Recurrent reciprocal deletions and duplications of 16p13.11: the deletion is a risk factor for MR/MCA while the duplication may be a rare benign variant

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ABSTRACT
Background: Genomic disorders are often caused by non-allelic homologous recombination between segmental duplications. Chromosome 16 is especially rich in a chromosome-specific low copy repeat, termed LCR16.

Methods and Results: A bacterial artificial chromosome (BAC) array comparative genome hybridisation (CGH) screen of 1027 patients with mental retardation and/or multiple congenital anomalies (MR/MCA) was performed. The BAC array CGH screen identified five patients with deletions and five with apparently reciprocal duplications of 16p13 covering 1.65 Mb, including 15 RefSeq genes. In addition, three atypical rearrangements overlapping or flanking this region were found. Fine mapping by high-resolution oligonucleotide arrays suggests that these deletions and duplications result from non-allelic homologous recombination (NAHR) between distinct LCR16 subunits with >99% sequence identity. Deletions and duplications were either de novo or inherited from unaffected parents. To determine whether these imbalances are associated with the MR/MCA phenotype or whether they might be benign variants, a population of 2014 normal controls was screened. The absence of deletions in the control population showed that 16p13.11 deletions are significantly associated with MR/MCA (p = 0.0048). Despite phenotypic variability, common features were identified: three patients with deletions presented with MR, microcephaly and epilepsy (two of these had also short stature), and two other deletion carriers ascertained prenatally presented with cleft lip and midline defects. In contrast to its previous association with autism, the duplication seems to be a common variant in the population (5/1682, 0.29%).

Conclusion: These findings indicate that deletions inherited from clinically normal parents are likely to be causal for the patients' phenotype whereas the role of duplications (de novo or inherited) in the phenotype remains uncertain. This difference in knowledge regarding the clinical relevance of the deletion and the duplication causes a paradigm shift in (cyto)genetic counselling.

Non-allelic homologous recombination (NAHR) between neighbouring intrachromosomal segmental duplications (also termed low copy repeats, or LCRs) is the main mechanism underlying genomic disorders. Several recurrent clinical syndromes are caused by either gains or losses of sequences flanked by segmental duplications. Since the initial discovery that Charcot–Marie–Tooth disease and HNPP (hereditary neuropathy with liability to pressure palsies) are caused by the duplication and the reciprocal deletion at 17p11.2, respectively, many other recurrent clinical syndromes have been shown to be caused by NAHR. The finding that around 4% of the human genome is made up of intrachromosomal segmental duplicons led to speculation that many more unrecognised recurrent rearrangement syndromes might exist. The advent of array comparative genome hybridisation (CGH) has enabled genome-wide screening for copy number variations (CNVs) in large patient populations leading to the identification of several novel low copy repeat-mediated rearrangements.

Chromosome 16 is especially rich in intrachromosomal segmental duplications. During recent primate evolution, chromosome 16 has undergone intense segmental duplication activity, and >10% of the euchromatic region of the p arm is composed of highly complex low copy repeats. During evolution, these blocks were generated in a stepwise fashion, generating multiple subunits termed LCR16a–t, with a size range of 20–600 kb and sharing >97% sequence similarity. The complex architecture of chromosome 16p therefore suggests it as an excellent candidate region for novel microdeletion syndromes. Recently, Ballif et al reported a novel microdeletion syndrome of 16p11.2–p12.2, which seems to be mediated by NAHR between 16p segmental duplicons. In addition to this novel syndrome, various studies analysing CNVs in patients with mental retardation and/or multiple congenital anomalies (MR/MCA) have reported imbalances of 16p13. However, the relevance of these findings remains unclear.

During the screening of 1027 patients with MCA and/or MR, we identified 6 deletions and 7 duplications of 16p12–p13, apparently caused by NAHR between LCR16. Our detailed analyses of these imbalances define 16p13.11 as a region of recurrent microdeletion/duplication and suggest that the deletion is a risk factor for MR/MCA but the clinical relevance of the duplication is uncertain.

