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Abnormalities of chromosome 16 have been found in many different entities, ranging from isolated cases to genetic syndromes involving multiple organs. In the past, these abnormalities have been classified according to the band involved in the rearrangement. From these data it appears that there is no simple relationship between the clinical findings and the breakpoints of the translocations reported. We report on a familial submicroscopic translocation involving chromosomes 8 and 16. The proband of the family had a clinical picture suggestive of a large deletion in the chromosome 16p13.3 area, as he was affected with tuberous sclerosis complex (TSC) and had α thalassaemia trait, and his half brother, who also had TSC, may have suffered additionally from polycystic kidney disease (PKD). FISH studies provided evidence for a familial translocation t(8;16)(q24.3;p13.3) with an unbalanced form in the proband and a balanced form in the father and in a paternal aunt. The unbalanced translocation caused the index patient to be deleted for the chromosome 16p13.3-pter region, with the most proximal breakpoint described to date for terminal 16p deletions. In addition, FISH analysis showed a duplication for the distal 8q region. Since the index patient also had hypomelanosis of Ito (HI), either of the chromosomal areas involved in the translocation may be a candidate region for an HI determining gene. Furthermore, it is noteworthy that both carriers of the balanced translocation showed a nodular goitre, while the proband has hypothyroidism.

Keywords: PKD1; TSC2; HI; partial trisomy/monosomy

We report on a patient affected with tuberous sclerosis complex (TSC), α thalassaemia trait, and hypomelanosis of Ito (HI), whose half brother, also affected with TSC, had died from renal complications.

Tuberous sclerosis complex (TSC) is an autosomal dominant disease characterised by skin lesions, mental handicap, seizures, and the development of hamartomas in many different organs and tissues. TSC determining loci have been mapped to chromosome 9q34 (TSC1) and 16p13.3 (TSC2). Both have been identified and characterised. The major gene for autosomal dominant polycystic kidney disease (PKD1) has also been identified and maps to chromosome 16p13.3, proximally adjacent to the TSC2 locus. A number of patients with large deletions disrupting both the TSC2 and the PKD1 genes who have TSC and childhood onset polycystic kidney disease have been reported. The α gene cluster has also been mapped to chromosome band 16p13.3 distal to the TSC2 locus. Deletions, variable in extent but limited to the terminal part of band 16p13.3, were reported in patients with α thalassaemia/mental retardation syndrome (ATR-16). Apart from the haematological abnormality presenting as either Hb H disease or α thalassaemia trait, the other clinical findings of this condition are mild to moderate mental handicap and a broad spectrum of associated dysmorphic features. Therefore, TSC2, PKD1, and ATR-16 could be involved in a contiguous gene syndrome with characteristic phenotypic abnormalities. This was suspected in the patient reported here.

Hypomelanosis of Ito (HI) is a neurocutaneous disorder characterised by hypopigmented whorls, streaks, and patches typically distributed along the lines of Blaschko; one or more abnormalities of the central nervous system, eyes, hair, teeth, and musculoskeletal system have also been described in about 70% of HI patients. The genetic basis of HI is still debated but published data indicate the existence of a wide variety of chromosomal mosaicism in different cases. In addition, a subgroup of affected females with non-mosaic balanced X;autosome translocations have been reported. The phenotype in these cases appears to be related to the presence of mosaic functional disomy rather than a disruption of an X linked gene. From these data it appears that there is no common genetic background to this syndrome. In our patient the presence of clinical findings clearly indicative of HI, in combination with findings suggestive of a contiguous gene syndrome involving the distal chromosome 16 region, has prompted us to evaluate the genetic background of this association. In this paper, the clinical findings and the cytogenetic and molecular analyses of the patient and his relatives are reported.

Case report

The male proband (fig 1) was born at term after a normal pregnancy and delivery. His birth weight was 2500 g. The parents were healthy and unrelated. The proband’s paternal half brother was diagnosed as having TSC (fig 2). Besides cortical tubers and subependymal nodules, brain MRI showed a Dandy-Walker
malformation. He died at 18 years of age following intraperitoneal haemorrhage owing to renal angiomyolipoma.

