LETTER TO JMG

Loci for primary ciliary dyskinesia map to chromosome 16p12.1-12.2 and 15q13.1-15.1 in Faroe Islands and Israeli Druze genetic isolates

D Jeganathan, R Chodhari, M Meeks, O Færoe, D Smyth, K Nielsen, I Amirav, A S Luder, H Bisgaard, R M Gardiner, E M K Chung, H M Mitchison

Primary ciliary dyskinesia (PCD; Immotile cilia syndrome; OMIM 242650) is an autosomal recessive disorder resulting from dysmotility of cilia and sperm flagella. Cilia and flagella function either to create circulation of fluid over a stationary cell surface or to propel a cell through fluid. These related structures are highly complex organelles composed of over 200 different polypeptides. The core or axoneme of cilia and flagella comprises a bundle of microtubules and many associated proteins. The microtubules are formed from α and β tubulin protofilaments and are arranged in a well recognised ‘9+2’ pattern: nine peripheral microtubule doublets in a ring connected around a central pair of microtubules by radial spoke proteins. The peripheral microtubules have dynein motor proteins attached and are connected with each other by nexin links.

In human beings, ciliated epithelium can be found lining the respiratory tract, including the sinuses and middle ear, the brain ependyma, the female oviduct, and the male vas deferens. Cilia in the respiratory tract play an important part in airway clearance of respiratory secretions. In primary ciliary dyskinesia, impaired mucociliary clearance causes recurrent respiratory tract infections including chronic otitis media, rhinitis, and sinusitus, often leading to permanent lung damage (bronchiectasis). Patients are also often subfertile due to sperm tail immotility and immotile oviduct cilia. About half of the patients have defects of laterality, usually complete mirror-image reversal of the left-right axis (situs inversus) and this association is known as Kartagener syndrome. Primary ciliary dyskinesia has an estimated incidence of 1 in 20 000 live births.

In four Druze families from the Golan region of Israel to a 17 cM region on chromosome 15q13.1-15.1, with a maximum lod score of 3.2 at \( a \) (proportion of linked families) = 0.7, using GENEHUNTER.

This study provides further evidence of the genetic heterogeneity underlying primary ciliary dyskinesia and has established a framework to facilitate isolation of two genes for primary ciliary dyskinesia. Determining the molecular basis of primary ciliary dyskinesia will provide insight into the genetic control of cilia assembly and function and the pathway which determines the vertebrate left right axis.

**Key points**

- Primary ciliary dyskinesia is an autosomal recessive disorder characterised by recurrent sinopulmonary infections, bronchiectasis, and subfertility, due to dysfunction of the cilia. Fifty percent of patients with primary ciliary dyskinesia have defects of laterality (situs inversus) and this association is known as Kartagener syndrome. Primary ciliary dyskinesia has an estimated incidence of 1 in 20 000 live births.

- To identify loci for this genetically heterogeneous condition, genome wide linkage scans and subsequent fine mapping were performed in two different isolated populations with distinct ciliary ultrastructural defects, from the Faroe Islands and the Druze community in northern Israel.

- A locus was mapped in seven families from the Faroe Islands to a 2.8 cM interval on chromosome 16p12.1-12.2, with a maximum lod score of 3.15, obtained using GENEHUNTER. A locus was mapped in three out of four Druze families from the Golan region of Israel to a 17 cM region on chromosome 15q13.1-15.1, with a maximum lod score of 3.2 at \( a \) (proportion of linked families) = 0.7, using GENEHUNTER.

**Abbreviation:** PCD, primary ciliary dyskinesia
found in a patient with Kartagener syndrome and normal cilia ultrastructure. The exact role of DNAH11 in primary ciliary dyskinesia has yet to be elucidated. Two other genes for primary ciliary dyskinesia have been localised: CILD2 to 19q21 and another locus to 15q24 (M P Witt, personal communication).

To identify loci for PCD, genome wide linkage scans and subsequent fine mapping were performed in two different isolated populations with distinct cilia ultrastructural defects, from the Faroe Islands and the Druze community in northern Israel.