METHODS
Selection of patients
This study involved patients with MR/MCA, ascertained from three sources: (1) those diagnosed by the clinical geneticist of Leuven, Belgium (n = 500), (2) children and young adults from a variety of UK clinical genetics centres, community learning disability teams and other sources,
including hospital neuropediatricians (n = 372), and (3) DNA from autopsies of fetuses with ≥1 congenital anomalies at Children’s Hospital and Regional Medical Center (Seattle, WA) after death or elective termination (n = 155). All were reported to have a normal karyotype at 550 G-band resolution, and in many cases cryptic subtelomeric rearrangements and other specific genetic abnormalities had been excluded.

Array comparative genome hybridisation

Patients were analysed using two different bacterial artificial chromosome (BAC) array CGH platforms. Patient samples from Leuven, Belgium (n = 500) were hybridised to a custom BAC array with clones spaced at approximately 1 Mb intervals throughout the genome, according to the protocol of Menten et al. Regions were scored as CNVs if one clone passed the threshold of 4 x the normal standard deviation (SD), and if ≥2 flanking clones passed the threshold of log2(3/2)−2 x SD. Patient samples from the UK (n = 372) and USA (n = 155) were hybridised to a custom BAC array consisting of ~2000 clones targeted to regions of the genome flanked by segmental duplications. Regions were scored as CNVs if the log2 ratio of ≥2 consecutive clones each exceeded 2 x SD of the autosomal clones in dye-swap replicate experiments.

An additional patient with a 16p13.11 duplication was identified by array CGH to human 105K genome-wide oligonucleotide arrays (Agilent Technologies, Diegem, Belgium) according to the manufacturer’s instructions. In brief, genomic DNAs from the patient and from a single sex-matched reference patient were separately double-digested using the restriction endonucleases AluI and Rsal (Promega, Leiden, The Netherlands) and purified using Microcon centrifugal filter devices (Millipore Corporation, Missouri, Minneapolis, USA). Then 1.5 µg of the digested products were differentially labelled by random priming with Cy3-dUTP and Cy5-dUTP (Perkin Elmer, Foster City, California, USA) and cohybridised to the array for 48 hrs at 65°C in a rotating oven. Parental DNAs were also hybridised using this method. The hybridised arrays were washed and scanned (Microarray Scanner; Agilent). Image data were extracted using Feature Extraction V.8.5 software (Agilent) and the data analysed using CGH Analytics V.5.4 software (Z-score method setting; Agilent).

To refine the breakpoints of these rearrangements, we utilised oligonucleotide arrays. One oligoarray consisting of 385 000 isothermal custom made probes (length 45–75 bp) covering a number of chromosomal regions, including this 5 Mb region of chromosome 16p (mean density, 1 probe per 131 bp) (NimbleGen Systems, Madison, Wisconsin, USA). Hybridisations were performed as described previously, and samples from a single normal man were used as the reference (GM15724; Coriell, Camden, New Jersey, USA).

The second oligoarray used (GeneChip Human Mapping 262K NspI; Affymetrix, Santa Clara, California, USA) contains 262 264 25 oligonucleotides. In this experiment, 250 ng genomic DNA was processed according to the manufacturer’s instructions (Affymetrix GeneChip Human Mapping 500K Manual; http://www.affymetrix.com). Copy number was assessed using DNA-Chip Analyzer (dChip) software 2006. Regions of copy number gain and loss were found using the hidden Markov model output of dChip.

Real-time quantitative PCR

Real-time quantitative PCR (qPCR) was performed as previously described with minor modifications. Primers were designed from RepeatMasker sequence (www.repeatmasker.org/) using Primerexpress V.2.0.0 oligo design software (Applied Biosystems, Lennik, Belgium), and validated with in silico PCR and genome searching using Blat software (http://genome.ucsc.edu/). Single-nucleotide polymorphisms (SNPs) were excluded from the primer sequence (SNP track in UCSC Browser). Real-time qPCR was performed using a commercial preparation (Q-PCR MasterMix Plus for SYBR Green 1 withoutUNG (uracil-N-glycosylase); Eurogentec, Liege, Belgium) according to the manufacturer’s instructions. Each reaction was performed in duplicate in a final volume of 15 µl containing 6–30 ng/µl genomic DNA, 1.25 µM forward/reverse primer, and 7.5 µl SYBR Green mastermix.

