Submicroscopic duplication in Xq28 causes increased expression of the MECP2 gene in a boy with severe mental retardation and features of Rett syndrome

M Meins, J Lehmann, F Gerresheim, J Herchenbach, M Hagedorn, K Hameister, J T Epplen

Rett syndrome is an X linked mental retardation syndrome almost exclusively affecting girls, and has long been regarded as an X linked dominant condition lethal in hemizygous males.1 Mutations in the gene encoding the methyl-CpG binding protein 2 (MECP2) were demonstrated as the cause of Rett syndrome,2 and confirmed by a number of studies. The vast majority (95%) of MECP2 mutations occurs de novo. Girls affected by “classic” Rett syndrome show mental retardation and regression, with a typical pattern of symptoms including initially normal development, stagnation, loss of acquired abilities, stereotypic hand movements, regression of speech, profound psychomotor retardation, epilepsy, and autism, although molecular diagnostics has proven that variant clinical forms exist.3-4

It has recently been shown that missense mutations in MECP2 can cause severe neonatal encephalopathy in boys.5 Classic Rett phenotypes in boys have so far only been reported in rare cases of somatic mosaicism or XXY karyotypes.6-11 In girls, larger intragenic deletions are responsible for about 11–16% of typical Rett syndrome without point mutations in the coding exons.12-13 Larger deletions have not yet been found in boys, and duplications of MECP2 have not yet been reported as a cause for typical Rett syndrome at all. We have established quantitative PCR for diagnosis of deletions affecting MECP2, and in this paper, we report a boy manifesting clinical features of Rett syndrome and a submicroscopic duplication within the cytogenetic band Xq28 encompassing the entire MECP2 gene.

CLINICAL FEATURES

The boy is the second child of healthy, unrelated parents, whose older brother had developed normally. There is no family history of mental retardation or developmental disorders. The patient was born in the 41st week after an uneventful pregnancy. Birth was spontaneous but with protracted labour (birth weight 3940 g, length 54 cm, head circumference 36.2 cm). Head growth was normal and did not decelerate (head circumference 54.5 cm at 7.5 years), but growth of length was retarded (length 117 cm at 7.5 years). Psychomotor development was retarded from birth. Initially, reduced movements, muscular hypotonia, and insufficient weight gain were noticed. The patient could not turn at the age of 15 months, and could not sit up until the age of 4 years. The first stereotypic hand movements were noticed at the age of 4 years. At the age of 6 years, he was crawling and able to walk a few steps with assistance. He was able to hold things and play with toys, but showed gradual loss of purposeful hand use around the same age. There was no spasticity or fixed scoliosis. The patient never learned to speak, but made babbling sounds to communicate basic needs.

During the first hospitalisation at the age of 10 months, magnetic resonance imaging (MRI) showed mildly enlarged inner and outer liquor spaces, but no retardation of myelination. In the following years, thorough screening for metabolic disorders including liquor tests revealed normal results. No signs of energy metabolism disorders, organoacidopathies, aminoacidopathies, peroxisomal or lysosomal disorders, or storage disorders were detected. There was no organomegaly. Ophthalmological examination showed mild...
hyperopia, but no retinopathy or optic atrophy. Nerve conduction velocities and electromyogram were normal. Owing to insufficient weight gain, a gluten enteropathy was suspected at the age of 1 year. A gluten free diet has been followed since then, although gliadin antibodies had not been found and enteroscopy had never been carried out to verify the diagnosis. Weight normalised gradually, and was in the normal range at the age of 6½ years.

No seizures were noted in the first years. EEG showed signs of unspcific encephalopathy, with theta waves, but no epileptogenic potentials between the age of 3 and 4½ years. At 6 years, the parents observed phases of absence in the child. Diagnostic evaluation confirmed generalised epilepsy with absences, and myotonic–astatic and tonic seizures. EEG was markedly abnormal, with hypersynchronous activity (spike and slow wave complexes, multifocal but most pronounced in the right hemisphere) and a very slow basal rhythm in the awake EEG. Antiepileptic therapy was induced, but treatment of epilepsy proved to be difficult. Monotherapy with different drugs (topiramate, clobazam, lamotrigine) was unsatisfactory. Current medication with lamotrigine and sulthiame has led to a decrease in seizure frequency, but the patient still has at least one seizure daily.

