Paternal origin of the de novo deleted chromosome 4 in Wolf-Hirschhorn syndrome

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Abstract
The parental origin of the de novo deleted chromosome 4 was studied in five cases of Wolf-Hirschhorn syndrome using polymorphic probes mapping in the 4p16.3 region. In all the patients the deleted chromosome was found to be of paternal origin and these results, together with similar ones obtained by another group, make the preferential paternal origin of the de novo chromosome 4 deletion highly significant.

The parental origin of numerical and structural chromosome anomalies has been difficult to assess for years. Acrocentric chromosome polymorphisms, heterochromatic variants, and specific genetic markers are only occasionally informative.

Current DNA techniques provide a more precise means for studying the origin of chromosomal anomalies in man and recently several studies have indicated the possible existence of genomic imprinting, a phenomenon first discovered in the mouse (see Hall for a review).

The Wolf-Hirschhorn syndrome (WHS), characterised by low birth weight, developmental delay, microcephaly, hypertelorism, downward slanting palpebral fissures, prominent glabella, short philtrum, cleft lip and palate, low set, abnormal ears, and other possible abnormalities such as seizures and genital defects, results from monosomy of the distal short arm of chromosome 4.2 Most cases are sporadic.

We studied the parental origin of the deleted chromosome 4 in five patients with the WHS using probes mapping in the 4p16.3 region.

Materials and methods
Sex, age, and clinical data of the five patients are shown in the table. All five patients had severely delayed growth, profound mental retardation, Greek warrior helmet face, and recurrent convulsive attacks.

Chromosome preparations were made from cultures of blood lymphocytes and high resolution banding was obtained according to Dutrillaux and Viegas-Pequignot.3 DNA was extracted directly from blood lymphocytes. For RFLP detection, 2 μg of each DNA sample was digested to completion with the appropriate restriction enzyme (AccI, PstI, PvuII) as recommended by the supplier (Boehringer, Mannheim). The resultant DNA fragments were resolved according to size by agarose gel electrophoresis in TAE buffer. The DNA fragments in the gel were denatured in situ with 0.2 mol/l NaOH, 0.6 mol/l NaCl. The denatured DNA fragments were transferred to a nylon filter (Hybond N-Amersham) by Southern blotting and fixed by UV.

DNA probes (pBS674E-D, 252-3, and D5 corresponding to D4S95, D4S115, and D4S90, respectively) were labelled with (32P)-dCTP (Amersham) by random oligonucleotide priming4 and then hybridised to the filter for 20 hours at 44°C in 50% formamide, 5 x SSC, 1 x Denhardt's solution, 20 mmol/l NaHPO4, 10% Na dextran sulphate, 0.1% SDS, and 100 μg/ml of salmon sperm DNA. The filters

Table  Clinical findings.

| Patients | 1   | 2 | 3  | 4   | 5 |  |  |  |  |  |
|-----------|-----|---|----|-----|---| |   |   |   |   |
| Date of birth | F | F | F | F | F | M | | | | |
| Sex | 17.788 | 9.982 | 20.184 | 27.983 | 26.588 | | | | | |
| Paternal age at birth | 26 | 41 | 41 | | | | | | | |
| Maternal age at birth | 22 | 32 | 39 | 32 | 28 | | | | | |
| Birth weight (g) | 2450 | 1800 | 1720 | 2050 | 2520 | | | | | |
| Height (cm) | 49 | 45 | 46 | 49 | | | | | | |
| Age at last examination | 2/2/12 | 8/4/12 | 4/9/12 | 7/2/12 | 2/2/12 | | | | | |
| Weight (kg) | 6.8 | 7.3 | 13.6 | 7.9 | | | | | | |
| Prominent glabella | + | + | | | | | | | | |
| Hyperelorism | + | + | | | | | | | | |
| Malformed ears | + | + | | | | | | | | |
| Stabismus | + | + | | | | | | | | |
| Iris defect | + | + | | | | | | | | |
| Broad nose | + | + | + | + | | | | | | |
| Short philtrum | + | + | + | + | | | | | | |
| Cleft mouth | + | + | + | + | | | | | | |
| Cleft lip or palate | + | + | + | + | | | | | | |
| Sacral sinus or dimple | + | + | + | + | | | | | | |
| Heart defect | + | + | + | + | | | | | | |
| Renal malformations | + | + | + | + | | | | | | |
| Craniofacial | + | + | + | + | | | | | | |
| Mental retardation | Profound | Profound | Profound | Profound | Profound | | | | | |
were washed twice in 2×SSC at 44°C for 15 minutes, and once in 2×SSC at 60°C for 15 minutes before autoradiography.

**Results**

In patients 1, 2, 3, and 4 chromosome analysis showed a deletion of the region 4p15.3→4pter. In patient 5 the abnormal chromosome 4 was derived from a translocation with a pericentromeric region of an acrocentric chromosome as indicated by the presence of the nucleolar organiser region. DA-DAPI staining, specific for chromosome 15, was negative. The monosity of patient 5 included the region 4p16.1→pter. The parents of the patients all had normal karyotypes.