Control populations

The first control population comprised 722 unrelated individuals from Belgium who had been referred for clinical genetic testing for haemochromatosis or cystic fibrosis. Genomic DNA of each individual was extracted from blood lymphocytes according to standard procedures, and assayed by real-time qPCR using primer pair 3 (Eurogentec, Seraing, Belgium) for detection of copy number changes of 16p13.1. Thresholds were set at a fold difference of 0.8 and 1.3. All samples surpassing these thresholds were analysed twice to confirm the presence of copy number changes.

A second control population, comprising 960 unrelated Caucasian adults (age 40–70 years) from the USA, were genotyped using a chip array (HumanHap300 Genotyping BeadChips; Illumina, San Diego, California), comprising ~317 000 HapMap SNPs distributed throughout the genome. Each individual was enrolled in the Pharmacogenomics and Risk of Cardiovascular Disease (PARC) study, which aims to identify genetic contributors to the variable efficacy of statin drugs on cardiovascular disease risk (http://www.pharmgkb.org/do/serve?objId=58&objCIs=Project). Hybridisations, data analysis and copy number analysis, focused on this region of 16p, were performed according to published protocols.

CASE REPORTS

Patients carrying 1.65 Mb 16p13.11 deletions

Patient 1 (ID 224725)

This adult patient is the only affected member of five siblings. She has severe MR, therapy-resistant epilepsy and behavioural problems. She has short stature (143 cm, less than third percentile (P3) of 155 cm) and microcephaly (occipitofrontal circumference (OFC) 51 cm; P3 = 52.2 cm). She has short nose, smooth philtrum, wide mouth and fine palpebral fissures. She has difficulty in expressive language and has an ataxic gait.

Patient 2 (ID 335606)

This adult proband and his brother were referred with severe MR. The proband has short stature (150 cm; P3 = 168 cm), microcephaly (OFC 51 cm; P3 = 52.2 cm), pectus excavatum and limb spasticity. He is being treated for epilepsy.

Patient 3 (ID 22698)

This adult man with moderate MR is the only child of non-consanguineous parents. His stature and OFC are normal and he is obese (105 kg; >P97). He is not dysmorphic, is extremely talkative, and displays intermittent verbal aggression and self-mutilation.
Patients carrying 1.65 Mb 16p13.11 duplications

Patients carrying larger atypical 16p13.11 rearrangements

RESULTS

Recurrent microdeletion/duplication of 16p13.11
patients with deletions, NDE1 was believed to be a good candidate for a dosage-sensitive gene that might underlie the features of these deletions. In order to test the hypothesis that the deletion acts by unmasking the presence of a recessive mutation on the remaining allele, we sequenced the NDE1 gene in four of our patients with deletions (1–4). Primers covering all eight exons and the 5′ and 3′ untranslated regions (supplementary table 1 online) were used for direct sequencing of genomic DNA, but no mutations were found.

The microdeletion associates with the MR/MCA phenotype

Although neither 16p13.11 duplications or deletions have been found in 210 unrelated HapMap individuals,20 nor in 122 other individuals sampled from the normal population,10,20,21 a larger and population matched sample size was needed in order to draw a statistically meaningful conclusion as to their pathogenic significance. Therefore, the copy number of the commonly rearranged 16p13.1 region in 722 population matched controls ascertainment from the Belgian population, and in a further 960 Caucasian controls drawn from the USA, were evaluated. These analyses did not detect any deletions of this region in the 1682 controls tested, but did reveal the presence of five 16p13.11 duplications. Although we do not have access to detailed clinical information for these five controls, the method used to ascertain them suggests that they are unlikely to have significant developmental abnormalities, but we cannot exclude possibility that they might have abnormal learning, memory or behavioural characteristics. Combining these data with previously published analysis of 532 controls results in a total control population of 2014, including 5 carriers of 16p13.1 duplications, but no carriers of deletions. This compares with 5 deletions and 7 duplications ascertained from 1027 patients with MR/MCA. We therefore conclude that deletions of 16p13.1 are significantly associated with patient phenotype (p = 0.0048, Pearson x² test with simulated p value, based on 10 000 replicas), but show incomplete penetrance, as demonstrated by their presence in some apparently unaffected relatives. The incidence of duplications in association with disease is not significantly different from that in controls (p = 0.1273, Pearson’s x² test). This observation leads us to a number of possible conclusions regarding the duplication including that it might (1) be truly clinically benign, (2) be...
DISCUSSION