MRI showed unspecific white matter changes, which may also be secondary and caused by epilepsy, including small cystic structures in the supratentorial white matter surrounding the trigonum (probably enlarged Virchow-Robin spaces). Cortex relief, and size of inner and outer liquor spaces, brain stem, and cerebellum were interpreted as normal.

At the age of 6½ years, the boy showed severe global retardation and autistic features. The parents described regression of motor abilities over 6 months with loss of crawling and assisted walking, and suggested coincidence with onset of epilepsy. However, motor abilities did not recover significantly after onset of medication. Speech development was still not recognisable. Stereotypic hand movements and teeth grinding were observed. Dysmorphological evaluation showed only mild dysmorphic features such as a narrow midface and undescended testis. The extremities were frequently pink and cold, indicating mild peripheral vasomotor disturbance. The patient is now 8 years old and has increasing problems with swallowing, resulting in salivation and decrease in weight gain. No breathing irregularities have been observed as yet. Further regression of basic communication skills and loss of purposeful hand use and interest in toys has been noted.

MATERIALS AND METHODS

Molecular genetic analysis

Mutation screening in MECP2 was performed by PCR amplification of coding exons in overlapping fragments, followed by single strand conformational polymorphism (SSCP) analysis.

The analysis included all parts of the open reading frame in exons 2–4 of the full length transcript MECP2A, and also the part of exon 1 coding in the alternative transcript MECP2B recently reported.14 Band shifts indicative of small intragenic aberrations were not detected (not shown).

Quantification of MECP2 gene dosage, characterisation of the duplicated region, and fine mapping of the duplication breakpoints were performed using a quantitative PCR approach with SYBR-Green 1 detection, and the comparative threshold cycle method.15 16 Analysis was carried out on the iCycler iQ real time PCR detection system (Bio-Rad, CA, USA) and performed repeatedly for three independent MECP2 ampiclons (each three times, in duplicate). Two primer pairs for the fourth exon (primers Rett ex4F1/ex4R1, and Rett ex4F2/ex4R2) and one for the third (primers Rett ex3F/ex3R), and reference ampiclons in the ALB and PMP22 genes were used (Table 1). Size of the duplication was analysed using a primer set for amplicons covering parts of Qxq27–q28 (Table 1). Genomic sequences were obtained from the UCSC site (http://genome.ucsc.edu/).17 Primers were designed with lengths of 18–24 nucleotides, G+C contents 50–65%, PCR product length 75–150 bp. Specificity and exact position (physical distance) of primers were verified using the BLAT interface at the UCSC site. Standard curves and PCR efficiency were run to confirm applicability of the comparative threshold cycle method.

Quantitative PCR reactions contained 0.6 μmol/l each primer and 12.5 μl SYBR Green PCR Master Mix (ABGene, UK) in a total of 25 μl. Assays included DNA standards, no template control, or 2.5 ng/μl of the patient DNA in two replicates. Cycling conditions were 50°C for 2 minutes, 95°C for 15 minutes, and 40 cycles of 95°C for 30 seconds, then 62°C for 1 minute (data collection step), followed by a melting curve analysis (95°C for 1 minute, 55°C for 10 seconds, temperature increase by 0.5°C every 10 seconds (data collection) up to 95°C) to confirm specificity of the PCR reaction.

Quantification of target amplicons was performed relative to reference amplicons with the comparative threshold cycle method. Quantitative data were normalised against the average of two or four female controls (MECP2 ampiclons, PMP22 genes, Table 1) and also the ALB and PMP22 genes, with the comparative threshold cycle method. Quantitative data were normalised against the average of two or four female controls (MECP2 ampiclons, PMP22 genes, Table 1) and also the ALB and PMP22 genes.

Table 1 Primer pairs for amplicons used for quantitative PCR. Position of amplicons in Mb refers to UCSC site.

