA point mutations. It is possible that it is inherited autosomal dominantly like mtDNA deletions. In such cases, cosegregation of the mutation in affected family members is important to determine its pathogenicity. A population based association study is another method for confirming a significant role of homoplasmic or heteroplasmic mtDNA mutations. The association should also be confirmed by other studies on the same and different ethnic groups.

By directly sequencing a mutation hot spot of mtDNA (3130-3423 bp) from 30 patients with type 2 diabetes mellitus (DM), we identified a G3316A homoplasmic mutation.7 The prevalence of this mutation was significantly higher in patients with glucose intolerance than in those with normal glucose tolerance.7 This missense mutation in the ND-1 gene, which substitutes alanine for threonine, was present at an increased frequency in patients with type 2 DM compared with non-diabetic subjects in other studies in Japanese8 or European9 populations. The same mutation was also identified in a patient through screening patients with hypertrophic cardiomyopathy, suggesting a role of this homoplasmic mutation in the development of mt cytopathy (manuscript in preparation). Although homoplasmic mtDNA mutations do not fulfil the classical criteria for pathogenicity, another recent study indicated that homoplasmic mutations are significantly associated with type 2 DM (p=0.0144). These findings suggest that the homoplasmic mutations are also of pathohological importance in mt cytopathy. Investigations on Leber’s hereditary optic neuropathy (LHON) suggest a role of the nuclear gene in the pathogenesis of clinical symptoms of mt cytopathy. Previous investigations, however, failed to identify any nuclear gene abnormalities in patients with mt cytopathy. We consider that homoplasmic mutations are also important in the development of mt cytopathy, as nuclear DNA may be involved in its pathogenesis.

Concerning the A3243G mutation, we suspect that nuclear gene abnormalities may be responsible for the different clinical phenotypes of type 2 DM or MELAS (mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes) associated with the same A3243G mutation.10 Recent investigations indicate that nuclear encoded gene mutations are associated with Leigh syndrome.11,12 These observations highlight the importance of nuclear gene-mtDNA interaction in the pathogenesis of mt dysfunction. They also suggest that homoplasmic mtDNA mutations are important in developing mt cytopathy, such as mt myopathies, diabetes mellitus, or cardiomyopathies. Although difficulties exist in confirming a pathogenic role of homoplasmic mtDNA mutations, some homoplasmic mutations are probably associated with mt dysfunction causing mt cytopathy. We propose that investigations of mtDNA abnormalities in patients with mt dysfunction should include homoplasmic mutations which cosegregate with clinical or pathological manifestations of mt cytopathy or are present with an increased frequency in affected patients.

Institute of Clinical Medicine, University of Tsukuba, 1-1-1, Tennoji, Tsukuba City, 305-8575 Japan

MASATO ODAWARA
HISATKA MAKI
NOBUHIRO YAMADA

Institute of Clinical Medicine, University of Tsukuba, 1-1-1, Tennoji, Tsukuba City, 305-8575 Japan

References

5. Odawara M, Sasaki K, Yamashita K. A G-to-A substitution at nucleotide position 3316 in mitochondrial DNA is associated with Japanese
Identification and clinical presentation of β thalassaemia mutations in the eastern region of Saudi Arabia

EDITOR—The autosomal recessive disease β thalassaemia is a common single gene disorder that poses a serious health problem in many parts of the world. According to the Human Gene Mutation Database (http://www.hgmd.org) and the β-globin Gene Server (http://globin.cse.psu.edu) about 300 sequence variants in the β-globin gene have been identified up to the present. Mutations in the β-globin gene have been found at carrier frequency rates ranging from 1% in some areas of Saudi Arabia to 15% in others. Both β+ and β− thalassaemia have been reported.1 Studies on the molecular pathogenesis of β thalassaemia have shown that the mutations encountered in Arab countries close to the Mediterranean basin are the same as those reported in other Mediterranean populations. In the Gulf region, in Saudi Arabia, UAE, and Iraq, the Asian pattern of mutations seems to be prevalent.1−3 The precise genetic changes prevalent in the different regions of the large country of Saudi Arabia and analysis of the genotype/phenotype relationship of the disease in Saudi patients still remain inadequately studied.

The present study aimed to investigate the mutational pattern of the β globin gene and to explore the relationship between these mutations and disease presentation in a group of patients with β thalassaemia major from the eastern region of Saudi Arabia. For this purpose, 31 children diagnosed with β thalassaemia major who over the past two years had regularly attended the paediatric clinics of Qatif Central Hospital or Dammam Maternity and Children Hospital were selected. Within this group of patients there were four pairs of sibs and one pair of first cousins. The whole β globin gene of all patients was amplified using standard PCR techniques and six specially designed different primers for amplification and sequencing. Nucleotide sequencing was performed by electrophoresis of the PCR products into an automatic capillary ABI Prism Genetic Analyzer type 310 (Perkin-Elmer, USA).