Molecular studies were performed using probes pBS674E-D, 252-3, and D5 which are localised in 4p16.3 distal to D4S10.6

RFLP analysis of pBS674E-D (D4S95), hybridised with a filter of genomic DNA digested by Accl, showed the paternal origin of the deleted chromosome 4 in patients 2 and 5 (fig 1).

RFLP analysis of 252-3 (D4S115), hybridised with a filter of genomic DNA digested by PstI, showed the paternal origin of the deleted chromosome 4 in patients 1, 2, 3, and 4 (fig 2).

The paternal origin of the deleted chromosome 4 in patients 3 and 4 was confirmed by the RFLP analysis of D5 (D4S90), hybridised with genomic DNA digested by PvuII (fig 3).

**Discussion**

All our patients showed a de novo terminal deletion of the short arm of chromosome 4 including the region 4p15.3→pter. In patient 5 monosomy 4p16.1→pter was the result of a de novo unbalanced translocation with an unidentified acrocentric chromosome. Our results are in agreement with previous reports suggesting that monosomy 4p16 is sufficient for the full expression of the Wolf-Hirschhorn syndrome, whose locus should be distal to D4S10.7 The paternal origin of the abnormal chromosome has been shown for all of our five patients using probes mapping in the deleted region.

Quarrell *et al*8 reported seven WHS patients with de novo deletions or rearrangements of the short arm of chromosome 4 showing paternal origin of the abnormal chromosome. Pooling our data and those of Quarrell *et al*,9 the preferential paternal origin of the de novo chromosome anomaly is significant (0.02 < p < 0.01).

A chromosome imprinting effect may account for these results. The best known imprinting effect in man is related to the deletion of band q11–q13 of chromosome 15. The same deletion causes Angelman's syndrome if the deleted chromosome is of maternal origin.

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**Figure 1** RFLP analysis of the pBS674E-D probe (D4S95), hybridised with a filter of genomic DNA digested by Accl, of patient 5 (DF), his father (F), and mother (M). The probe recognises two groups of polymorphic alleles of 7.0 and 1.5 kb and of 4.4, 4.3, 4.2, and 4.1 kb, respectively. In the proband only the maternal 1.5 kb allele is present while the paternal 7.0 kb allele is absent.

**Figure 2** RFLP analysis of the 252-3 probe (D4S115), hybridised with a filter of genomic DNA digested by PstI, of patients 1 (CG), 2 (SSa), 3 (SSe), 4 (MP), and their parents (F=father, M=mother). The 252-3 probe recognises more than six alleles between 2.2 and 2.6 kb. In all four patients only the maternal allele is present.

**Figure 3** RFLP analysis of probe D5 (D4S90), hybridised with genomic DNA digested by PvuII, of patients 3 (SSa) and 4 (MP) and their parents (F=father, M=mother). The probe recognises two alleles of 5.0 and 5.6 kb. Only the maternal 5.6 kb allele is present in the two patients.
and the Prader-Willi syndrome if the deleted chromosome is of paternal origin.8

The deletion of the paternal chromosome 4 and maternal hemizygosity for the same region would be responsible for the expression of the WHS. We can postulate that the maternal origin of the chromosomal anomaly remains undetected, being either lethal in the embryo or without phenotypic effect.

However, the observation that patients with derivative 4p monosomy owing to familial translocation always show the WHS, irrespective of the parental origin of the anomaly, is against this hypothesis. In a review of published reports, Narahara et al16 found that 13% of the 4p monosomies associated with WHS were the result of familial translocation. Among the 15 cases reported, five were of paternal and 10 of maternal origin.

It seems, therefore, that among these cases there was no selection against the deletions of the short arm of chromosome 4 of paternal origin and that the paternal chromosome 4 could be more prone to mutational events than the maternal one.

A similar discrepancy in the parental origin between familial and sporadic cases has been found in Beckwith-Wiedemann syndrome with an excess of maternal transmission in the former and paternal transmission in sporadic cases with chromosome 11p15.1 duplication.10

An imprinting phenomenon also related to chromosome 4 has been postulated to play some role in the expression of Huntington's disease (HD). The paternal transmission of the HD gene is correlated with an earlier onset and a more severe expression of the disease.11

Thus, it could be suggested that the distal region of the short arm of chromosome 4 in man is likely to undergo genomic imprinting. In the mouse, the region corresponding to the distal portion of 4p in man does not appear to be subject to imprinting.11

Finally, it must be noted that the ratio between male and female WHS patients is 1:2. A distorted sex ratio has been observed in several chromosomal anomalies and is usually interpreted as resulting from differential survival in one sex. It is conceivable that the imprinting phenomenon may be responsible for the sex ratio distortion.

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