At birth, the proband was noted to have omphalocele, dysmorphic face, and left talipes equinovarus, requiring corrective plaster casts until the age of 6 months. At the age of 3 years, the diagnosis of TSC was made on the basis of the presence of hypopigmented skin spots, mental retardation, cortical tubers, and subependymal nodules on the brain CT scan. From 11 years of age, he developed complex partial seizures which were successfully treated with carbamazepine. At this time, physical examination showed facial angiofibromas, fibrous forehead plaque, three hypopigmented spots, dysmorphic facial features with a triangular face, high forehead, hypertelorism, epicanthic folds, broad nasal root, narrow and high arched palate, hypertrophic alveolar ridges, supernumerary teeth, microcephaly, and a generalised muscular hypotrophy (fig 1A). The left leg was 2 cm shorter than the right.

He had a well demarcated 1.5 cm wide hypopigmented streak striating from the left groin and extending linearly to the medial malleolus (fig 1B). Another irregular hypopigmented area was present on the left lower abdomen. Psychomotor development was severely delayed. Haematological investigations showed mild hypochromic microcytic anaemia (Hb 9.8 g/dl, MCV 65.8 fl, MCH 22.2 pg) with normal levels of Hb A₂. Ophthalmological examination and cardiac and abdominal ultrasound were normal.

Brain MRI showed multiple cortical and subcortical tubers and one periventricular subependymal nodule. Generalised cerebral atrophy with enlarged lateral ventricles and inferior vermal hypoplasia were also observed (fig 1D).

Radiographs of the lower limbs confirmed that the right femur was 2 cm longer than the left, with an area of osteosclerosis in the right distal femur.

Follow up renal ultrasound at the age of 12 years 6 months showed bilateral multiple renal cysts, the largest of which was 10 mm in diameter. These findings were confirmed by renal CT scan.

No pigmentary abnormalities were present in the patient’s parents. His father showed no signs of TSC after extensive examination, which included fundoscopy, renal and cardiac ultrasound, and brain MRI. He did have symptoms of hyperthyroidism; a nodular goitre was diagnosed. Recently, a nodular goitre with normal thyroid function was also diagnosed in the father’s sister (fig 2, II.4), who was otherwise healthy without signs of TSC. In the proband, laboratory investigations showed high TSH and low T4 levels; thyroid echography was normal.

Materials and methods

CYTOGENETICS

Chromosome analysis was performed according to standard procedures with GTG banded chromosomes from cultured peripheral blood lymphocytes. The slides were used directly for FISH.

DNA ANALYSIS

DNA was isolated from peripheral blood samples using the salting out method. Southern blot analysis was done on HindIII or EcoRI digested DNA with probes (4B2, E0.7, and E1A1H.6) from the TSC2 cDNA labelled by the random primer method. The VNTR at the α globin locus (3’HVR) was analysed. In addition, the microsatellite markers KG8, 16AC2.5 (D16S291), and SM7 (D16S283) were analysed.

FISH ANALYSIS

For routine TSC2 deletion screening, the plasmid CW23 (3’ TSC2 gene) and the cosmids CW9D, about 30 kb distal to the TSC2 gene, were used (fig 3G). The breakpoint analysis of the 16p13 region was performed with the cosmids from the PKD1 region LA3 (N54) and cGGG4b (GGG12). In addition, PACs 97.10G, 1.8F, and 96.4b, located proximal to the PKD1 gene, were used.
An unbalanced submicroscopic translocation

