Identification of an unbalanced cryptic translocation t(9;17)(q34.3;p13.3) in a child with dysmorphic features

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Abstract

We report a case of an unbalanced cryptic telomeric translocation 46,XY,der(17)t(9;17)(q34.3;p13.3) in a boy with dysmorphic features and developmental delay. The proband had intrauterine growth retardation, postnatal short stature, and mild microcephaly. Magnetic resonance imaging showed incomplete myelination, but no evidence of lissencephaly. Cytogenetic analysis of the proband's peripheral blood showed an abnormal 17p. Fluorescence in situ hybridisation (FISH) with a Miller-Dieker cosmid probe did not detect a deletion for that area. Further analysis with a 17p telomere specific probe identified an unbalanced telomeric translocation. The same probe was used to determine the presence of an apparent balanced translocation t(9;17)(q34.3;p13.3) in the mother of the proband. The balanced translocation was confirmed with two cosmids that map distally on 9q34.3. Two phenotypically normal half sibs, a maternal aunt, a maternal uncle, and the maternal grandmother were found to be balanced translocation carriers as well. A subtle translocation is one mechanism that can produce an abnormal phenotype in a patient who had a normal karyotype at lower band resolution levels.

The incidence of cryptic translocations is not known, but they may represent a major contributor to human pathology. Recently several cases of cryptic translocations associated with abnormal phenotypes have been published.1,2 The detection of subtle aberrations represents a major challenge in clinical cytogenetics and requires analysis of banded prometaphase (high resolution) chromosomes to identify the abnormal chromosome followed by molecular or molecular cytogenetic confirmation.

Deletions of chromosome 17 band p13 are associated with the Miller-Dieker sequence which is characterised by lissencephaly, severe mental retardation, and characteristic facial features. Isolated lissencephaly has also been described in patients with deletions of 17p13.7 Smaller deletions of 17p, not encompassing the Miller-Dieker region, but associated with an abnormal phenotype have not been described.

A well characterised abnormal phenotype is a feature of partial duplication of 9q. The main characteristics include joint contractures, dolichocephaly, beaked nose, retrogнатia, deep set eyes, slender limbs, arachnodactyly, and mental retardation. Heart defects have also been reported.8

In this communication we describe a cryptic translocation, t(9;17)(q34.3;p13.3), detected in a chromosomally unbalanced child with dysmorphic features and developmental delay. The clinical features do not include lissencephaly or other features of the Miller-Dieker sequence, and are presumably the result of partial monosomy of 17p and partial trisomy of 9q.

Materials and methods

Blood chromosome analysis was performed on the proband, his mother, two half sibs, a maternal aunt, a maternal uncle, and the maternal grandmother. Routine cytogenetic techniques including high resolution chromosomes prepared using ethidium bromide9 and GTG banding were used. Fluorescence in situ hybridisation (FISH) analysis was performed using a Miller-Dieker specific cosmid probe (D17S379) (Oncor); a 17p telomere specific probe which is the most distal locus mapped on 17p13.3 (D17S34)10 (Oncor); a chromosome 17 library, pBS17 (gift of Dr D Pinkel, University of California, San Francisco); one 9q34.2 cosmid, 5B11; and two 9q34.3 cosmids, 3AE11 and Tan1. The 9q cosmids were a gift from Dr D Kwiatkowski, Harvard Medical School, Boston. The 5B11 cosmid contains the single copy marker D9S113 and maps to 9q34.2 (D Kwiatkowski, personal communication). The Tan1 cosmid contains the TAN1 gene (human homologue of the Dmsothila notch gene) which maps very distal on 9q34.3. The 3AE11 cosmid contains the anonymous marker D9S67 and maps more proximally, but still within band 9q34.3. The non-commercial probes were labelled with biotin using a nick translation kit from Gibco BRL. Single colour hybridisations were performed for each of the probes used.13 Confirmation of the chromosome identity was accomplished by destaining the slides after the FISH analysis and subsequent GTG or QTQ banding.14

Case report

The proband was the product of a pregnancy complicated by a hepatitis B infection in a 21 year old gravida 2 mother. Sonograms during pregnancy showed progressive intrauterine
of the brain showed incomplete myelination but no lissencephaly. At the age of 4 years, he was proportionately small (below the 5th centile for height, weight, and head circumference). He showed moderate developmental delay with more severe delay in expressive language (fig 1).

Fig 2 displays the pedigree of this family. The maternal grandmother had eight spontaneous abortions and two apparently normal children in addition to the proband's mother. The proband's mother reported two spontaneous abortions, at 13 and 18 weeks of gestation. The proband had two phenotypically normal half sibs. The three children were from different fathers, none of whom was available for testing. The maternal aunt had a pregnancy termination at 23 weeks of gestation because of a congenital heart defect detected on ultrasound. At necropsy, the fetus was an appropriate size for gestational age with congenital heart disease and hypospadias.