We describe five patients carrying identical 1.65 Mb deletions of 16p13.11 encompassing 15 genes. In addition, we found five patients carrying apparently reciprocal duplications of this same region. The rearrangement breakpoints are located in low copy repeats implying that non-allelic homologous recombination between these flanking LCRs mediates these rearrangements. Three further patients presenting with larger atypical rearrangements showed breakpoints that also mapped to clusters of LCR16.

Despite careful parental analysis, observations of rearrangements of 16p13.11 make it difficult to distinguish between disease-causing events (generally presumed to be de novo) and benign variants (that do not contribute to a phenotype). Two deletions and one duplication were found to be inherited from an apparently normal parent, and another duplication was inherited from a clinically mildly abnormal parent. Conversely, we also found a duplication that occurred de novo. Previous studies have reported 16p13.11 deletions occurring both de novo and by inheritance from a normal parent, while duplications were reported to be inherited from normal parents in two families.22 23 One interpretation of these observations could be that rearrangements of this region are benign variants, and that the observed phenotypes are coincidental with the presence of the imbalance. However, one case–control study reported a significantly higher incidence of the del16p13.11 in patients with MR/MCA, implying that the del16p13.11 is a risk factor contributing to the MR/MCA phenotype. The duplication is present in equal frequency in the normal and the patient population, indicating this variant is compatible with a normal phenotype. The identification of this dup16p13.11 in a patient with fragile X (patient 9) in our study lends support to this hypothesis. Recently, Ullmann et al24 reported three carriers of dup16p13.11 in a cohort of 182 people with autism. Because the duplication was found in 5 out of 2014 normal participants in our study, the duplication seems overrepresented in the autistic population (p = 0.023, Fisher exact test). More studies are needed to strengthen this association.

Three of the four adult patients with 16p13.11 deletions had both microcephaly and seizures, and the two fetuses with the deletions had brain anomalies, one of which also had relative microcephaly. The same three adult patients also have small stature. Small stature and dysmorphic features were also a feature of one of the patients described by Ullman et al.11 In contrast, our fourth adult patient and a previously described deletion carrier25 had normal head circumference (55.3 cm), while one previously reported patient had macrocephaly.11 Although the typical 16p13.11 duplication may be a benign variant, it is striking that four of our duplication carriers not only presented with MR but also behavioural problems. Similarly, members of two of three families with duplications reported by Ullman et al11 had similar behavioural problems. Although we do not have data on the behavioural phenotypes of all patients with MR/MCA tested using the arrays, the occurrence of this type of behaviour in this patient population seems higher than average, and hence, it seems plausible that dup16p13.11 carriers may have a predisposition for aggressive behaviour.

To date, most genomic imbalances have been classified as either benign or pathogenic and most microdeletion syndromes are presumed to be well-defined clinical conditions. However, even well-known genomic disorders can be phenotypically heterogeneous and more variable than originally thought, owing to incomplete penetrance or variable expression. The variability

Atypical rearrangements of chromosome 16p12–p13

In addition to the common recurrent 1.65 Mb microdeletion/duplication of 16p13.11 observed in 10 patients, 3 atypical rearrangements were found. Two patients (11 and 12) carried a larger duplication of ~3.4 Mb in size, overlapping the typical duplication. The distal breakpoint of these atypical duplications was located between 15.0–15.4 Mb and the proximal breakpoint was located within a third LCR16 cluster (18.3–18.4 Mb). Results of real-time qPCR with primer pair 2 (supplementary table 2 online) were normal whereas the results using primer pair 3 showed the presence of a duplication (fig 2). This result confirms that the duplication starts in a more proximal LCR16 than the typical duplication. This duplicated region includes 12 RefSeq genes. The normal mother of patient 11 was found to be a carrier of this same duplication.