Figure 3  (A) In situ hybridisation on the proband’s metaphases (fig 2, III.3) shows a deletion of the 16p13.3 region with CW9D (arrowhead) and (C) a partial trisomy for the 8q24.3 region with probe 2053b (arrowhead). (B) Metaphases of the proband’s father show a balanced translocation t(8;16)(q24.3;p13.3) with the probes CW9D (16p13.3) (arrow) and 2053b (8q24.3) (arrowhead). (D) The breakpoint on 16p13.3 is visualised by the probe 1.8F, with signals present on 16p13.3 as well as on 8q24.3 (arrowheads). (F) Probe CHT 16 (5’ TG gene) remains on 8q24.3 (green signals), while the cosmid CW9D is translocated from 16p13.3 to 8q24.3 (red signals). (E) Ideogram of the cryptic translocation t(8;16)(q24.3;p13.3). (G) The molecular map of the translocation area is not drawn to scale. Probe 1.8F crossing the breakpoint is highlighted by a red bar. The vertical arrowhead indicates the breakpoint of the t(16;22)(p13;q11) as analysed by The European Polycystic Kidney Disease Consortium 1994.1
For the 8q24 breakpoint analysis, we used the following probes (fig 3G): cMYC, Drg1 PAC 28N23, TG gene cosmids CHT 3, 11, 16, and 18, and the subtelomeric probe 2053b3. The orientation of the TG gene and the TG cosmids is indicated in fig 3G (F Baas, L Kalaidijeva, unpublished results).

For the identification of chromosome 8, we used the α satellite centromere probe αp8 (D8Z1) directly labelled with tetramethylrhodamine-dUTP using the nick translation kit (Boehringer Mannheim). All other probes were labelled either with biotin or digoxigenin with the BIO- or DIG-NICK kit (Boehringer Mannheim). All other probes were not involved in the translocation (fig 3F).

The unbalanced form of the translocation in the proband was further characterised with 2053b3, which showed signals on the der(16) as well as on both chromosomes 8 (fig 3C).

Discussion
Contiguous gene syndromes are an important issue in clinical genetics. Keen clinical observation has contributed to the delineation of syndromes such as Kallman syndrome, DiGeorge syndrome, and Miller-Dieker syndrome.

Several contiguous gene syndromes involving the chromosome 16p13.3 region have been described. The combination of α thalassaemia, dysmorphic features, and mental retardation, together with a cryptic translocation t(8;16)(q24.3;p13.3) with the PKD1 gene on chromosome 8q24.3-qter region, has been described. The proband in this family described here had a clinical picture suggestive of a large deletion in the chromosome 16p13.3 area, as he was affected with TSC and had α thalassaemia trait. The death of his half brother, who also had TSC, at 18 years of age owing to renal complications indicated the possibility of involvement of the PKD1 gene. FISH studies provided evidence for a familial cryptic translocation t(8;16)(q24.3;p13.3) with an unbalanced form in the proband and a balanced form in the father and paternal aunt.
The unbalanced translocation caused the index patient to be monosomic for the chromosome 16p13.3 region with a breakpoint detected by PAC 1.8F, which represents the most proximal breakpoint described to date for terminal 16p deletions. In addition, FISH analyses showed trisomy for the distal 8q region as a result of an adjacent 1 segregation.

To our knowledge, constitutional translocations involving 8q24.3 are very rare, presumably because they escape detection by routine cytogenetic techniques. A specific phenotype associated with a partial trisomy 8q24-qter has not been defined. In contrast, balanced and unbalanced rearrangements including 8q24 have been noted in a variety of haematological and solid tumours.

The thyroid dysfunction, which was diagnosed in both unbalanced and balanced translocation carriers, is possibly of interest, because the chromosome 8q24.3 region harbours the thyroglobulin (TG) gene. However, since in all three patients, both the 3' and the 5' end of the TG gene were shown to remain on chromosome 8 by FISH analysis, disruption of the coding region of the gene seems unlikely.

The complex clinical picture of the proband can be explained to some extent by deletion of known or as yet unknown genes in the chromosome 16p13.3 region, as he clearly can be explained to some extent by deletion of some 8 by FISH analysis, disruption of the coding region of the gene seems unlikely. The gene for autosomal dominant polycystic kidney disease lies in a 750-kb CpG rich region. Germino GG, Weinstat-Saslow D, Himmelbauer H, et al. The gene for autosomal dominant polycystic kidney disease is a large genomic rearrangement. Genomics 1992;13:144-51.


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