Results of the nucleotide sequencing have enabled accurate identification of disease causing mutations both in the homozygous and heterozygous states in each of the 31 patients diagnosed with β thalassaemia major. In total, eight disease causing mutations were detected: CD39(C→T), IVS-1 3′-end-25bp, −2CD8(−AA), IVS-2+1(G→A), −1CD44(−C), +1CD8/9(+G), IVS-1+5(G→C), and IVS-1+5(G→T) which comprised allele frequencies of 32.1%, 22.6%, 15.1%, 15.1%, 7.5%, 3.8%, 1.9%, and 1.9%, respectively. An overall β thalassaemia detection rate of 100% was achieved (tables 1 and 2), thus reflecting the efficiency of the technique. The accuracy of the genetic analysis has a special diagnostic importance in view of the fact that certain haemoglobinopathies, for example, sickle cell anaemia, spherocytosis, and autoimmune haemolytic disease, are known to produce symptoms that mimic those of β thalassaemia major.4−6 The silent polymorphic mutation CD2(CAC→CAT) was very frequent among this group of children as it was encountered in 16 out of 31 patients with β thalassaemia major. On the other hand, the polymorphisms IVS-2+26 (T→G) and IVS-2+74(G→T) were less common and detected in only two patients each (Nos 29 and 37 and 17 and 45, respectively). A fourth polymorphism IVS-2+666(T→C) was also detected in two patients (Nos 17 and 45). These sequence variants are not shown in table 2.

The spectrum of mutations identified here confirms the notion that, for historical reasons, there is an overlap between Mediterranean and Asian mutations in Saudi Arabia.1 Five of the eight mutations detected here have been reported to exist among patients from other parts of the country, albeit with different allele frequencies.1 We report here the novel identification in the Saudi population of three mutations: the Turkish frameshift mutation −2CD8(−AA),4 the Kurdish frameshift mutation −1CD44(−C), and the silent polymorphic mutation CD2(CAC→CAT) which was frequent among this group of children and was encountered in 16 out of 31 patients with β thalassaemia major. On the other hand, the polymorphisms IVS-2+26 (T→G) and IVS-2+74(G→T) were less common and detected in only two patients each (Nos 29 and 37 and 17 and 45, respectively). A fourth polymorphism IVS-2+666(T→C) was also detected in two patients (Nos 17 and 45). These sequence variants are not shown in table 2.

Table 1 β globin gene mutations in patients with β thalassaemia major from the eastern region of Saudi Arabia

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Type of mutation</th>
<th>Nucleotide change</th>
<th>Type of thalassaemia</th>
<th>Independent alleles</th>
<th>Origin of mutation</th>
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<td>CD39(C→T)</td>
<td>Nonsense</td>
<td>Substitution C→T</td>
<td>β+ thalassaemia</td>
<td>17</td>
<td>32.1%</td>
<td>Mediterranean, European</td>
</tr>
<tr>
<td>IVS-1 3′-end-25bp</td>
<td>5′-end</td>
<td>Deletion of 25 bp</td>
<td>β− thalassaemia</td>
<td>12</td>
<td>22.6%</td>
<td>Asian, Indian</td>
</tr>
<tr>
<td>−2CD8(−AA)</td>
<td>Frameshift</td>
<td>Deletion of 2A</td>
<td>β− thalassaemia</td>
<td>8</td>
<td>15.1%</td>
<td>Turkish</td>
</tr>
<tr>
<td>IVS-2+1(G→A)</td>
<td>Frameshift</td>
<td>Deletion of G</td>
<td>β− thalassaemia</td>
<td>8</td>
<td>15.1%</td>
<td>Mediterranean, Tunisian, African-American</td>
</tr>
<tr>
<td>−1CD44(−C)</td>
<td>Frameshift</td>
<td>Deletion of C</td>
<td>β− thalassaemia</td>
<td>4</td>
<td>7.5%</td>
<td>Kurdish</td>
</tr>
<tr>
<td>+1CD8/9(+G)</td>
<td>Frameshift</td>
<td>Insertion of G</td>
<td>β− thalassaemia</td>
<td>2</td>
<td>3.8%</td>
<td>Asian, Indian</td>
</tr>
<tr>
<td>IVS-1+5(G→C)</td>
<td>Consensus change</td>
<td>Substitution G→C</td>
<td>β− thalassaemia</td>
<td>1</td>
<td>1.9%</td>
<td>Indian, Chinese, Melanesian</td>
</tr>
<tr>
<td>IVS-1+5(G→T)</td>
<td>Consensus change</td>
<td>Substitution G→T</td>
<td>β− thalassaemia</td>
<td>1</td>
<td>1.9%</td>
<td>Mediterranean, Blacks</td>
</tr>
</tbody>
</table>

Calculation of allele frequency:
There are 31 patients with β thalassaemia major.
No of alleles = 31×2 = 62 alleles.
There are 4 pairs of sibs; hence 62−8 = 54 alleles.
Subtract 1 allele for first cousin = 53 independent alleles.
Detection rate = 53/53×100% = 100%.
Table 2  The genotype, mean clinical indices, and disease presentation of Saudi children diagnosed with \( \beta \) thalassaemia major