The Faroes comprise a small group of islands in the North Atlantic Ocean located near Iceland, Scotland, and Norway with a relatively young population of mixed Norwegian, Danish, and British ancestry. The islands were colonised at the same time as Iceland, around 1100 years ago and the population size remained small until rapid expansion in the 1800s. The current population size is estimated at 48,000 and has arisen predominantly by indigenous expansion. The Drue community, a small middle eastern religious sect, was established slightly later, in the eleventh century AD. Members live predominantly in defined geographical areas of southern Syria, southern Lebanon, and northern Israel and they remain isolated mainly for religious reasons. Both populations are also isolated for geographical and cultural reasons, in the Faroe Islands associated with limited immigration and in the Druze with a high level of consanguinity.

With relatively few founders, a limited population size, and recent expansion, the Faroes and Druze populations are suitable for genetic mapping of a heterogeneous recessive disease. This has been demonstrated in the Faroe Island population, in which enrichment of disease incidence associated with specific gene mutations due to founder effects has been shown for cystic fibrosis and glycogen storage disease II. Similar findings have been reported for several conditions in the well studied Druze population including cystic fibrosis, Krabbe disease and mucolipidosis. However the Druze population has not always proved to be genetically homogeneous.

We report here the identification of two new PCD loci in these genetic isolates, located on chromosomes 16p12.1-12.2 and 15q13.1-15.1 in the Faroe Island and Druze population respectively.

SUBJECTS AND METHODS

This study was carried out using the two family sets shown in fig 1. Informed consent was obtained in accordance with protocols approved by the University College London Hospital NHS Trust ethical committee. The diagnosis of affected subjects was made according to established clinical criteria supported by abnormal ciliary motility studies and electron microscopy of brushings or biopsy of nasal mucosa. The Faroe Island resource consisted of seven families comprising 11 affected and 24 unaffected individuals (fig 1A). Clinical findings for some of the patients have been described previously. Only the affected child in UCL140 exhibited situs inversus. Electron microscopy defined an ultrastructural phenotype of absent outer dynein arms in Faroe patients (fig 2B). The patients were Faroese in origin, living on three of the islands only, except for the father in family UCL140, who was from Denmark. The families were treated as unrelated pedigrees in linkage analysis. There was unsupported verbal evidence for distant relatedness between families UCL196, UCL197, and UCL109, however no formal genealogical analysis has been possible to establish the precise relationships. There was one affected parent, the mother in family UCL198.

Four Druze Israeli families were studied comprising 7 affected and 22 unaffected individuals (Three are shown in fig 1B). The parents in three families, UCL122, UCL124, and UCL25, were first cousins, while the fourth family, UCL123, was non-consanguineous. In contrast to the Faroe Island population, Druze patients showed an unusually high incidence of situs inversus (six out of seven affected children). Electron microscopy defined an ultrastructural phenotype of partial absence of the inner dynein arms (fig 2C). Nasal brushings were processed for ultrastructural studies using established techniques and over 100 suitably oriented cross sections of cilia throughout the section were examined to confirm this structural defect. The four families were located in two neighbouring Druze villages comprising 7500 inhabitants, in the mountainous region of the Golan Heights. Families UCL122 and UCL124 were from one village and families UCL123 and UCL125 were from the other.

All of the patients with primary ciliary dyskinesia who were recognised within the two populations were ascertained and there is considerable population enrichment for primary ciliary dyskinesia in both the Faroe Island and Druze populations. The prevalence of primary ciliary dyskinesia in the Faroe Islands is around 1:4500 whilst the local prevalence amongst the Druze population studied is as high as 1:1000.