Results

Chromosome analysis of GTG banded preparations of PHA stimulated lymphocyte cultures of the proband showed an abnormal 17p at the 850 band level. Although the exact nature of the abnormality could not be identified, it was thought to be a de novo terminal deletion of 17p. Chromosome studies of the mother at the 725 band level of resolution were inconclusive. FISH analysis with a whole chromosome 17 library (pBS17) did not show a structural rearrangement of 17p involving another chromosome in either the mother or the proband. Further analysis with a Miller-Dieker cosmid probe (D17S379) specific for 17p13.3 showed positive signals on both chromosomes 17p in both the mother and child, ruling out a translocation or deletion of the Miller-Dieker region.

Following two subsequent miscarriages, the mother became pregnant again. Karyotyping of amniocytes indicated that the fetus also had the abnormal 17p. At birth, the child appeared phenotypically normal. The FISH analysis was repeated on the infant using a probe for the D17S34 locus. This locus is distal to the Miller-Dieker region. The results showed positive signals on the telomere of the short arm of one chromosome 17 and a second set of signals on the distal q arm of an unidentified C group chromosome. Destaining and subsequent Q and G banding indicated that the C group chromosome was a 9, suggesting the presence of a reciprocal translocation between 17p13.3 and 9q. The presence of the reciprocal translocation was confirmed using two 9q34.3 specific cosmid probes, Tan1 and 3AE11, on both the mother and the two half sibs. Hybridisation of these two cosmids on metaphase spreads of the proband showed three signals: two on 9q34.3 and one on 17p13.3 (fig 3). Cosmid 5B11 (9q34.2) hybridised on 9q in the mother and the proband establishing the translocation breakpoint between 5B11 and 3AE11. The abnormal proband is therefore the result of an adjacent 1 segregation of the maternal
translocation with a karyotype: 46,XY,−17, +der(17),t(9;17)(q34.3;p13.3)mat. This karyotype results in monosomy 17p13.3−ter and trisomy 9q34.3−ter.

Further family studies indicated that the maternal aunt, uncle, and grandmother are also carriers of the familial translocation t(9;17)(q34.3;p13.3) (fig 4). Analysis of fetal cord blood of the maternal aunt's pregnancy termination showed that the male fetus also had the same unbalanced translocation that was originally detected in the proband.

Discussion
The extent of the segmental aneusomy for chromosome 17 (fig 4) may be estimated to be approximately 2 Mb or less. This is based on calculations that the Miller-Dieker locus, which is not deleted, is located approximately 2 Mb from the telomere. An association between monosomy for this region of chromosome 17 and an abnormal phenotype has not been described in published reports. However, a deletion of the D17S34 locus has been described in 50% of paediatric medulloblastomas, 66% of highly anaplastic astrocytoma, and 21% of pilocytic astrocytoma. In a series of 20 medulloblastomas, it was found that the p53 tumour suppressor gene was mutated infrequently. All of the children with a deletion of the D17S34 locus fared very poorly, as compared to those without a deletion. These results suggest the presence of a new tumour suppressor gene distal to the p53 locus. The possible implication of the deletion of the D17S34 locus in our patient is unknown.

The partial duplication of chromosome 9q leading to a partial trisomy is a relatively uncommon event. Although limited in number, these cases have been well documented. Most reports of partial duplication 9q are of much larger duplications than the one described in this study, and the most common breakpoints are q21−qter and q32−qter. The length of the segmental aneusomy with breakpoints at 9q21 or 9q32 range from four to eight fold that of our patient (fig 4). Moreover, all of the published cases were unbalanced products of parental translocations involving a variety of segmental monosomies with the exception of a family reported by Allderdice et al. An insertion of chromosome 9 resulted in seven recombinant family members with duplication of band 9q34.

![Figure 4](image-url)
The general clinical features of partial trisomy 9q include low birth weight, dolichocephaly, severe physical and mental retardation, stereotyped movement of the extremities, low set, malformed ears, deep set eyes, prominent, beaked nose, small, down turned mouth, micrognathia, and long tapering fingers. Congenital heart disease has also been documented in some cases. A review of published patients with partial duplications of 9q equal to or smaller than 9q31-qter is presented in the table. Our index patient shared some of those features such as low birth weight, failure to thrive and continued small stature, down turned mouth, small jaw, low set, malformed ears, and clinodactyly. Because he lacked several of the more specific features such as dolichocephaly, deep set eyes, long tapering digits, and flexion contractures, his condition was not immediately recognizable as 9q duplication. Also, our patient's mental retardation and delayed development is less severe than other patients with partial duplication of 9q.

This patient, together with those previously reported with duplication of 9q34, provides evidence in support that the size of the duplication appears to influence the severity of the phenotype in partial duplication of 9q.

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