<table>
<thead>
<tr>
<th>Patient No</th>
<th>Genotype</th>
<th>Mean ( Hb ) ( A_2 ) (%)</th>
<th>Mean age at diagnosis (y)</th>
<th>Mean annual No of blood transfusions</th>
<th>Disease presentation</th>
</tr>
</thead>
<tbody>
<tr>
<td>1, 2, 3, 4, 5, 6, 15 &amp; 30</td>
<td>CD39 (C→T) / CD39 (G→T)</td>
<td>3.3</td>
<td>0.8</td>
<td>12.8</td>
<td>All 8 severe</td>
</tr>
<tr>
<td>17</td>
<td>CD39 (C→T) / IVS-1 +5 (G→C)</td>
<td>2.5</td>
<td>0.3</td>
<td>12.0</td>
<td>Severe</td>
</tr>
<tr>
<td>26</td>
<td>CD39 (C→T) / IVS-1 +5 (G→T)</td>
<td>2.7</td>
<td>2.0</td>
<td>10.0</td>
<td>Severe</td>
</tr>
<tr>
<td>19 &amp; 45</td>
<td>CD39 (C→T) / IVS-2 +1 (G→A)</td>
<td>2.0</td>
<td>4.0</td>
<td>9.0</td>
<td>1 severe, 1 moderate</td>
</tr>
<tr>
<td>18</td>
<td>CD39 (C→T) / +1 CD8/9 (+G)</td>
<td>4.0</td>
<td>5.0</td>
<td>12.0</td>
<td>Severe</td>
</tr>
<tr>
<td>31</td>
<td>CD39 (C→T) / IVS-1 3'end-25bp</td>
<td>3.8</td>
<td>1.3</td>
<td>12.0</td>
<td>Severe</td>
</tr>
<tr>
<td>8, 20, 21, 22, 23 &amp; 31</td>
<td>IVS-1 3'end-25bp / IVS-1 3'end-25bp</td>
<td>3.6</td>
<td>2.7</td>
<td>8.7</td>
<td>4 severe, 2 mild</td>
</tr>
<tr>
<td>44</td>
<td>IVS-1 3'end-25bp / +1 CD8/9 (+G)</td>
<td>1.0</td>
<td>3.0</td>
<td>12.0</td>
<td>Severe</td>
</tr>
<tr>
<td>7, 10, 35 &amp; 36</td>
<td>-2CD8 (AA) / -2CD8 (AA)</td>
<td>2.3</td>
<td>3.3</td>
<td>10.0</td>
<td>3 severe, 1 moderate</td>
</tr>
<tr>
<td>20, 34 &amp; 37</td>
<td>IVS-2 +1 (G→A) / IVS-2 +1 (G→A)</td>
<td>2.0</td>
<td>4.3</td>
<td>7.3</td>
<td>2 moderate, 1 severe</td>
</tr>
<tr>
<td>13, 14 &amp; 33</td>
<td>-1CD44 (C→) / -1CD44 (C→)</td>
<td>4.5</td>
<td>4.0</td>
<td>12.0</td>
<td>All 3 severe</td>
</tr>
</tbody>
</table>

Patients 1+2, 3+4, 13+14, 21+22 are sibs. Patient 5 is a first degree cousin of patients 3 and 4.

-1CD44 (C→) and the Mediterranean/Black consensus mutation IVS-1+5 (G→T). It is highly unlikely that these mutations arose independently in the Saudi population. On the contrary, there is historical evidence that the Arabian, Turkish, and Kurdish populations have interacted in the past through trade and the introduction of Islam in Turkey. The introduction of the Mediterranean/Black mutation in Saudi Arabia can be explained by a similar historical reason, that is, gene flow facilitated by trade and expansion of Islam in the Mediterranean region and in Africa. Similarly, evidence of a common ethnic origin of the cystic fibrosis mutation 3120+1G→A in Arab, African, Greek, and African-American populations has recently been reported. However, we have detected the rare Asian Indian mutation +1CD8/9 (+G) in the compound heterozygous state in two patients. It is likely that the Indian mutation may have been introduced to this region by gene flow since the mutation has recently been identified in patients from the geographically close island of Bahrain, which is a known historical centre for international trade between Arabia, India, and Asia. Similarly, we have found that the splice junction frameshift mutation IVS-1 3'end-25bp, first reported in Asia and India, was the second most prominent mutation with an allele frequency of 22.6% in this group of patients. This mutation has recently been reported as the most common mutation in Bahrain with the highest allele frequency of 40%. Therefore, all these findings provide evidence that the eastern coast of Saudi Arabia, unlike the inner desert parts of the Arabian Peninsula, was particularly prone to gene flow from Turkey, Iran, and the Indian subcontinent. This mutation has also been observed in patients with the same genotype may well find its basis in the number of active \( \alpha \) globin genes. Genetic analysis of the \( \alpha \) globin gene has not been performed in this study. In two patients who are carriers of the mutations IVS-1+5 (G→C) and IVS-1+5 (G→T), known to cause \( \beta \) thalassaemia, the mutations apparently did not confer protection against the adverse phenotypic expression of the disease. A possible explanation is that the two mutations are encountered here in the compound heterozygous state with CD39 (C→T), which is known to cause a severe form of the disease.