Genome wide scans of 10 cM density were performed in these two populations using four of the Faroe Island pedigrees (UCL96, 97, 98, and 109) and all four Druze pedigrees (UCL122, 123, 124, and 125). Genomic DNA was extracted from white blood cells using standard methodology. Over 350 hundred microsatellite markers from the Genethon map were genotyped in each family by polymerase chain reaction and fluorescent based semi-automated methodology using methods previously described. Alleles were assigned using Genescan and Genotyper software (Applied Biosystems). Linkage analysis was performed under the assumption of autosomal recessive inheritance with a penetrance of 0.9, a disease allele frequency of 0.007 with equal allele frequencies (0.1) for each marker and a phenoctype rate of 0.00001. This disease allele frequency reflects the worldwide incidence of primary ciliary dyskinesia of 1:20 000. Analysis was also performed using the disease allele frequencies that reflected more closely the actual population frequencies we have determined for each population as described above: 0.015 for the Faroe Island families (incidence 1:4500) and 0.03 for the Druze families (incidence 1:1000). Multipoint analyses were performed using the GENEHUNTER program.

For subsequent fine mapping, six novel microsatellites were determined in the laboratory from the genomic sequence of BAC clones spanning the selected region. The primer pairs used to amplify these polymorphisms were: 5'-TGTTCCTTAGACGTTTCAGC-3' / 5'-ACTGTACCTTCCCCAAAGCG-3' (16/14125), 5'-TGCAAAACAGACTGACACCAC-3' / 5'-GCTTCAAACTCTCTAGCTC-3' (16/10321), 5'-CACGCTTGGCTAGACTAATG-3' / 5'-CTTTACCCAGTTGCAGCATACC-3' (15/14), 5'-CTGGCCTATGCACTTCCACGAGGATTGTGTTCGCT-3' / 5'-TCTCATGACTTTCAGTAATGCTC-3' (15/20), 5'-TCTCATGACTTTCAGTAATGCTC-3' / 5'-TCTCATGACTTTCAGTAATGCTC-3' (15/23) and 5'-GTTGCGCTTCAATAATCC-3' / 5'-AGTACCTAACATTCAAGG-3' (15/36).

Haplotypes were manually constructed using the most parsimonious allele configuration to minimise recombinants. Génethon marker order and genetic distances were determined from the deCODE Genetics high resolution genetic map. Additional markers were positioned in the deCODE framework map based on their relative position within the human genome sequence available from the UCSC Genome Browser, April 2003 Build 33 sequence freeze.
Figure 1  Pedigrees consistent with linkage on chromosome 16p12.1-12.2 and 15q13.1-15.1. (A) Faroe Island and (B) Druze Israeli haplotypes. Filled symbols indicate individuals affected with primary ciliary dyskinesia, asterisks indicate patients with situs inversus, and a double line indicates first cousin marriage. Genetic markers used in the initial genome scan are shown in bold and the box indicates the minimum critical interval encompassing each locus. For each marker, alleles are coded numerically such that the same allele number correlates to the same allele size across families. The frameworks of microsatellite markers used were as follows with genetic distances indicated in Kosambi cM:

For markers:
- D16S3046, 2.59; D16S3076, 0.003; D16S403, 0.1; D16S412, 0.5; D16S417, 1.3; UCL109, 0.36; 16/4125, 0.4; 16/10321, 0.16; D16S401, 0.01; D16S3133, 0.31; D16S3093, 2.09; D16S1002, 6.02; D15S975, 1.99; D15S1048, 1.57; D15S165, 1.99; D15S1010, 1.19; 15/20, 0.87; D15S144, 0.57; D15S1007, 1.09; D15S1040, 0.96; 15/23, 0.92; D15S122, 0.88; D15S971, 0.27; 15/36, 1.12; D15S118, 4.02; D15S1012. Genetic distances were taken from the DeCODE map except for markers 16/4125, 16/10321, D16S319, 15/14, D15S1010, 15/20, 15/23, D15S122 and 15/36. These were positioned relative to the DeCODE marker framework using Human Genome Project draft sequence information as described in the text.
Physical distances were taken from this genomic sequence map.