<table>
<thead>
<tr>
<th>Name</th>
<th>Nucleotide sequence</th>
<th>Position</th>
</tr>
</thead>
<tbody>
<tr>
<td>Test amplicons</td>
<td></td>
<td></td>
</tr>
<tr>
<td>L1CAM in1 R</td>
<td>TCGAAGGAGTTGGGACCG</td>
<td>151 608</td>
</tr>
<tr>
<td>L1CAM in1 F</td>
<td>TCCTGAGCGGCTAATTGG</td>
<td>151 618</td>
</tr>
<tr>
<td>LCA10 in1 F</td>
<td>CTCGCGGAGTTCATGCC</td>
<td>151 639</td>
</tr>
<tr>
<td>LCA10 in1 R</td>
<td>TCGGCGGAGTTCATGCC</td>
<td>151 639</td>
</tr>
<tr>
<td>AVPR2 in1 R</td>
<td>TTACCATTCCTCAGGGTG</td>
<td>151 689</td>
</tr>
<tr>
<td>AVPR2 in1 F</td>
<td>TCTAATGACCTGCGAGAG</td>
<td>151 689</td>
</tr>
<tr>
<td>HCFC ex17 F</td>
<td>CCTTGCGAGGTCTGAGCC</td>
<td>151 698</td>
</tr>
<tr>
<td>HCFC ex17 R</td>
<td>CTCGCGGAGTTCATGCC</td>
<td>151 698</td>
</tr>
<tr>
<td>IRAK1 in9 F</td>
<td>GCACCGTACTGCTCACC</td>
<td>151 749</td>
</tr>
<tr>
<td>IRAK1 in9 R</td>
<td>GTGACTCCTGCTCAGGG</td>
<td>151 749</td>
</tr>
<tr>
<td>Rett ex4 A1</td>
<td>CAGCGTGCTACTGACTGTC</td>
<td>151 764</td>
</tr>
<tr>
<td>Rett ex4 R1</td>
<td>CAGCGTGCTACTGACTGTC</td>
<td>151 764</td>
</tr>
<tr>
<td>Rett ex4 F2</td>
<td>TTTCTCGGAGTTCATGCC</td>
<td>151 765</td>
</tr>
<tr>
<td>Rett ex4 R2</td>
<td>TTACCATTCCTCAGGGTG</td>
<td>151 765</td>
</tr>
<tr>
<td>Rett ex3 R3</td>
<td>ATGTATGACCTGCGAGAG</td>
<td>151 766</td>
</tr>
<tr>
<td>Rett ex3 F3</td>
<td>ATGTATGACCTGCGAGAG</td>
<td>151 766</td>
</tr>
<tr>
<td>KGQ1273 F</td>
<td>TCTTGAGCGGTGGGAGAG</td>
<td>151 848</td>
</tr>
<tr>
<td>KGQ1273 R</td>
<td>CCGAGACGAGGACGACG</td>
<td>151 848</td>
</tr>
<tr>
<td>TKTL ex12 F</td>
<td>GAACACCCGCGACGACG</td>
<td>152 027</td>
</tr>
<tr>
<td>TKTL ex12 R</td>
<td>GAACACCCGCGACGACG</td>
<td>152 027</td>
</tr>
<tr>
<td>FJNA 3 F</td>
<td>CCTGGAGTGGGAGAGAG</td>
<td>152 044</td>
</tr>
<tr>
<td>FJNA 3 R</td>
<td>CCTGGAGTGGGAGAGAG</td>
<td>152 044</td>
</tr>
<tr>
<td>FJNA in29 F</td>
<td>CCTGGAGTGGGAGAGAG</td>
<td>152 053</td>
</tr>
<tr>
<td>FJNA in29 R</td>
<td>CCTGGAGTGGGAGAGAG</td>
<td>152 053</td>
</tr>
<tr>
<td>FJNA in25 F2</td>
<td>CCTGGAGTGGGAGAGAG</td>
<td>152 055</td>
</tr>
<tr>
<td>FJNA in25 R2</td>
<td>CCTGGAGTGGGAGAGAG</td>
<td>152 055</td>
</tr>
<tr>
<td>FJNA in21 F</td>
<td>CTTGCGCIACGCTGAGCC</td>
<td>152 057</td>
</tr>
<tr>
<td>FJNA in21 R</td>
<td>CTTGCGCIACGCTGAGCC</td>
<td>152 057</td>
</tr>
<tr>
<td>FJNA ex18 B</td>
<td>GAGTACGACCGCTGCCGAG</td>
<td>152 058</td>
</tr>
<tr>
<td>FJNA ex18 R</td>
<td>GAGTACGACCGCTGCCGAG</td>
<td>152 058</td>
</tr>
<tr>
<td>FJNA in14 F</td>
<td>TCCAGTGGCGAGGACGACG</td>
<td>152 060</td>
</tr>
<tr>
<td>FJNA in14 R</td>
<td>TCCAGTGGCGAGGACGACG</td>
<td>152 060</td>
</tr>
<tr>
<td>FJNA in6 R</td>
<td>TCCAGTGGCGAGGACGACG</td>
<td>152 062</td>
</tr>
<tr>
<td>FJNA in6 R2</td>
<td>TCCAGTGGCGAGGACGACG</td>
<td>152 062</td>
</tr>
<tr>
<td>FJNA in1 F</td>
<td>CTTGCGCIACGCTGAGCC</td>
<td>152 066</td>
</tr>
<tr>
<td>FJNA in1 R</td>
<td>CTTGCGCIACGCTGAGCC</td>
<td>152 066</td>
</tr>
<tr>
<td>EMD 3 UTR R</td>
<td>CATGACGACTGACGACG</td>
<td>152 070</td>
</tr>
<tr>
<td>EMD 3 UTR F</td>
<td>CATGACGACTGACGACG</td>
<td>152 070</td>
</tr>
<tr>
<td>Reference amplicons</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PMP22 ex3 F</td>
<td>GCCACACGGAGGAGAGAG</td>
<td>17p11.2</td>
</tr>
<tr>
<td>PMP22 ex3 R</td>
<td>GCCACACGGAGGAGAGAG</td>
<td>17p11.2</td>
</tr>
<tr>
<td>ALB ex12 F</td>
<td>ATACGACCGCAGGACGACG</td>
<td>4q11–q13</td>
</tr>
<tr>
<td>ALB ex12 R</td>
<td>ATACGACCGCAGGACGACG</td>
<td>4q11–q13</td>
</tr>
</tbody>
</table>
hybridised with a 32P labelled probe generated from a PCR of genomic DNA of the index patient were digested with FLNA and MECP2 from cosmid LLNLc110C1837Q (GenBank accession no. AF031077), containing a total of 12 kb of genomic sequence from the large second intron of MECP2. The cosmid clone was obtained from the Resource Center of the German Human Genome Project (RZPD, Berlin, Germany). After culturing and DNA preparation, cosmid DNA was briefly sonicated and labelled directly with dCTP, separated on an agarose gel, blotted onto a Hybond membrane (Amersham, Germany) and UV-cross-linked. The labelling and the nick translation were performed using the BioNick labelling system (Q-Biogene) according to the instructions of the manufacturer. Dual colour FISH was performed with the cosmid probe, and with a probe mix generated from PCR amplified fragments of the FLNA gene (four PCR fragments containing a total of 5.5 kb between FLNA introns 18 and 29) labelled directly with rhodamine. Hybridisations were carried out for 12–18 h at 37°C following a standard protocol. Slides were evaluated using an Axioscope 2 Plus microscope (Zeiss, Germany) and the Isis software (Metasystems, Germany).

