Rett syndrome (RTT) is a severe neurodevelopmental disorder affecting females almost exclusively and is characterized by a wide spectrum of clinical manifestations. Mutations in the X-linked methyl-CpG-binding protein 2 (MECP2) gene have been found in up to 95% of classical RTT cases and a lesser proportion of atypical cases. Recently, mutations in another X-linked gene, cyclin-dependent kinase-like 5 (CDKL5) have been found to cause atypical RTT, in particular the early onset seizure (Hanefeld variant) and one female with autism. In this study we screened several cohorts of children for CDKL5 mutations, totaling 316 patients, including individuals with a clinical diagnosis of RTT but who were negative for MECP2 mutations (n = 102), males with X-linked mental retardation (n = 9), patients with West syndrome (n = 52), patients with autism (n = 59), patients with epileptic encephalopathy (n = 33), patients with Aicardi syndrome (n = 7) and other patients with intellectual disability with or without seizures (n = 54). In all, seven polymorphic variations and four de novo mutations (c.586C>T [p.S196L]; c.58G>C [p.G20R]; c.2504delC [p.P835fs]; deletion of exons 1 - 3) were identified, and in all instances of the latter the clinical phenotype was that of an epileptic encephalopathy. These results suggest that pathogenic CDKL5 mutations are unlikely to be identified in the absence of severe early-onset seizures and highlight the importance of screening for large intragenic and whole gene deletions.

Keywords: CDKL5, Rett syndrome, infantile spasms, epileptic encephalopathy, intellectual disability, mutation

Rett syndrome (RTT; OMIM#312750) is an X-linked dominant neurodevelopmental disorder that manifests predominantly in females with profound intellectual impairment (Hagberg et al., 1983), and has an estimated incidence of 1 in 8,500 by the age of 15 years (Laurvick et al., 2006). This disorder is characterized by a wide spectrum of phenotypic severity (Hagberg et al., 2002).

In 1999, mutations in the X-linked gene methyl-CpG-binding protein 2 (MECP2) gene were identified (Amir et al., 1999), and it is now recognized that MECP2 mutations may be found in 90 to 95% of individuals with classical RTT (Williamson & Christodoulou, 2006). Recently, mutations in another X-linked gene, cyclin-dependent kinase-like 5 (CDKL5) have been found to cause a RTT-like phenotype with early onset seizures and profound intellectual impairment (Bahi-Buisson et al., 2008; Evans et al., 2005; Scala et al., 2005; Tao et al., 2004; Weaving et al., 2004).

There are features of various disorders associated with intellectual disability that overlap with RTT, suggesting that these could be candidates for CDKL5 mutation screening. Mutations in the CDKL5 gene have been found particularly in the Hanefeld variant of RTT, with characteristic early-onset seizures, usually of the infantile spasm type (Scala et al., 2005).
A male with cognitive impairment and seizures was found to have a large deletion that disrupted the CDKL5 gene (Huopaniemi et al., 2000). Moreover, Tao et al. suggested that CDKL5 may be associated with clinical features that overlap with those of other neurodevelopmental disorders such as autism and Angelman syndrome (Tao et al., 2004), and one patient in our original cohort with a pathogenic CDKL5 mutation had autism but no seizures (Weaving et al., 2004). These observations, coupled with the previous observation that disruption of the CDKL5 gene can be associated with X-linked infantile spasms (ISSX) (Kalscheuer et al., 2003), and the more recent finding of a CDKL5 encephalopathy in which females have severe epilepsy and poor neurocognitive development without a RTT phenotype (Archer, et al., 2006), prompted the speculation that CDKL5 mutations may underlie other clinical phenotypes.

In this study we explored whether CDKL5 mutations may be associated not only with RTT but with other clinical disorders presenting with cognitive impairment, social dysfunction and/or seizures.

Materials and Methods

Patients

A total of 316 patients were selected for CDKL5 screening. The cohort consisted of MECP2 mutation-negative RTT patients, mainly with atypical variants, and patients with other clinical features that overlap with RTT.

Clinical Cohorts

RTT. The RTT group formed 36% of the patients recruited for this study. All samples were previously negative for mutations of MECP2 gene. Mutation testing included screening all four exons of MECP2 and MLPA studies for gene deletions or duplications. Of the 102 RTT patients, 10 had the classical phenotype and 92 had atypical RTT. Seizures occurred in 41 out of 67 patients for whom this information was available.