RESULTS
A region consistent with linkage in the four Faroe Island families was identified on chromosome 16p12.1-13.1. No evidence for linkage at any of the known PCD loci was found. Fine mapping was undertaken in the entire seven family resource which included the three additional families UCL135, UCL139, and UCL140. Linkage analysis using GENEHUNTER was performed across a 9 cM region between markers D16S3046 and D16S3093. This gave a maximum multipoint lod score of 3.15 between markers D16S412 and 16/10321. Using a disease allele frequency calculated from the actual recorded Faroe Island population disease incidence rather than worldwide incidence of primary ciliary dyskinesia, the maximum lod score obtained was 3.13. This is probably a conservative estimate of the true degree of linkage as the families were only analysed as unrelated pedigrees. Haplotype analysis indicated the key recombinant events defining the critical region on chromosome 16p12.1-12.2 (fig 1A). A paternal recombination in family UCL98 at D16S403 defined the telomeric limit of the region. The centromeric limit was defined by a maternal recombination event in family UCL139 at D16S3133. The D16S403-D16S3133 critical interval spans 2.8 cM which corresponds to a physical distance of 2.37 Mb.

Although no statistically significant evidence of a common disease associated haplotype amongst the families could be proven, three markers in the D16S403-D16S3133 interval did show a suggestion of linkage disequilibrium with a higher frequency of certain alleles on disease chromosomes compared to control chromosomes. The control data were taken from genotypes on the families’ obligate normal pedigrees. Haplotype analysis indicated the key recombinant events defining the critical region on chromosome 16p12.1-12.2 (fig 1A). A paternal recombination in family UCL98 at D16S403 defined the telomeric limit of the region. The centromeric limit was defined by a maternal recombination event in family UCL139 at D16S3133. The D16S403-D16S3133 critical interval spans 2.8 cM which corresponds to a physical distance of 2.37 Mb.

Although no statistically significant evidence of a common disease associated haplotype amongst the families could be proven, three markers in the D16S403-D16S3133 interval did show a suggestion of linkage disequilibrium with a higher frequency of certain alleles on disease chromosomes compared to control chromosomes. The control data were taken from genotypes on the families’ obligate normal pedigrees. Haplotype analysis indicated the key recombinant events defining the critical region on chromosome 16p12.1-12.2 (fig 1A). A paternal recombination in family UCL98 at D16S403 defined the telomeric limit of the region. The centromeric limit was defined by a maternal recombination event in family UCL139 at D16S3133. The D16S403-D16S3133 critical interval spans 2.8 cM which corresponds to a physical distance of 2.37 Mb.

Although no statistically significant evidence of a common disease associated haplotype amongst the families could be proven, three markers in the D16S403-D16S3133 interval did show a suggestion of linkage disequilibrium with a higher frequency of certain alleles on disease chromosomes compared to control chromosomes. The control data were taken from genotypes on the families’ obligate normal pedigrees. Haplotype analysis indicated the key recombinant events defining the critical region on chromosome 16p12.1-12.2 (fig 1A). A paternal recombination in family UCL98 at D16S403 defined the telomeric limit of the region. The centromeric limit was defined by a maternal recombination event in family UCL139 at D16S3133. The D16S403-D16S3133 critical interval spans 2.8 cM which corresponds to a physical distance of 2.37 Mb.

Although no statistically significant evidence of a common disease associated haplotype amongst the families could be proven, three markers in the D16S403-D16S3133 interval did show a suggestion of linkage disequilibrium with a higher frequency of certain alleles on disease chromosomes compared to control chromosomes. The control data were taken from genotypes on the families’ obligate normal pedigrees. Haplotype analysis indicated the key recombinant events defining the critical region on chromosome 16p12.1-12.2 (fig 1A). A paternal recombination in family UCL98 at D16S403 defined the telomeric limit of the region. The centromeric limit was defined by a maternal recombination event in family UCL139 at D16S3133. The D16S403-D16S3133 critical interval spans 2.8 cM which corresponds to a physical distance of 2.37 Mb.

Although no statistically significant evidence of a common disease associated haplotype amongst the families could be proven, three markers in the D16S403-D16S3133 interval did show a suggestion of linkage disequilibrium with a higher frequency of certain alleles on disease chromosomes compared to control chromosomes. The control data were taken from genotypes on the families’ obligate normal pedigrees. Haplotype analysis indicated the key recombinant events defining the critical region on chromosome 16p12.1-12.2 (fig 1A). A paternal recombination in family UCL98 at D16S403 defined the telomeric limit of the region. The centromeric limit was defined by a maternal recombination event in family UCL139 at D16S3133. The D16S403-D16S3133 critical interval spans 2.8 cM which corresponds to a physical distance of 2.37 Mb.