One further patient (patient 15) carried a 1.6–2.1 Mb deletion that flanked the common rearrangement region. This atypical deletion had its distal breakpoint in the second cluster and its proximal breakpoint in the third LCR16 cluster. The region includes 2 RefSeq genes. This imbalance was inherited from a phenotypically normal mother. A summary of all 13 rearrangements found is shown in table 1.

Figure 2  Real-time quantitative PCR results with different primer sets flanking the breakpoint regions. (A) In all individuals carrying the common deletion/duplication (patients 1–10), the distal breakpoints occur between primers pp1 and pp2, and the proximal breakpoint is defined by primers pp4 and pp5. (B) The extent of the atypical duplication and deletion identified in patients 11 and 13 were delineated by primersets pp2/pp3 and pp4/pp5, respectively, for distal breakpoints and between pp6 and pp7 for the proximal breakpoint. The presence of two copies for a locus was defined by a fold difference of 1 whereas a fold difference of 0.5 or 1.5 corresponds to a deletion or a duplication, respectively.
of the del22q11 phenotype originally led to their different clinical classification as DiGeorge syndrome (heart and thymus defects) (OMIM 188400), Sprintzen syndrome (speech difficulties) or velocardiofacial syndrome (VCFS) (conotruncal anomaly face) (OMIM 192430). Recently, several reports have been published about atypical patients with 22q11 deletions. 24 25 Equally, in dup22q11 carriers, the phenotype may range from severe MR through to completely unaffected, and various minor developmental anomalies are noted. 26 27 In addition, 22q11 duplications can be inherited from apparently normal parents.26 28 Therefore, it is possible that 16p13.11 duplications might also be causative and the heterogeneous phenotype of our patients explained in part by (1) the unbiased selection criteria, (2) variability due to other genetic or possibly environmental determinants, (3) incomplete penetrance, (4) variable expression or (5) unmasking of recessive alleles.29 In particular, owing to the presence of del16p13.11 in a normal parent of one of our probands, we set out to test the latter hypothesis. Because microcephaly was observed in two of the three adult patients with typical deletions and in one of the two fetuses with deletion, NDE1 was considered an excellent candidate gene for this phenotype. NDE1 is strongly expressed in brain, 30 and forms complexes with LIS1, a dosage-sensitive gene that is crucial for neuronal migration and cerebral development, and that is known to underlie Miller–Dieker lissencephaly syndrome (OMIM 247200). Furthermore, Nde1-null mice show microcephaly.31 However, sequencing of all exons of NDE1 in four patients with deletions did not reveal any mutation on the remaining allele, suggesting that this is not the mechanism responsible for the phenotype in our patients. Another plausible candidate gene is NTAN1 (asparagine-specific N-terminal amidase). Mouse models deficient for this enzyme showed alterations in activity, social behaviour and memory.32 However although this region is reported in the Redon database (http://projects.tcag.ca/variation/) to have CNVs, learning and memory defects and aberrant social behaviour could not be excluded among controls and therefore the NTAN1 gene remains a good candidate gene.

Imprinting is a mechanism that could potentially explain the presence of these rearrangements in unaffected relatives. 11 However, there are no known imprinted genes on chromosome 16 (http://www.geneimprint.com/site/genes-by-species). Furthermore, for both deletions and duplications of 16p we observed the inheritance of these imbalances from normal parents through both the maternal and paternal germ lines, indicating that imprinting does not significantly influence patient phenotype of this disorder.

In addition to the common 1.65 Mb rearrangement observed in the 10 patients reported here, 3 ‘‘atypical’’ chromosomal imbalances either overlapping or flanking this common region were found in patients with MR/MCA. Breakpoints for all three imbalances were also located within LCR16 sequences. However, the atypical 3.4 Mb duplication seems to be mediated by different LCR16s compared with the atypical deletion. Therefore, the complex structure of the LCR16s in this region seems to be involved in generating a variety of different chromosomal

**Figure 3** Detection of 16p12–p13 imbalances defined by the 262k NspI SNP array. Data from the common 16p13.11 1.65 Mb rearrangements are shown. Each plot has physical probe position on 16p (x-axis) against probe intensity ratio (y-axis). Red shading, common deleted region; green shading, duplication in patients 1–4, 6 and 7. Chr, chromosome.
rearrangements. The finding of variably sized rearrangements on chromosome 16p is similar to that observed for other recurrent genomic disorders, such as the Prader–Willi/Angelman syndrome, Smith–Magenis syndrome, and the 15q24 deletion syndrome, in which recombination within alternate LCRs can result in recurrent deletions and duplications of different sizes.