Cytogenetic analysis
Cytogenetic analysis on cultured blood lymphocytes had been performed earlier. G1T and QFQ banded metaphases at a resolution of 550–600 bands revealed no numerical or structural aberration (not shown).

Fluorescence in situ hybridisation (FISH) analyses were carried out on metaphase spreads using a probe generated from cosmid LLNLc110C1837Q (GenBank accession no. AF031077), containing a total of 12 kb of genomic sequence from the large second intron of MECP2. The cosmid clone was obtained from the Resource Center of the German Human Genome Project (RZPD, Berlin, Germany). After culturing and DNA preparation, cosmid DNA was briefly sonicated and labelled directly with dCTP, separated on an agarose gel, blotted onto a Hybond membrane (Amersham, Germany) and UV-cross-linked. The labelling and the nick translation were performed using the BioNick labelling system (Q-Biogene) according to the instructions of the manufacturer. Dual colour FISH was performed with the cosmid probe, and with a probe mix generated from PCR amplified fragments of the FLNA gene (four PCR fragments containing a total of 5.5 kb between FLNA introns 18 and 29) labelled directly with rhodamine. Hybridisations were carried out for 12–18 h at 37°C following a standard protocol. Slides were evaluated using an Axioscope 2 Plus microscope (Zeiss, Germany) and the Isis software (Metasystems, Germany).