In summary, we report the first identification of three mutations, the Turkish frameshift mutation -2CD8 (AA), the Kurdish frameshift mutation -1CD44 (C→), and the Mediterranean/Black mutation IVS-1+5 (G→T) in patients with \( \beta \) thalassaemia major from the eastern region of Saudi Arabia. Documentation of the spectrum of \( \beta \) thalassaemia mutations could facilitate national screening and educational programmes which would be important with respect to the problem of the haemoglobinopathies in this region.

We are grateful to Dr Samia Flimban of the Maternity and Children Hospital in Dammam for supporting this study. Our thanks are extended to Miss Michaella Finsel for her assistance in the preparation of the manuscript. We gratefully acknowledge the financial sponsorship of this work by the Alexander von Humboldt-Stiftung, Bonn (Bad Godesberg), Germany.

EL-HARITH A EL-HARITH
WOLFGANG KÜHNAU
JÖRG SCHMIDTKE
MANFRED STUHRMANN
Institute of Human Genetics, Medical School of Hannover, Carl-Neuberg Strasse 1, D-30623 Hannover, Germany.

ZAKI NASSERALLAH
Paediatric Department, Qatif Central Hospital, Qatif, Saudi Arabia

ABDALLAH AL-SHAHRI
Paediatric Department, Maternity and Children Hospital, Dammam, Saudi Arabia

Rapid screening for the most common β thalassaemia mutations in south east Asia by PCR based restriction fragment length polymorphism analysis (PCR-RFLP)

EDITOR—The heterogeneity of the molecular lesions which underlie the failure of erythropoietic cells to synthesise normal haemoglobin in β thalassaemia¹ is a complicating factor in its molecular diagnosis. However, although more than 100 different mutations have been identified, mostly single base substitutions or small deletions and insertions in the β globin gene, in many populations the bulk of β thalassaemia is caused by a population specific spectrum of only a small number of mutations.¹ The strategy for the detection of mutations in patients, therefore, normally involves screening in the first instance for a small number of mutations that are the most common for the population concerned.²

Two of the most commonly used screening procedures are dot blot or reverse dot blot hybridisation³ and the amplification refractory mutation system (ARMS).³ While these procedures are satisfactory in the hands of the more experienced specialised laboratories, the exacting conditions demanded by the above procedures, a situation which is perhaps shared by many other countries in which β thalassaemia is common. We have endeavoured, therefore, to develop a more robust and accurate alternative method for the detection of β thalassaemia mutations in south east Asia, based on restriction endonucleases that recognise naturally occurring or PCR generated restriction sites associated with the β thalassaemia mutations. The approach is widely used in the detection of pathological mutations in mitochondrial DNA⁴ and has also been applied in the molecular diagnosis of β thalassaemia.⁵

A strategy has been devised to allow rapid detection of nine of the most common mutations in south east Asia which requires the amplification of two segments only of the β globin gene. The mutations are at positions IVS-1 nt5, IVS-1 nt1, codon 26, codon 15, codon 17, codon 19, codon 30, IVS-1 nt2, and codon 41-42 of the β globin gene (fig 1 (top), table 1), which together account for around 70-90% of β thalassaemia mutations in most populations of south east Asia.⁶ The PCR amplifications use primer sets TLF62028-TLR62320 and TLF62392-TLR62703. Primer TLR62320 includes a G at the position equivalent to nt8 of intron 1 instead of the normal A to create a GCTAGC site for Cac8I in the presence of the IVS-1 nt5 G>C mutation. A Cac8I site is also created in the presence of the IVS-1 nt2 T>C mutation which represents less than 1% of the β thalassaemia alleles in Indonesia. The mutations G to T at IVS-1 nt1, G to A at codon 26, and A to G at codon 19 abolish the natural occurring sites for Bsd1, MnlI, and MaeIII, respectively. The mutations G to A at codon 15, A to T at codon 17, and G to C at codon 30 create sites for SfiI, BfaI, and Bsp1286I, respectively. The detection of the 4 bp deletion of codon 41-42 is essentially testing, but do not have the skill to comply with the strict conditions demanded by the above procedures, a situation which is perhaps shared by many other countries in which β thalassaemia is common. We have endeavoured, therefore, to develop a more robust and accurate alternative method for the detection of β thalassaemia mutations in south east Asia, based on restriction endonucleases that recognise naturally occurring or PCR generated restriction sites associated with the β thalassaemia mutations. The approach is widely used in the detection of pathological mutations in mitochondrial DNA⁴ and has also been applied in the molecular diagnosis of β thalassaemia.⁵

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Table 1 PCR primers and restriction endonucleases used in the detection procedure

| Region | Primer sets* | Mutation | Restriction endonuclease
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
| I      | TLF62028-TLR62320 | IVS-1 nt5 | Cac8I
|        |               | IVS-1 nt1 | BfdI
|        |               | Codon 26 | MnlI
|        |               | Codon 15 | SfiI
|        |               | Codon 17 | BfaI
|        |               | Codon 19 | MaeII
|        |               | Codon 30 | Bsp1286I
| II     | TLF62392-TLR62703 | IVS-1 nt2 | Cac8I
|        |               | Codon 41 | TaqI

*The primers used were: TLF62028-5′ACCTCACCCTGCGGACCCAC3′ (common C in Old et al); TLR62320-5′CTATTTGGTGTCTCCTTAAACCTCTTCTTGTACCTTGGCTA3′; TLF62392-5′ATTTTTCCACCCCTAGGGGCCTGCGGTGTCCTACCCCTTGGACGAGGCTC3′; TLR62703-5′CCCCTTCCCTATGACGAGCTTA3′; modifications in nucleotide sequence are indicated by bold letters.