Figure 4  High-resolution oligonucleotide array mapping of seven 16p12.3–p13.11 rearrangements, of which four have a common distal breakpoint (14.7–14.75 Mb). For those four patients with the common 1.65 Mb rearrangement (red shading), the proximal breakpoints also map to a second LCR16 cluster (16.3–16.77 Mb). Another three patients have an atypical rearrangement: patients 11 and 12 show an atypical larger duplication, with the distal breakpoint between 15.0–15.4 Mb and the proximal breakpoint located within a third LCR16 cluster (18.3–18.4 Mb), and patient 13 has an atypical deletion with proximal breakpoint in the third LCR16 cluster and distal breakpoint in the second cluster. Data from normal control individuals show that there is marked copy number variation in the LCR16 clusters that define these three breakpoint regions. Note that the high degree of homology between these LCR16s also results in false-positive signals from probes that are identical to those within the true deletion/duplication in patients 5, 8 and 9. The image has a 5 Mb region of 16p12–p13 (chr16:14 000 000–19 000 000). For each individual, deviations of probe log2 ratios from zero are depicted by grey/black lines, with those exceeding a threshold of 1.5 SD from the mean probe ratio shown in green and red to represent relative gains and losses, respectively. Segmental duplications of increasing similarity (90–98%, 98–99%, and >99%) are represented by grey/yellow/orange bars, respectively.
Table 1 Genotype–phenotype correlation of patients with deletion or duplication of 16p12–p13