X chromosome inactivation
X chromosome inactivation was analysed by PCR amplification in the androgen receptor gene (AR) as described. Genomic DNA of the probands was digested with either MspI or methylation sensitive HpaII, or incubated with restriction buffer only. A 280 bp fragment of AR exon 1 was then amplified incorporating 32P labelled dCTP, separated on denaturing polyacrylamide gels, and evaluated using a Storm860 phosphorimager (Molecular Dynamics, CA, USA). The ratio of inactivation of the alleles in informative females was calculated from the band intensities measured by the ImageQuant 5.1 software (Molecular Dynamics).

Test of integrity of FLNA
The restriction map of FLNA shows a central 21.2 kb EcoRI fragment (EcoRI sites in intron 1 and exon 41 of FLNA). To test for integrity of one functional gene copy of FLNA, 10 μg of genomic DNA of the index patient was digested with EcoRI, and a Southern blot performed. The blot was hybridised with a 32P labelled probe generated from a PCR fragment made with FLNA primers int8F and int14R (outside the duplicated region), and evaluated by autoradiography.

MECP2 expression analysis
Total RNA of the patient, his mother, and male and female controls was extracted from lymphoblastoid cells generated by EBV transformation. Expression of MECP2 was analysed by one step RT real time PCR with SYBR Green detection and the comparative threshold cycle method. Primers Rett 2F and Rett 3-2R were used to amplify a 277 bp MECP2 mRNA fragment. Quantification was performed against a control amplicon of the GAPDH mRNA, using primers GAPDH-F (AGGTCCGAGTCACAAGGATTTG) and GAPDH-R (AAGCAG CCCTGGTGACCG). Reactions for MECP2 and GAPDH were carried out three times in duplicate using the Quantitect SYBR Green RT-PCR kit (Qiagen, Germany). Reaction tubes contained 0.4 μmol/l each primer of a pair, 10 μl QuantiTect SYBR Green, 0.2 μl QuantiTect RT mix, and 20 ng RNA (total volume 20 μl). Fluorescein (0.2 μl diluted 1:1000) was added for internal calibration of the iCycler system. Cycling conditions were 50°C for 30 minutes, 95°C for 15 minutes, and 40 cycles of 94°C for 15 seconds, then 60°C for 30 seconds, and 72°C for 30 seconds (data collection step), followed by a melting curve analysis. Quantification of relative MECP2 expression was performed as described for relative gene dosage calculation (see above).

RESULTS
The analysis of MECP2 gene dosage was performed repeatedly by independent comparison of three amplicons in MECP2 to autosomal reference amplicons, and suggested existence of two gene copies in the index patient, identical to the gene dosage found in girls. Chromosome analysis by conventional cytogenetics had earlier revealed a normal karyotype 46,XY in the boy (not shown). To verify a MECP2 duplication, additional amplicons 5’ and 3’ of the gene, situated in IRAK1 intron 9 and in STS XQ3273 (GenBank accession no. G66748) were analysed. Double dosage was found for both amplicons, indicating a complete duplication of MECP2 (fig 1). No such findings were found in a cohort of 75 female and 17 male patients suspected with Rett syndrome who had tested negative for smaller intragenic mutations.

EDTA blood samples had been received after informed consent for dosage analysis in the family of the index patient (fig 2A). An increased dosage for all MECP2 amplicons was found for the patient himself (III.2) and his mother (II.2), indicating two gene copies in the index patient and three copies in his healthy mother. Normal MECP2 dosage was detected in the healthy brother (III.1), father (II.1), and maternal uncle (II.3) (fig 2B).

The extent of the duplication was determined by application of further amplicons in Xq27–q28, situated in HCF1, AVPR2, LICAM, and FMR1 (centromeric to MECP2) and TKTL1, FLNA, EMD, G6PD, and F8 (telomeric to MECP2). The evaluation showed that the duplication involves a region including AVPR2 to TKTL1, but not the amplicons situated in LICAM and in FLNA intron1 (fig 1). Dosage of the more distant genes FMR1, EMD, G6PD, and F8 was also normal (not shown).

An amplicon in the first intron of LCA10 (GenBank accession no. AF514420), a predicted gene encoding for lung carcinoma associated protein, was analysed to determine possible involvement of LICAM. Single dosage for the LCA10 amplicon was found repeatedly in the assay. This suggests localisation of the proximal breakpoint to a 21 kb region between LCA10 intron 1 and AVPR2 intron 1, at least 8.4 kb 5’ of the first exon of LICAM. No regulatory sequences of LICAM are known further upstream, thus practically excluding LICAM contribution to the phenotype of this patient (fig 1).