†Bold numbers indicate fragments of distinguishable sizes.
be easily detected (fig 1A). Similarly, the 122 bp fragment allele (a 257 bp digested fragment). Heterozygosity could be distinguished readily from the mutant allele (indicated by a 293 bp undigested product) can be distinguished from the mutant allele (data not shown). In all the above cases, the PCR-RFLP results agreed with those of ARMS and were confirmed by DNA sequencing.

The detection procedure described here does not involve an allele specific hybridisation or an allele specific PCR amplification step and is thus less prone to non-specific reactions which could lead to false positive/negative results. We have applied our new procedure to the detection of the underlying mutations in a number of difficult samples in which ARMS gave ambiguous results. In all cases the PCR-RFLP method proved to be more reliable and gave definitive identification of the underlying mutation, as confirmed by DNA sequencing data (data not shown). The nine mutations included here account for 70% of β thalassaemia alleles in Thailand, 90% in Malaysia, 53% in India, and 68-90% in Indonesia depending on the ethnic population. The procedure, therefore, is suitable as the front line screening for the molecular diagnosis of β thalassaemia in south east and perhaps also in eastern and southern Asia.

This work was supported by the RUT grant No IIIo/13/I/-/IPD from the National Research Council (Indonesia) to Iswari Setianingsih, and grant in aids from PT Krakatau Steel and PT Inti through the Agency for Strategic Industries (Indonesia).
Clinical and molecular findings in a patient with a deletion on the long arm of chromosome 12

Editor—Reports of congenital abnormalities resulting from deletions on the long arm of chromosome 12 are rare. A number of genes have been mapped to 12q, which include a gene for Noonan syndrome (NS) in some families and the gene for insulin-like growth factor I (IGF-I). The patient presented here was referred for assessment regarding the diagnosis of NS in view of her short stature, dysmorphic facies, and developmental delay and was found to have a de novo interstitial deletion on chromosome 12q. Despite some of the similar clinical findings to NS in this patient, molecular analysis showed that the deletion mapped approximately 17 cM centromeric to the critical region for NS. To our knowledge, there have been no similar cases of interstitial deletion reported on chromosome 12q.

The patient, a 15 year old girl was the first born child to a 23 year old mother and an unrelated 21 year old father. Her younger brother, aged 11 years, was fit and well. The family history was unremarkable. The pregnancy was normal. She was born at term as an emergency caesarean section for fetal distress. Her birth weight was 2860 g. She was admitted to the special care baby unit for 24 hours for observation. The neonatal period was complicated by pyloric stenosis for which surgery was carried out on day 16. During the postoperative period, she developed severe candidiasis and lactose intolerance. At the age of 1 year she was challenged with milk and seemed to have recovered from the intolerance. Developmentally she was able to sit unsupervised at the age of 8 months and walked independently at the age of 2 years. Her speech was delayed and she was unable to say two words together until the age of 3 years. She has had no visual or hearing problems. Her height has always been below the 3rd centile. At the age of 11 years, just as she was entering puberty, she was diagnosed as having growth hormone deficiency. Her peak growth hormone level on glucagon stimulation test was 7 mU/l. She was started on treatment with growth hormone and she showed a good response with sustained growth over a three year period. She had no known cardiac abnormalities. She suffered from recurrent nose bleeds but there was no other history of bleeding problems. Physical examination at the age of 15 years indicated that her height and weight were just below the 3rd centile and her head circumference was on the 3rd centile. She had pectus excavatum, but her nipples were not widely spaced. She had bilateral ptosis, hypertelorism, and low set and posteriorly rotated ears (fig 1). Her hair was thin, fine, and sparse. Her posterior hairline was trident and low. Her neck was short with mild webbing. Cardiovascular examination showed a grade II ejection systolic murmur at the second left intercostal space. Echocardiogram showed normal dimensions and arrangements of the cardiac chambers and heart valves. The velocity of blood flow in the proximal pulmonary artery was slightly increased and this was thought to be the origin of the systolic murmur. Neurological examination was normal, but she had relatively poor coordination. Coagulation studies, including intrinsic clotting factor assays, were normal. Growth hormone secretion was normal with a peak response of 40.7 mU/l during the insulin tolerance test. Basal levels of IGF-I were normal (IGF-I 371 ng/ml, normal range 70–420 ng/ml).

Chromosome analysis by GTG banding was carried out on peripheral lymphocyte cultures. This showed an interstitial deletion of chromosome 12 (fig 2), karyotype 46,XX,del(12)(q21.2q23.2). Parental chromosomes were normal. FISH studies were not performed.