West syndrome. This heterogeneous group of patients consisted of 52 patients of whom 47 were males and 5 were females. The majority were sporadic cases. All patients were previously screened for mutations of the ARX gene, with no mutations identified.

Autism. The autism spectrum disorder group (59 subjects) included 4 females and 55 males. The males were recruited from the AGRE (Autism Genetic Resource Exchange) set and included only families with greater than one affected male, suggestive of X-linked inheritance. The vast majority of the affected males, within each family, shared a common haplotype across the Xp22 region.

Epileptic encephalopathy. A cohort of 30 females and 3 males with epileptic encephalopathies was studied. Inclusion criteria included refractory epilepsy with seizure onset under 6 months and cognitive impairment. The diagnosis of RTT had been entertained in two cases; both were negative for MECP2 mutations. 25 were negative for mutations of the gene encoding the alpha 1 subunit of the sodium channel, SCN1A, which is frequently mutated in Dravet syndrome.

Non-syndromic X-Linked Mental Retardation (XLMR). The nonsyndromic XLMR cohort numbered 9, and consisted of 1 female and 8 males and all had seizures.

Other related disorders. Seven female subjects had a clinical diagnosis of Aicardi syndrome. They all had the ocular anomalies typical of Aicardi syndrome, as well as agenesis or dysgenesis of the corpus callosum and seizures. The 54 remaining patients (8 males and 46 females) were incompletely classified but had clinical features of interest according to the selection criteria for this study, including intellectual impairment and 9 subjects had seizures.

Methods

DNA was extracted using the ‘salting out’ method (Miller et al., 1988). The 20 coding exons of CDKL5 (exons 2–21) were amplified by PCR amplification of genomic DNA. Each reaction (volume 25 μl) contained 25 ng of genomic DNA, 0.5 μM of each primer, 0.2 mM of dNTPs, 0.75 U HotMaster Taq DNA Polymerase (Eppendorf, North Ryde, NSW, Australia), 1x HotMaster buffer with a final concentration of 2.5 mM MgCl2. The thermocycling conditions were as follows: 94°C for 2 minutes (1 cycle); 94°C for 20 sec, 65°C for 10 sec, 70°C for 20 sec (2 cycles); 94°C for 20 sec, (63°C to 55°C, [decreased by 2°C per cycle] for 10s per cycle), 70°C for 20 sec (35 cycles); 72°C for 4 min. Investigation of CDKL5 transcripts identified an alternative isoform (Williamson S, personal communication), resulting in the need to redesign the exon 18 primers. Primer sequences used are available on request.

The 20 coding exons of CDKL5 were screened by denaturing high performance liquid chromatography (dHPLC) and direct sequencing. The cohort of patients with epileptic encephalopathies was screened for mutations as previously described (Scala et al., 2005). Additional screening for identified mutations was performed by either restriction digests or custom TaqMan SNP Genotyping Assays (Applied Biosystems, Carlsbad, CA, USA). The c.586C>T (p.S196L) variation leads to the loss of an Ahd I restriction site, the size of the uncut product is 280 bp, whereas in the wildtype PCR product two bands of 60 and 220 bp are produced. Control alleles and parental samples were therefore screened for the p.S196L missense mutation using a Ahd I restriction digest. Screening for the c.554+11G>A sequence variation was carried out using a Bsm F I (New England Biolabs, Ipswich, MA, USA) restriction digest. A custom TaqMan SNP Genotyping Assay was used to screen for the c.978-23T>C variation.

Long-range PCR and cloning were carried out to determine whether the p.S196L mutation was located...
on the same allele as c.554+11G>A. Both variations were amplified within one amplicon around 4 kb in length using Expand Long Template PCR System (Roche Applied Science, Castle Hill, NSW, Australia) according to manufacturer's instructions. PCR cloning was carried out using CopyControl cDNA, Gene & PCR Cloning kit (Epicentre, Madison, WI, USA) with minor changes to manufacturer's instructions.