Further amplicons in the FLNA gene were applied for fine mapping of the distal breakpoint between TKTL1 exon 12 and FLNA intron 1. The distal breakpoint was finally located to an approximately 2 kb segment between an amplicon in FLNA intron 14 and an amplicon at the border of exon 18 to intron 18 of FLNA (fig 1). The aberration thus includes complete duplication of 12 genes and predicted transcripts (AVPR2, ARHAGA4, ARDI, RENBP, HCF1, IRAK1, MECP2, OPN1LW, OPN1MW, TKTL1, CorfJ12, and Corf2), plus partial duplication of FLNA (and possibly of predicted transcript LCA10).

The mother of the index patient was informative for the trinucleotide repeat polymorphism at the AR site. The analysis demonstrates severely skewed X inactivation in the mother. Quantification of the X inactivation of the two alleles.
indicated a ratio of more than 10:1 for the patient’s mother, whereas a ratio of 7:3 and 6:4 was found for the two informative female controls c2 and c3 (fig 2C). The index patient, his brother, and his maternal uncle all carry the same, active allele at the AR locus. This is also the allele preferentially unmethylated in the mother, indicating recombination between the AR gene at Xq11 and MECP2 at Xq28 in the index patient (fig 2C).

FISH analysis with a probe for MECP2, generated from cosmid LLNLc10C1837Q, showed only one signal in the telomeric region of Xq in all analysed metaphases (fig 3). This suggested an intrachromosomal duplication with integration next to the originating segment. Dual colour FISH was applied with the same probe and a probe mix from the duplicated region of FLNA. In one metaphase, a pattern of fluorescent signals compatible with an orientation central–FLNA(partial)–MECP2–MECP2–FLNA–tel was observed. This result, however, which suggests an inverted tandem duplication with integration into the distal breakpoint, could not be verified in other metaphases, probably due to a limited resolution of this ∼430 kb duplication in the FISH analysis. Southern blot analysis with a probe outside the duplicated region revealed the expected 21 kb central EcoRI fragment of FLNA in the index patient, his mother, and controls, confirming integrity of FLNA (data not shown).

Expression of MECP2 was analysed at the mRNA level in lymphoblastoid cells. No significant difference was found between male and female samples, as expected for a gene underlying X inactivation in females. In contrast, quantification of transcript levels in the index patient suggests a double dose of MECP2 transcription (fig 2D). The patient’s healthy mother had normal values.

**DISCUSSION**

Xq28 is a chromosomal region frequently affected by rearrangements, and contains several genes mutated in mental retardation and neurological disease, such as MTM1, ABCD1, LICAM, MECP2, FLNA, and EMD.21–25 The gene product of MECP2, the gene mutated in Rett syndrome, is involved in regulation of transcription by interaction with methylated DNA. In vitro, MECP2 has been found to act as a transcriptional repressor, although the target genes of MECP2 have yet to be identified. The precise effect of MECP2 mutations is only partly understood. It was previously speculated that MECP2 mutations would be lethal in boys, although it is now thought that the much higher incidence of Rett syndrome in girls is mainly caused by an overwhelming ratio of mutations on paternally derived X chromosomes.26 Nevertheless, relatively few reports of Rett syndrome in males exist. The classic Rett phenotype has been described in males with Klinefelter syndrome or with somatic mosaicism.27 While in most other cases, MECP2 mutations in boys have been associated with a more severe clinical course culminating in neonatal encephalopathy.26 In contrast, there have been numerous reports on point mutations, small intragenic deletions, and larger deletions in MECP2 in girls, and a possible genotype–phenotype correlation has been studied in detail. Some authors have suggested that partial deletions and truncating mutations may be associated with a more severe phenotype. Other investigators have not observed this correlation, leading to the suggestion that Rett syndrome may be caused by loss of MECP2 function regardless of the exact mutation involved.27