Venous blood was sampled from the patient, her normal brother, and her unaffected parents and genomic DNA was isolated. Seventeen microsatellite markers (D12S291, D12S96, D12S90, D12S335, D12S313, D12S80, D12S92, D12S337, D12S88, D12S81, D12S82, D12S101, D12S218, D12S346, IGF-I, D12S78, D12S84) of chromosome 12q were analysed. PCR amplification of 50 ng genomic DNA was performed in a 15 µl reaction mixture containing 30 ng of each primer, 200 µmol/l dNTPs, 50 mmol/l KCl, 1.5 mmol/l MgCl2, 10 mmol/l Tris-HCl, 0.01% gelatin, 0.1% Triton X-100, and 0.1 U...
SuperTaq DNA polymerase (HT Biotechnology Ltd). In all reactions, 30 cycles (one minute at 94°C, two minutes at 55°C, and two minutes at 72°C with a final seven minute elongation step) were carried out in an automated thermal cycler (Hybaid). The amplified products were separated by electrophoresis on 10% polyacrylamide gels. The gels were silver stained and dried. Haploinsufficiency of markers D12S313, D12S80, D12S88, and D12S101 was found. Haplotype analysis indicated that the deletion was paternal in origin and mapped between markers D12S313 and D12S218. The deletion represented a minimum region of about 18 cM positioned approximately 17 cM proximal to D12S28. The deletion was mapped to chromosome 12q22-24.1,6 has been found in isolated deficiency of IGF-I, the gene for which has been mapped to chromosome 12q22-24.1, had been seen by the clinical geneticists in Edinburgh. He was found to have marked developmental delay, short stature, hydrocephalus, prominent eyes, and long, thin fingers. He did not have any facial features of NS and no congenital heart defect (Dr David Fitzpatrick, Department of Clinical Genetics, Western General Hospital, Edinburgh, personal communication). Isolated deficiency of IGF-I, the gene for which has been mapped to chromosome 12q22-24.1, has been found in pygmys of the Central African Republic.8 In view of our patient’s short stature, dysmorphic facies, and increased pulmonary valve blood flow, it was suspected that the deletion might involve either the IGF-I gene or the critical region for NS on chromosome 12q. Analysis using microsatellite markers showed that the deletion was proximal to the critical region for NS and also proximal to the IGF-I gene (fig 3), making either scenario unlikely. Some of the genes which lie in the area deleted are shown in fig 3. The patient reported by Tonoki et al8 had features similar to those found in NS and the authors suggested that the deleted region in their patient may contain a gene for NS. Similarly, the deleted segment in our patient may also contain a gene for NS. Since the deletions in these patients do not overlap, it would mean that three genes responsible for NS would have to be situated on chromosome 12q, a considerable distance apart. This seems an unlikely event. Although the deletion in our patient lies outside the critical
Martín O Savage

PEDIATRIC ENDOCRINOLOGY SECTION, ST BARTHOLOMEW’S HOSPITAL, LONDON, EC1A 7BE, UK

Correspondence to: Dr Brady, Kennedy-Galton Centre, Northwick Park and St Mark’s NHS Trust, Watford Road, Harrow, Middlesex HA1 3UJ, UK

Amelogenesis imperfecta, sensorineural hearing loss, and Beau’s lines: a second case report of Heimler’s syndrome

Editor—Hearing loss owing to genetic causes has a reported prevalence of 1 in 1000 births and among these 15–30% are associated with other abnormalities, although only a small number are associated with oral and dental disorders.1 Heimler et al2 reported two sibs with a combination of sensorineural hearing loss, amelogenesis imperfecta, and nail abnormalities (McKusick No 234580). We describe a further case here and extend the phenotypic spectrum of this syndrome.

A 12-year-old girl presented with a combination of unilateral sensorineural deafness and amelogenesis imperfecta. She was born at term following a normal pregnancy and had a birth weight of 3200 g (50th centile). There was no consanguinity within the family; her mother was aged 25 and her father was aged 29 at the time of conception. She had no major illnesses in the first years of life and all her developmental milestones were achieved within normal limits. At the age of 7, it was discovered that she had unilateral hearing loss and subsequent investigation showed that she had profound sensorineural deafness on the left, hearing on the right being normal. At the time her mother felt that she may have had reduced hearing in the left ear, her hearing on the right being normal. At the time her mother felt that she may have had reduced hearing in the left ear, her hearing on the right being normal. At the time her mother felt that she may have had reduced hearing in the left ear, her hearing on the right being normal. At the time her mother felt that she may have had reduced hearing in the left ear, her hearing on the right being normal. At the time her mother felt that she may have had reduced hearing in the left ear, her hearing on the right being normal. At the time her mother felt that she may have had reduced hearing in the left ear, her hearing on the right being normal. At the time her mother felt that she may have had reduced hearing in the left ear, her hearing on the right being normal. At the time her mother felt that she may have had reduced hearing in the left ear, her hearing on the right being normal.
stream education. Her family history was unremarkable; her parents were unrelated and there was no history of sensorineural deafness or enamel defects on either side of the family. She has one younger brother who is unaffected.