Large deletions of the CDKL5 gene were screened for using real-time quantitative PCR (QPCR) using either the same primers as used in DHPLC or new primers designed using Primer3 software (Rozen & Skaletsky, 2000). Glyceraldehyde-3-phosphate dehydrogenase was used as a genomic reference. Primer sequences are available upon request. Each reaction of 10 µl contained 40 ng of genomic DNA, 0.5 μM of each primer, 0.2 mM of dNTPs, 0.5 U Taq polymerase (New England Biolabs, Ipswich, MA, USA), 1x ThermoPol buffer with a final MgCl2 concentration of 2.0 mM and 1x SYBR green (Invitrogen, Carlsbad, CA, USA). Thermocycling was carried out in a RotorGene 3000A thermocycler (Corbett Life Science, now QIAGEN, Doncaster, Victoria, Australia) with the following cycling conditions: an initiation denaturation of 94°C for 4 min, followed by 40 cycles of 94°C for 20 sec, 56°C for 20 sec and 70°C for 20 sec.

Analyses of results were carried out using the accompanying software.

**Results**

**Sequencing**

The entire coding region of the CDKL5 gene (exons 2 to 21) was screened by direct sequencing in our cohort of patients. Seven polymorphic variations and four probably or potentially pathogenic mutations were identified (Table 1).

**c.586C>T (p.G20R) Missense Mutation**

This 7-year-old girl had an epileptic encephalopathy. She had intractable seizures, profound early onset developmental regression, feeding difficulties requiring gastrostomy insertion, generalized hypotonia, precocious puberty and cortical visual impairment.

This girl was the younger of two children to unrelated Australian parents. The pregnancy and perinatal history were normal. Her development was normal until 4 months when she regressed. Her head control deteriorated, she smiled and vocalized less than previously, and she did not fix and follow as well. She then made some slow developmental gains but regressed again at 3.5 years. She sat at four years but has never walked. She had cortical visual impairment, however she would look at faces and follow people around a room. Rather than look directly at an object or person she tended to observe from the corners of her eyes.

Seizures started at two months of age, shortly after her first immunization. The seizures comprised epileptic spasms, partial tonic seizures with asymmetric posturing and myoclonic seizures. A vagal nerve stimulator was inserted at 4 years, which improved seizure frequency and severity. At 7 years, her seizures remained refractory on a combination of clobazam and topiramate.

At 6 months, video-EEG monitoring showed subtle spasms progressing to a tonic seizure with extension of the right upper and lower limbs and flexion on the left side, evolving to a series of spasms. The ictal rhythm comprised non-lateralizing low amplitude fast activity in the frontal region spreading to the central region. The spasms were associated with bilateral frontotemporal discharges. At 5.5 years, her EEG background showed intermittent slowing with frequent trains of left frontotemporal discharges with independent discharges in the frontal and temporal regions bilaterally. MRI brain was normal.

At 5 years, she had precocious puberty with the onset of breast and pubic hair development and an early growth spurt.

On examination at 7 years, her head circumference was 49 cm (< 2nd percentile). She had subtle dysmorphic features with a full lower lip, straight eyebrows and deep-set eyes. She had a café au lait macule over her right ankle. She had small feet, her left foot length was 15.5 cm (< 3rd percentile) and her peripheries were warm and well perfused. She demonstrated midline hand clasping and hand mouthing movements. She showed limited visual fixation. Her breathing pattern was normal and her back was straight. Cardiovascular and respiratory examinations were also normal. Her general muscle mass was normal. She had generalized hypotonia, with intermittent tremulousness and dystonic posturing of her feet. She had a gastrosomy button in situ. In ankle/foot/knee orthoses, she was able to stand with assistance.

She was found to be heterozygous for the missense mutation, c.58G>C in exon 2, which changes the amino acid glycine (nonpolar neutral side chain) to arginine (polar positively-charged side chain) at position 20 of the protein (Figure 1a). The mutation was not present in either parent or 200 control alleles. Figure 1b shows the alignment of the human wild-type and the p.G20R mutant CDKL5 sequence against eight CDKL5 orthologs. The region is highly conserved, and is part of the ATP binding site of the putative kinase domain, common to seven CDKL5 orthologs, as well as other members of the mitogen-activated protein (MAP) kinase and cyclin-dependent kinase (CDK) families (Montini et al., 1998). Disruption of the sequence at the kinase domain may potentially reduce the efficiency of the kinase activity of CDKL5, and this mutation is highly likely to be the pathogenic cause of the epileptic encephalopathy in this patient.