We report here a familial duplication of a submicroscopic Xq28 segment in a boy with severe mental retardation and features of Rett syndrome. Psychomotor development was primarily retarded. Regression and loss of purposeful hand use and other acquired abilities, stereotypic movements, autistic features, epileptic seizures, and feeding problems occurring between the ages of 4½ and 6½ years led to suspicion of Rett syndrome. Quantitative PCR revealed a duplication involving MECP2. As there are at least 12 genes
and predicted transcripts included in the duplication, we cannot rule out that other genes may contribute to the clinical phenotype, although none of these genes other than MECP2 (and the colour opsin genes) is known to play a fundamental role in neural development and maintenance. There is convincing experimental evidence that complete, functional gene copies exist for both L1CAM and FLNA, the two nearest genes responsible for well known neurological phenotypes. Although L1CAM is not included in the duplication, fine mapping of the distal breakpoint indicated partial duplication of FLNA. Protein synthesis from the partially duplicated gene copy lacking the promoter and at least exons 1–13 is most unlikely, especially as periventricular heterotopia was excluded by MRI. In combination with the clinical phenotype, the results indicate that duplication of MECP2 may be the major if not the only cause for the mental retardation syndrome in our patient. Even though primary psychomotor retardation and normal head growth are atypical findings, the patient shows many diagnostic signs of Rett syndrome.

Owing to the uninformative family history, it remains unclear whether submicroscopic duplications involving MECP2 could cause Rett syndrome or other deleterious conditions in female patients. The finding of extremely skewed X inactivation in the index patient’s healthy mother, who also carries the duplication, suggests this hypothesis. This is further supported by the finding of elevated MECP2 mRNA levels in lymphoblastoid cells of the index patient, but not in his mother, compared with male and female controls. Importantly, in Mecp2 transgenic mice, the overexpression of murine Mecp2 causes a neurological phenotype similar to that in Mecp2 deficient mice. 28

In conclusion, our results indicate that duplications of the MECP2 gene caused by intrachromosomal duplications of Xq28 are rare, but are sufficient to cause a clinical phenotype similar to Rett syndrome in boys and possibly girls. These findings may also have implications for development of potential gene therapy strategies for Rett syndrome. The case demonstrates that alteration of methylation patterns due to pure loss of MECP2 function is not the only mechanism involved in pathogenesis of Rett syndrome, but that elevated dosage of MECP2 may be more critical than previously thought.

ACKNOWLEDGEMENTS

We thank the parents for their cooperation. We also thank J Karimzad Hagh and D Falkenstein for expert technical assistance.

Authors’ affiliations

M Meins, F Gerresheim, J Herchenbach, M Hagedorn, J T Epplen, Department of Human Genetics, Ruhr-University Bochum, Germany

J Lehmann, K Hameister, Fachklinik fuer Kinderneurologie und Sozialpaediatrie Konigsborn, Unna, Germany

Competing interests: there are no competing interests

Correspondence to: Dr M Meins, Department of Human Genetics, Ruhr-University Bochum, Universitaetsstrasse 150, 44801 Bochum, Germany; moritz.meins@ruhr-uni-bochum.de

Received 8 June 2004

Revised 12 August 2004

Accepted 16 August 2004

www.jmedgenet.com
REFERENCES

Submicroscopic duplication in Xq28 causes increased expression of the MECP2 gene in a boy with severe mental retardation and features of Rett syndrome

M Meins, J Lehmann, F Gerresheim, J Herchenbach, M Hagedorn, K Hameister and J T Epplen

*J Med Genet* 2005 42: e12
doi: 10.1136/jmg.2004.023804

Updated information and services can be found at: [http://jmg.bmj.com/content/42/2/e12](http://jmg.bmj.com/content/42/2/e12)

These include:

**References**
This article cites 26 articles, 3 of which you can access for free at: [http://jmg.bmj.com/content/42/2/e12#BIBL](http://jmg.bmj.com/content/42/2/e12#BIBL)

**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.

**Topic Collections**
Articles on similar topics can be found in the following collections

- Calcium and bone (307)
- Clinical diagnostic tests (356)
- Epilepsy and seizures (197)
- Genetic screening / counselling (886)
- Molecular genetics (1254)
- Reproductive medicine (519)
- Clinical genetics (256)

**Notes**

To request permissions go to: [http://group.bmj.com/group/rights-licensing/permissions](http://group.bmj.com/group/rights-licensing/permissions)

To order reprints go to: [http://journals.bmj.com/cgi/reprintform](http://journals.bmj.com/cgi/reprintform)

To subscribe to BMJ go to: [http://group.bmj.com/subscribe/](http://group.bmj.com/subscribe/)