On examination she was on the 10th centile for height and the 25th centile for weight. She had a fair complexion (fig 1) and examination of her nails showed multiple transverse grooves (Beau's lines) on several fingers and toes (fig 2A, B). There was no evidence of leuconychia. Examination of her teeth showed dental overcrowding and extensive enamel discoloration (fig 3). Ground sections of permanent premolars, extracted for orthodontic purposes, showed dentine and enamel of normal thickness. It seems likely therefore that the amelogenesis imperfecta is a hypomineralised rather than a hypoplastic variant.

The combination of sensorineural hearing loss, amelogenesis imperfecta, and nail abnormalities was first reported by Heimler et al. They suggested that the syndrome could be the result of a single gene affecting derivatives of the ectodermal tissue because the abnormalities described have a common embryological origin in the ectoderm. This theory is made more probable by the reporting of a second case here.

Heimler et al described two sibs who both had profound bilateral sensorineural hearing loss, amelogenesis imperfecta of the permanent dentition, and Beau's lines. Inheritance of this syndrome was postulated to be autosomal recessive and our case does not allow us to draw any further conclusions on this. To date, no other cases of Heimler's syndrome have been identified (A Heimler, personal communication). The case described here had unilateral sensorineural hearing loss, a hypomineralised form of amelogenesis imperfecta, and Beau’s lines and it is likely that this is a similar association to the originally described syndrome, which extends the phenotypic spectrum (table 1).

It is interesting that the hearing loss was diagnosed at a relatively late age and the mother’s observations suggest that it had previously been normal. In the original report, deafness was diagnosed in the second sib at the age of 2½ years, hearing having been normal for the first two years. It thus seems that the hearing loss in this condition is not congenital.

Amelogenesis imperfecta is classified according to the predominant clinical and radiographic appearance of the enamel defect and on the mode of inheritance of the trait. The amelogenesis imperfecta described here is unusual in that only the permanent teeth are affected, which makes non-genetic causes less likely. The diagnosis of hypoplastic amelogenesis imperfecta in the original case report was

<table>
<thead>
<tr>
<th>Table 1</th>
<th>A comparison of phenotypes between the originally described cases and a new case of Heimler's syndrome</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Original case (sib 1)</td>
</tr>
<tr>
<td>Sensorineural hearing loss</td>
<td>Bilateral, diagnosed at 18 months</td>
</tr>
<tr>
<td>Primary dentition</td>
<td>Normal</td>
</tr>
<tr>
<td>Permanent dentition</td>
<td>Enamel hypoplasia</td>
</tr>
<tr>
<td>Nail abnormalities</td>
<td>Punctate leuconychia, Beau's lines</td>
</tr>
</tbody>
</table>

Figure 1 The 12 year old girl with amelogenesis imperfecta, unilateral hearing loss, and nail abnormalities.

Figure 2 (A, B) Transverse grooves (Beau’s lines) on finger nails in index case.

Figure 3 Permanent dentition in index case illustrating extensive enamel discoloration of incisors, canines, and premolars.
made on radiographic evidence and a histopathological examination was not performed. The hypomeralised amelogenesis imperfecta in our case illustrates the variation in phenotype that can occur in this condition.

Beau’s lines are transverse lines across the nails that can arise from severe illnesses, such as sepsis, AIDS, or bullous pemphigoid, and can also be physiological in menstruating women. They can be quite subtle as in this case where they only became apparent once nail varnish had been removed. Our patient had no evidence of punctate leuconychia which was described in the original family, which could suggest that this feature may have been an incidental finding in the original report, as it is a common normal variant. Our case also emphasises the importance of careful examination of the nails in patients with a combination of impaired hearing, which may only be unilateral, and dental pathology.

Marc Tischkowitz
Catherine Cleenaghan
Sally Davies

**PTEN and LKB1 genes in laryngeal tumours**

**Editor—PTEN**, a tumour suppressor gene located in chromosome 10q23, is homologous to tyrosine and dual specificity phosphatases with a high degree of substrate specificity. This enzymatic activity is necessary for **PTEN/MMAC1** tumour suppressor function.1–4 Mutations of this gene have been identified in many glioma, glioblastoma, prostate, kidney, and breast carcinoma cell lines and in primary tumours including gliomas, and breast, thyroid, and kidney carcinomas.1–5 Germline mutations of the **PTEN** gene underlie Cowden disease, an autosomal dominant disorder associated with an increased risk of breast and thyroid cancer and possibly endometrial malignancy. Benign tumours of the intestine (hamartomas) and skin (such as trichilemmomas) also occur.1–5

**LKB1**, a candidate tumour suppressor gene, encodes a serine/threonine kinase which is highly homologous (84%) to Xenopus serine/threonine kinase XEEK1.6 Germline mutations in **LKB1** have been associated with Peutz-Jeghers syndrome (PJS).7–9 Jenne et al10 report that their success in identifying the gene by analysing only two candidate sequences was based on strong linkage disequilibrium. This is surprising, as while linkage disequilibrium is a powerful tool in disease gene identification, no linkage disequilibrium has been reported in PJS and the patients typically display different mutations.10 PJS is characterised by hamartomatous intestinal polyposis, mucocutaneous pigmentation, and increased risk of cancer of multiple organ systems.11 LKB1 germline mutations are typically of inactivating nature, often causing truncation of the protein product.11,12 Genes involved in hereditary cancer syndromes are often targets of somatic mutations. In the case of the **LKB1** gene, several studies, with the exception of one study on colorectal cancer,13 have reported a low frequency of **LKB1** somatic mutations in colorectal, testicular, breast, and gastric cancers.11–14

