MECP2 mutation in non-fatal, non-progressive encephalopathy in a male

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Abstract
To study the clinical overlap between Rett (RTT) and Angelman syndromes (AS), we screened the MECP2 gene in a cohort of 78 patients diagnosed as possible AS but who showed a normal methylation pattern at the UBE3A locus. MECP2 missense (R106W, G4285S), nonsense (R255X, R270X), and frameshift mutations (803delG) were identified in 6/78 patients including 4/6 female cases consistent with RTT, one female case with progressive encephalopathy of neonatal onset, and one isolated male case with non-fatal, non-progressive encephalopathy of neonatal onset. This study shows that MECP2 mutations can account for a broad spectrum of clinical presentations and raises the difficult issue of the screening of the MECP2 gene in severe encephalopathy in both males and females.

Keywords: MECP2 gene; Rett syndrome; Angelman syndrome; encephalopathy

Rett syndrome (RTT) is an X linked condition characterised by the cluster of acquired microcephaly, ataxia, psychomotor regression with loss of purposeful hand skills in females, and lethality in males (MIM 312750). The vast majority of cases are sporadic, but rare familial forms have allowed the disease gene to be mapped to chromosome Xq28. Recently, RTT has been ascribed to mutations of the MECP2 gene, which encodes a protein involved in transcription repression and gene silencing, via a methyl-CpG binding domain (MBD) and a transcription repression domain (TRD). The screening RTT patients for MECP2 gene mutations has shown random X inactivation in over 90% of RTT females, the paternal origin of de novo MECP2 mutations, and the maternal inheritance of mutations in familial forms, with a skewed X inactivation pattern in circulating white blood cells of healthy female carriers. Angelman syndrome (AS) is an epileptic encephalopathy with microcephaly, absent speech, ataxia, and inappropriate laughter mapped to chromosome 15q11 and ascribed to deletion, uniparental disomy, and mutations of either the imprinting centre or the UBE3A gene. Considering that RTT shares common clinical features with AS, we hypothesised that some patients regarded as possible AS cases might have been misdiagnosed and could in fact suffer from RTT. For this reason, we studied the MECP2 gene in a series of male and female children whose encephalopathy was not accounted for by AS.

Methods
A total of 78 children (40 females and 38 males), referred for clinical features consistent with the diagnosis of Angelman syndrome but displaying a normal methylation pattern at the UBE3A locus, were further screened for MECP2 gene mutations.

The MECP2 coding sequence and flanking introns were amplified by PCR with a set of nine pairs of primers (table 1) and analysed by silver staining single strand conformation polymorphism (SSCP). For PCR amplification, the reaction mixture (20 µl) contained 100 ng of leucocyte DNA, 20 pmol of each primer, 0.1 µmol/l dNTP, and 1 IU Taq DNA polymerase (Roche). Thirty five cycles of amplification were performed, each cycle consisting of 30 seconds denaturation at 96°C, 30 seconds annealing, and 30 seconds elongation. PCR products were heated for 10 minutes at 96°C, loaded onto a GeneGel Excel 12.5/24 kit (Amersham Pharmacia Biotech), and electrophoresed for 2.5 hours at 15°C. When an abnormal SSCP pattern was identified, genomic DNA was sequenced on both strands by the fluorometric method (Big Dye Terminator Cycle Sequencing kit, Applied Biosystems).

Results
Nucleotide variations were identified in 6/78 patients including 4/6 female cases consistent with Rett syndrome, one female case of severe early onset encephalopathy, and one male case (tables 2 and 3). MECP2 mutations in females included missense (R106W) or nonsense mutations (R255X, R270X) or frameshift deletion (803delG), which involved either the
methyl binding domain or the transcription repression domain of the protein (table 2). It is worth noting that all mutations occurred in CpG dinucleotides. Most interestingly, a male patient with non-fatal, non-progressive encephalopathy was found to carry a point mutation in a CpG doublet (1282 G>A in exon 3), changing a glycine into a serine at the carboxyl-terminal end of the protein.

This 3 year old boy was born to a healthy mother after a normal pregnancy and delivery. Family history was unremarkable. Hypotonia and hyperlaxity were noted early, but he thrived normally on breast feeding. However, his motor milestones were severely delayed (head control 7 months, sitting unaided 13 months, voluntary grasp 9 months, finger tip grasp 18 months, standing with support 2 years). The mother had noticed frequent periods of fatigue during the day and a phobia of doors shutting. He was anxious and uncomfortable with frequent facial grimacing and poor eye contact. At 3 years of age, balance remained poor with restless, uncoordinated, and rough movements of the limbs and trunk and he had no speech. However, he did not lose skills and retained purposeful hand skills. Neurological examination showed no ataxia, spasticity, acquired microcephaly, or cranial nerve or fundus involvement. Mild distal lower limb hypotrophy and mild dysmorphic features were noted (fig 1). Electroencephalogram showed bradyarrhythmia and absence of paroxysmal anomalies. Brain MRI was unremarkable and RG banded karyotype at 800 band resolution showed normal chromosomes, 46,XY. The G428S mutation was inherited from the healthy carrier mother (II.3) who has not passed it to her healthy son (III.6, fig 2). Random X inactivation in her white blood cell DNA was found at the androgen receptor locus (not shown). The G428S mutation was also found in the two normal aunts (II.1 and II.2) but was absent from I.2, III.2, III.4, and a panel of 220 control chromosomes. Finally, haplotype analysis at the MECP2 locus in the family makes germinal mosaicism in I.1 the most likely hypothesis.

Discussion

The systematic study of the MECP2 gene in a series of 78 children previously tested for possible Angelman syndrome has resulted in the detection of 6/78 mutant genotypes. Three lines of evidence support the deleterious nature of these base changes namely, (1) the involvement of CpG dinucleotides which are mutation hot spots, (2) the occurrence of the mutations in domains of the protein which are highly conserved across species (not shown), and (3) the absence of the corresponding base changes in 220 control chromosomes.

While 4/6 cases were clinically consistent with the diagnosis of RTT, 2/6 cases failed to meet the classical diagnostic criteria (table 3). Indeed, one female had a progressive encephalopathy of neonatal onset, a feature which has long been regarded as an exclusion criterion in RTT. More importantly, while this condition is currently regarded as lethal in males, a MECP2 mutation was found in a male patient with non-progressive encephalopathy, no seizures, and a normal head circumference. It is worth noting also that, at variance with classical RTT, the patient had no history of hand stereotypy, hyperventilation, or teeth grinding. Similarly, at variance with classical AS, he had no ataxia, epilepsy, typical EEG, or bursts of laughter. His abnormal movements were difficult to describe and raise the question of a combined neurological and behavioural phenotype. MECP2 mutations have seldom been described in males.6 7 9–13 In fact, a total of seven male cases have been reported so far and 3/7 had maternal relatives with either typical or variant forms of

<table>
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<tr>
<th>Patients</th>
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<td>F</td>
<td>RTT</td>
<td>763 C&gt;T</td>
<td>TRD</td>
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<td></td>
<td></td>
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<td>(G428S)</td>
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C-ter: carboxyl-terminal domain.

Table 2  Clinical presentation in the 6/78 patients with a MECP gene mutation

Figure 1  (A) Front view of the male patient and (B) profile. Note deep set eyes, arched eyebrows, prominent nasal bridge, and down turned corners of the mouth.

Figure 2  Segregation of the MECP2 mutation in the family of case 6.
In one case, the necropsy of the brain showed di...