<table>
<thead>
<tr>
<th>Patient (Deciphercode)</th>
<th>Phenytype</th>
<th>Pattern of inheritance</th>
<th>Type of imbalance</th>
<th>Distal breakpoint (Mb)</th>
<th>Proximal breakpoint (Mb)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (CHG00002371)</td>
<td>Moderate MR, norm stature (183 cm), microcephaly (51 cm), epispy, ataxia</td>
<td>Parents not available for testing</td>
<td>Deletion</td>
<td>14.7–14.75</td>
<td>16.3–16.77</td>
</tr>
<tr>
<td>2 (CHG00002372)</td>
<td>Severe MR, short stature (150 cm), microcephaly (51 cm), pectus excavatum, limb spasticity</td>
<td>Parents not available for testing</td>
<td>Affected brother does not carry deletion</td>
<td>14.7–14.75</td>
<td>16.3–16.77</td>
</tr>
<tr>
<td>3 (CHG00002374–)</td>
<td>Moderate MR, normal stature (183 cm), normal head circumference (55.3 cm), behavioural problems</td>
<td>Parents not available for testing</td>
<td>14.7–14.75</td>
<td>16.3–16.77</td>
<td></td>
</tr>
<tr>
<td>4 (CHG00001230)</td>
<td>Term fetus; autopsy showed holoprosencephaly, nose agenesis, midline upper lip notch, midline cleft palate, dysplastic external ear and atretic auditory canal on right, preauricular skin tags bilaterally, relative microphalpy</td>
<td>Phenotypically normal father carries deletion</td>
<td>14.7–14.75</td>
<td>16.3–16.77</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>Fetus at 21 weeks; autopsy showed post-hemorrhagic hydrocephalus with marked ventriculomegaly, cortical thinning, hypoplastic falx cerebri, cleft lip on right, two preauricular skin tags on right, and cleft T1 and T3 vertebral bodies. Physical growth parameters were consistent with gestational age</td>
<td>Parents not available for testing</td>
<td>14.7–14.75</td>
<td>16.3–16.77</td>
<td></td>
</tr>
<tr>
<td>6 (CHG00001046)</td>
<td>Moderate MR, normal stature (176 cm), normal head circumference (57.4 cm), behavioural problems, Hirschsprung disease</td>
<td>Mother does not carry duplication</td>
<td>Duplication</td>
<td>14.7–14.75</td>
<td>16.3–16.77</td>
</tr>
<tr>
<td>7 (LEI)00002370</td>
<td>MR, mild developmental delay, learning disabilities. Originally reported by Kriek et al.</td>
<td>de novo imbalance</td>
<td>14.7–14.75</td>
<td>16.3–16.77</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>Severe learning disabilities with limited use of language, poor vocabulary and repetitive speech, epilepsy. Challenging, agitated behaviour marked by shouting, hand-clapping, kicking, hitting and throwing objects at people, although this has improved with age</td>
<td>Phenotypically normal father carries duplication</td>
<td>14.7–14.75</td>
<td>16.3–16.77</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>Moderate developmental delay, behavioural problems (increased impulsivity, limited attention span). Large simple ears, thick lips, large tongue, large puffy hands and small nails. Also has an expansion of the PAX6A1 triplet repeat</td>
<td>Parents not available for testing</td>
<td>14.7–14.75</td>
<td>16.3–16.77</td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>Microcephaly found at 20 weeks gestation. At 4 years of age OFC 44 cm (P3 = 48.6 cm). Brachycephaly, telecanthus, abnormal eyebrows, deep set eyes, epicanthic folds, pinched nasal tip, prominent nose, small jaw, VSD, umbilical hernia, deep palmar and plantar creases, speech delay, hyperactive behaviour with aggressive episodes. Mother has small head (no OFC)</td>
<td>Mother with mild phenotype carries the duplication</td>
<td>14.7–14.75</td>
<td>16.3–16.77</td>
<td></td>
</tr>
<tr>
<td>11 (CHG00000993)</td>
<td>Feeding and respiratory problems as neonate. Asymmetric face with left facial nerve paresis, short neck with reduced mobility, bilateral epicanthal folds, strabismus, choroid colobomata, atresia of right choanae, ASDII, unique right kidney with double ureters, aplasia of semicircular canals, abnormal middle ear bones</td>
<td>Phenotypically normal mother carries duplication</td>
<td>Duplication</td>
<td>15.1–15.4</td>
<td>18.05–18.45</td>
</tr>
<tr>
<td>12</td>
<td>MR, multiple congenital anomalies. Originally reported by Sharp et al.</td>
<td>Parents not available for testing</td>
<td>Phenotypically normal mother carries deletion</td>
<td>15.1–15.4</td>
<td>18.3–18.5</td>
</tr>
<tr>
<td>13 (CHG00002373)</td>
<td>Marked developmental delay, IQ = 38, short stature (150 cm), microcephaly (50,5 cm), neonatal seizures</td>
<td>Parents not available for testing</td>
<td>Deletion</td>
<td>16.3–16.77</td>
<td>18.3–18.4</td>
</tr>
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</table>

MR, mental retardation; OFC, occiptofrontal circumference.

In conclusion, we report a novel genomic disorder likely caused by NAHR between copies of LCR16. Although in some cases this is inherited from a normal parent, we found a strong association of the deletion with developmental disorders. Reciprocal duplications were observed as both inherited and de novo events, and were also identified in several controls, suggesting that the duplication by itself confers either no phenotype at all or a range of phenotypes of varying severity. Alternatively, the duplication may require additional predisposing factors to have a phenotypic effect. Our findings have important implications for genetic counseling. Traditionally, chromosomal imbalances inherited from a normal parent were considered benign, while de novo chromosomal imbalances were considered pathogenic. Although our results suggest that the inherited 16p13.11 deletion is likely causal for the phenotype, the clinical significance of both de novo and inherited duplications remains uncertain and they may be benign variants. The study of additional patients and normal individuals with 16p13.11 rearrangements is required to reinforce this hypothesis and to obtain better insight in the potential pathology associated with the observed microdeletion and microduplication events.

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Acknowledgements: We are grateful to Dr R Krauss and the PARC project for the use and analysis of Illumina SNP genotyping data, the MicroArray Facility, Flanders Interuniversity Institute for Biotechnology (VIB) for their help in the spotting of the arrays and the Mapping Core and Map Finishing groups of the Wellcome Trust Sanger Institute for the initial clone supply and verification. We also thank Dr A Khan


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