Although no statistically significant evidence of a common disease associated haplotype amongst the families could be proven, three markers in the D16S403-D16S3133 interval did show a suggestion of linkage disequilibrium with a higher frequency of certain alleles on disease chromosomes compared to control chromosomes. The control data were taken from genotypes on the families’ obligate normal pedigrees.

DISCUSSION
These results provide statistically significant support for loci for primary ciliary dyskinesia on chromosomes 16p12.1-12.2 and 15q13.1-15.1. Since primary ciliary dyskinesia is a genetically and clinically heterogeneous disorder the selection of patients with an identical ultrastructural phenotype and families from isolated populations should minimise the risk of genetic heterogeneity. The incidence of inbreeding is often high in these populations which may allow the application of homozygosity or linkage disequilibrium mapping to identify and refine the disease gene localisation. This is a powerful approach and has proved successful in mapping many autosomal recessive diseases including...
primary ciliary dyskinesia, even in the presence of heterogeneity. This study uses PCD family groups from two genetically isolated populations from the Faroe Islands and the Golan Heights Druze community, both of which were founded and have expanded relatively recently. There is significant enrichment for primary ciliary dyskinesia in both these populations presumably due to isolation and inbreeding, the incidence being around 1:4500 in the Faroe Islands and 1:1000 in the Druze population studied.

In both populations the initial assumption was that the existence of single ancestral Faroe Island or Druze mutation would account for all the patients in each group. However, in the current study such linkage disequilibrium has not been detected. At the Faroes locus no common haplotype was observed among the affected subjects even amongst families UCL96, UCL97, and UCL109, who may be interrelated, and the allele sharing observed was not statistically significant. Identification of linkage disequilibrium by additional marker typing at both loci would be useful to further refine the critical interval and pinpoint the localisation of the disease gene.

The extent of linkage disequilibrium encompassing a disease gene allele is dependent on course on a number of factors including natural selection and physical features such as the local recombination and gene conversion rate. Population scale effects include the population size, demographic and admixture history. A large population under mutation drift equilibrium displays low levels of linkage disequilibrium while high linkage disequilibrium correlates with a small population due to genetic drift. If the population is reduced, then allelic diversity is lowered and genetic drift is increased. Simulation studies on human populations predicts that slow early growth, such as that which occurred in the Faroe population, can be a key factor in increasing the extent of linkage disequilibrium in an isolated population.

The age of the disease and marker alleles can be regarded as one of the most important considerations; the exact timing of mutation drift equilibrium may have been eroded by ancient recombination. The extent of linkage disequilibrium in an isolated population displays low levels of linkage disequilibrium while high linkage disequilibrium correlates with a small population due to genetic drift. If the population is reduced, then allelic diversity is lowered and genetic drift is increased. Simulation studies on human populations predicts that slow early growth, such as that which occurred in the Faroe population, can be a key factor in increasing the extent of linkage disequilibrium in an isolated population.

The age of the disease and marker alleles can be regarded as one of the most important considerations; the exact timing of mutation drift equilibrium may have been eroded by ancient recombination. The extent of linkage disequilibrium in an isolated population displays low levels of linkage disequilibrium while high linkage disequilibrium correlates with a small population due to genetic drift. If the population is reduced, then allelic diversity is lowered and genetic drift is increased. Simulation studies on human populations predicts that slow early growth, such as that which occurred in the Faroe population, can be a key factor in increasing the extent of linkage disequilibrium in an isolated population.