The aetiology of laryngeal cancer is considered to be multifactorial and genetic alterations are likely to play a role in it. The **PTEN** and **LKB1** genes have been recently characterised and appear to cause somewhat similar phenotypes when mutated in the germline. Because of their tumour suppressor function, both **PTEN** and **LKB1** are possible candidates as genes which could be involved in laryngeal tumorigenesis. To test this hypothesis, we evaluated the role of **PTEN** and **LKB1** somatic mutations in malignant and premalignant laryngeal tumours.

This study was based on laryngeal tumour specimens collected from 16 patients treated at Helsinki University Central Hospital, Department of Otorhinolaryngology and Head and Neck Surgery. Thirteen of these patients had laryngeal carcinoma and three had laryngeal papilloma. Of the patients with papilloma, one had juvenile onset and two had adult onset disease. One of these adult onset patients had a malignant transformation of his laryngeal tumour into epidermoid carcinoma (table 1). The tumour samples were resected during operations and fresh frozen. A 5 µm section of each tumour was stained with haematoxylin to ensure that the sample contained at least 60% of tumour tissue. DNA was extracted from the laryngeal tumour samples with phenol-chloroform according to the standard procedure.

The nine exons of the **PTEN** gene were sequenced by means of nested primers designed within the flanking intronic sequence. PCR conditions and primers have been described previously.13 After PCR, 5 µl of each amplicon was run on a 2% agarose gel to verify the specificity of the PCR reaction. The rest was purified with QIAquick PCR purification kit (QIAGEN GmbH, Hilden, Germany).

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<th>Table 1 Clinical data of the patients</th>
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*All laryngeal carcinomas were histologically squamous cell carcinomas.
†Neck metastasis.
‡With malignant transformation.
Direct sequencing of PCR products was performed with the ABI PRISM Dye Terminator or ABI PRISM dRhodamine cycle sequencing kits (Perkin-Elmer Applied Biosystems Division, Forster City, CA). Cycle sequencing products were analysed on an Applied Biosystems model 377 DNA sequencer (PE/ABI) or 310 Genetic Analyzer (PE/ABI).

Mutation analysis of the \textit{LKB1} gene was performed by single strand conformation polymorphism (SSCP) analysis. Primer sequences and PCR conditions used in this study have been described previously.\textsuperscript{19} After PCR, 5 µl of each reaction product was mixed with 5 µl of denaturing loading buffer (98% formamide, 20 mmol/l EDTA, 0.05% bromphenol blue, and 0.05% xylene cyanol), denatured for five minutes at 94°C, and subjected to electrophoresis on 0.4 mm \times 30 cm \times 45 cm gels containing \(0.6 \times\) mutation detection enhancement solution (AT Biochem, Malvern, PA) and 0.6 \times TBE buffer. Electrophoresis was conducted at 4 W overnight. PCR fragments were visualised in gels by silver staining. In order to validate the SSCP results, amplicon of exon 1 in the \textit{LKB1} gene from all samples were directly sequenced (as described above).

To determine whether the \textit{PTEN} and \textit{LKB1} genes are mutated in laryngeal tumours, we screened 16 laryngeal tumour samples by genomic sequencing and SSCP assay, respectively. We performed direct sequencing of amplicon for \textit{PTEN} mutation analysis; no mutations in the coding sequences and exon/intron boundaries were found. The search for \textit{LKB1} mutations, SSCP assay was applied in conjunction with PCR. Difference in mobility pattern on the SSCP assay usually suggests a variant, the nature of which should be examined by sequencing. In our hands SSCP analysis of \textit{LKB1} has always shown known mutations and it is reasonable to assume a 70% to 80% sensitivity, which is commonly reported for the method.\textsuperscript{19}

To validate the SSCP results, exon 1 was directly sequenced from each sample. No mutations in exon 1 and the respective exon/intron boundaries were observed. The mutation detection methods used in this study would not have detected some mutation types, such as large genomic deletions or alterations in the promoter region. Yet the complete absence of changes indicates that somatic mutations of \textit{PTEN} and \textit{LKB1} are not frequent in laryngeal tumours.

The molecular events which induce laryngeal tumorigenesis, especially laryngeal carcinogenesis, are not well characterised. Proto-oncogenes seem to be the target of the risk factors (cigarette smoking, alcohol abuse, ionising radiation, and human papillomavirus infection) that are commonly considered to be associated with laryngeal squamous cell carcinoma. Several tumour suppressor genes have been shown to play important roles in human tumours, including head and neck cancers. Mutations of the p53 gene are frequent events in primary squamous cell carcinomas of the head and neck as well as in SCCHN cell lines. While many cancer genes are associated with laryngeal tumorigenesis,\textsuperscript{20} our study suggests that \textit{PTEN} and \textit{LKB1} are not among them.