The age of the disease and marker alleles can be regarded as one of the most important considerations; the exact timing of mutation drift equilibrium may have been eroded by ancient recombination. The extent of linkage disequilibrium in an isolated population displays low levels of linkage disequilibrium while high linkage disequilibrium correlates with a small population due to genetic drift. If the population is reduced, then allelic diversity is lowered and genetic drift is increased. Simulation studies on human populations predicts that slow early growth, such as that which occurred in the Faroe population, can be a key factor in increasing the extent of linkage disequilibrium in an isolated population.

The age of the disease and marker alleles can be regarded as one of the most important considerations; the exact timing of mutation drift equilibrium may have been eroded by ancient recombination. The extent of linkage disequilibrium in an isolated population displays low levels of linkage disequilibrium while high linkage disequilibrium correlates with a small population due to genetic drift. If the population is reduced, then allelic diversity is lowered and genetic drift is increased. Simulation studies on human populations predicts that slow early growth, such as that which occurred in the Faroe population, can be a key factor in increasing the extent of linkage disequilibrium in an isolated population.

The age of the disease and marker alleles can be regarded as one of the most important considerations; the exact timing of mutation drift equilibrium may have been eroded by ancient recombination. The extent of linkage disequilibrium in an isolated population displays low levels of linkage disequilibrium while high linkage disequilibrium correlates with a small population due to genetic drift. If the population is reduced, then allelic diversity is lowered and genetic drift is increased. Simulation studies on human populations predicts that slow early growth, such as that which occurred in the Faroe population, can be a key factor in increasing the extent of linkage disequilibrium in an isolated population.
A human syndrome caused by immotile cilia.


Schneider H, Bruckner M. Of mice and men: dissecting the genetic pathway that controls left-right asymmetry in mice and humans. Am J Med Genet 2000;97:258–70.


Venturin M, Guarneri P, Natacci F, et al. Mental retardation and cardiovascular malformations in NF1 microdeleted patients point to candidate genes in 17q11.2 (J Med Genet 2003;41:35–41). We would like to offer our sincere apologies to the authors of this paper for a number of errors that were introduced regarding the incorrect use of the term “learning disability”. The instances of “learning disability” in the Key points box, and in Tables 1 and 2 should be “mental retardation”. These errors are much regretted and the corrected versions are shown here.
Table 2  Clinical features of the 14 newly described patients carrying NF1 microdeletion characterised by refined fluorescent in situ hybridisation (FISH) analysis

<table>
<thead>
<tr>
<th>Patient</th>
<th>Age (years)</th>
<th>Sex</th>
<th>Deletion type</th>
<th>Growth defects</th>
<th>Dysmorphic</th>
<th>Mental retardation</th>
<th>Cardiovascular malformation</th>
<th>Other features</th>
</tr>
</thead>
<tbody>
<tr>
<td>119</td>
<td>4</td>
<td>M</td>
<td>REP</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>118</td>
<td>5</td>
<td>M</td>
<td>cen-REP</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>93</td>
<td>6</td>
<td>M</td>
<td>REP</td>
<td>No*</td>
<td>Yes†</td>
<td>IQ48</td>
<td>VSD (upper part)</td>
<td>–</td>
</tr>
<tr>
<td>65</td>
<td>6</td>
<td>M</td>
<td>REP</td>
<td>Short stature 10th centile</td>
<td>Yes‡</td>
<td>IQ54</td>
<td>Mitral insufficiency</td>
<td>MCLS, kyphoscoliosis, pectus excavatum, genu valgus, pes planus, umbilical hernia</td>
</tr>
<tr>
<td>72</td>
<td>7</td>
<td>M</td>
<td>REP</td>
<td>No</td>
<td>Yes‡</td>
<td>–</td>
<td>IQ50</td>
<td>–</td>
</tr>
<tr>
<td>76</td>
<td>8</td>
<td>F</td>
<td>REP</td>
<td>No</td>
<td>Yes*</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>94</td>
<td>8</td>
<td>F</td>
<td>REP</td>
<td>No</td>
<td>Yes**</td>
<td>No</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>75</td>
<td>9</td>
<td>F</td>
<td>REP</td>
<td>No</td>
<td>Yes††</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>85</td>
<td>11</td>
<td>M</td>
<td>REP</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>7</td>
<td>11</td>
<td>M</td>
<td>REP</td>
<td>No</td>
<td>Yes††‡</td>
<td>Speech impairment</td>
<td>–</td>
<td>MCLS</td>
</tr>
<tr>
<td>82</td>
<td>23</td>
<td>F</td>
<td>REP</td>
<td>Short stature 9th centile</td>
<td>No</td>
<td>–</td>
<td>Hearing impairment, Noonan-like</td>
<td>–</td>
</tr>
<tr>
<td>77</td>
<td>U</td>
<td>F</td>
<td>REP</td>
<td>Overgrowth ≥97th centile</td>
<td>Yes††‡</td>
<td>Speech impairment,</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>78</td>
<td>U</td>
<td>F</td>
<td>REP</td>
<td>–</td>
<td>Yes***</td>
<td>Speech impairment</td>
<td>–</td>
<td>Delayed motor development, short and broad feet, fifth finger clinodactyly</td>
</tr>
</tbody>
</table>

*Hypertelorism, epicanthic folds, low set ears, low posterior hairline.
†Hypertelorism, downslanting eye, strabismus, large and prominent nose with high and broad bridge, bulbous nasal tip, large and low set ears, malar hypoplasia, wide and prominent philtrum, small mouth, small pointed chin.
‡Prominent forehead, hypertelorism, ptosis (O.DX), downslanting eyes; strabismus, large and prominent nose with high and broad bridge and bulbous nasal tip, large and low set ears, wide and prominent philtrum, low posterior hairline.
*Coarse face, hypertelorism.
**Epicanthic folds, broad and wild nasal bridge, broad nasal tip.
††Epicanthic folds, bulbous nose, narrow high palate, low forehead.
†‡Simple facial features.
**Epicanthic folds, bulbous nose, narrow high palate, low forehead.

<table>
<thead>
<tr>
<th>Clinical signs</th>
<th>Growth defects</th>
<th>Dysmorphic</th>
<th>Mental retardation</th>
<th>Cardiovascular malformation</th>
<th>Other features</th>
</tr>
</thead>
<tbody>
<tr>
<td>Growth defects</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Dysmorphic</td>
<td>–</td>
<td>Yes†</td>
<td>No</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Mental retardation</td>
<td>Yes††</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Cardiovascular malformation</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>MCLS</td>
</tr>
<tr>
<td>Other features</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>MCLS</td>
<td>–</td>
</tr>
<tr>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

Key points

- NF1 microdeletion syndrome is determined by haplo-insufficiency of the NF1 gene and its flanking regions; NF1 microdeleted patients show a more severe phenotype than observed in classical NF1 patients.
- The aim of this study was to verify the presence of specific clinical signs of NF1 microdeletion, by combining clinical and genetic evidence from 92 deleted patients, 14 newly characterised and 78 already published.
- Statistical analysis, done by comparing the frequency of 10 clinical signs between NF1 microdeleted patients and the whole NF1 population, showed that the most common extra-NF1 clinical signs in microdeleted patients were mental retardation, cardiovascular malformations, and dysmorphisms.
- Using bioinformatic tools, the deletion gene content of 44 genetically and clinically characterised patients was established. It is proposed that haploinsufficiency of OMG and/or CDK5R1 genes may be implicated in mental retardation. In relation to cardiovascular malformations, only JJAZ1 and CENTA2 can be considered as plausible candidate genes.
- When present in an NF1 patient, dysmorphisms, cardiac anomalies, and mental retardation are signs indicating NF1 microdeletion.
CORRECTION

J Med Genet 2004 41: 239-240
doi: 10.1136/jmg.2003.014761corr1

Updated information and services can be found at:
http://jmg.bmj.com/content/41/3/239

These include:

Email alerting service
Receive free email alerts when new articles cite this article. Sign up in the box at the top right corner of the online article.

Notes

To request permissions go to:
http://group.bmj.com/group/rights-licensing/permissions

To order reprints go to:
http://journals.bmj.com/cgi/reprintform

To subscribe to BMJ go to:
http://group.bmj.com/subscribe/