**c.586C>T (p.S196L) Missense Mutation**

The missense c.586C>T variation was identified in a female, the first child of nonconsanguineous parents. The patient was born at full term, and the perinatal period was uneventful. Normal development occurred
until 5 months of age when she could sit with support, reach for objects, had social smiling, recognition of her mother, good eye contact and nonspecific vocalization. Regression was noticed from the age of 5 months, when she no longer reached for objects, lost eye contact and had no useful hand activity. She developed hand-washing stereotypies and never produced any meaningful sounds. It was at this time that she developed infantile spasms, having 10–15 flexor spasms per day, which increased in frequency when she was drowsy. She was treated with ACTH, and subsequently with sodium valproate and clobazam without adequate control of seizures. When last reviewed at the age of 3 years, she continued to have frequent seizures, had developed hypothyroidism and was on lamotrigine. Her breathing pattern was normal. Her head circumference was 47 cm (20% percentile), weight was 14 kg (50% percentile), and height was 94 cm (40% percentile). She also had small feet but had normal muscle tone. Her EEG showed hypsarrhythmia.

She was found to be heterozygous for the missense mutation c.586C>T in exon 9, which changes the amino acid serine (polar neutral side chain) to leucine (nonpolar neutral side chain) at position 196 of the protein (Figure 1a). Figure 1c shows a segment of the

<table>
<thead>
<tr>
<th>Type of variant</th>
<th>Nucleotide</th>
<th>Amino acid change</th>
<th>No. of change</th>
<th>Diagnosis</th>
<th>Detected in Patients</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>Frameshift</td>
<td>c.2504delC</td>
<td>p.P835fs</td>
<td>1</td>
<td>EE (female)</td>
<td>Not found in either parent</td>
<td>Probably pathogenic.</td>
</tr>
<tr>
<td>Deletion</td>
<td>Exons 1 – 3 (and 5’ UTR)</td>
<td>No CDKL5 protein predicted</td>
<td>1</td>
<td>EE (female)</td>
<td>Not found in either parent</td>
<td>Pathogenic.</td>
</tr>
<tr>
<td>Missense</td>
<td>c.2372A&gt;C</td>
<td>p.Q791P</td>
<td>19</td>
<td>WS (3), RTT (15). EE (1; female)</td>
<td>ND</td>
<td>Seen in the father (Kalscheuer et al., 2003; Tao et al., 2004)</td>
</tr>
<tr>
<td>Intrinsic</td>
<td>c.2376+118T&gt;A (IVS16+118T&gt;A)</td>
<td>NP</td>
<td>21</td>
<td>WS (3), RTT (18).</td>
<td>ND</td>
<td>Known c.SNP (Evans et al., 2005)</td>
</tr>
<tr>
<td>Intrinsic</td>
<td>c.2377-31T&gt;C (IVS16-31T&gt;C)</td>
<td>NP</td>
<td>1</td>
<td>EE (1; female)</td>
<td>Heterozygous in unaffected mother. Not present in 200 control alleles. (not reported.) Probable polymorphism</td>
<td></td>
</tr>
<tr>
<td>Intrinsic</td>
<td>c.978-23T&gt;C (IVS11-23T&gt;C)</td>
<td>NP</td>
<td>1</td>
<td>Male, seizures, MR</td>
<td>Heterozygous in unaffected mother. Not present in 306 control alleles.</td>
<td>Probable polymorphism</td>
</tr>
<tr>
<td>Intrinsic</td>
<td>c.463+22T&gt;C (IVS7+22T&gt;C)</td>
<td>NP</td>
<td>1</td>
<td>RTT, seizures</td>
<td>Heterozygous in unaffected mother. Not present in 306 control alleles.</td>
<td>Probable polymorphism (Evans et al., 2005)</td>
</tr>
<tr>
<td>Silent polymorphism</td>
<td>c.[3003C&gt;T; 3084G&gt;A]</td>
<td>p.[H1001H; T1028T]</td>
<td>3</td>
<td>Atypical RTT (1;female), Angelman-like (1; male), WS (1; male)</td>
<td>ND</td>
<td>Probable polymorphism (Huppke et al., 2005; Tao et al., 2004)</td>
</tr>
</tbody>
</table>

Note: MR – Mental retardation; RTT – Rett syndrome; WS – West syndrome; EE – epileptic encephalopathy; ND – not determined; NP – none predicted.
protein kinase domain, demonstrating that the altered amino acid is highly conserved within this domain. The mutation was not present in either parent or 300 control alleles. It is likely that this mutation affects the protein kinase activity of CDKL5.

We also identified the c.554+11G>A (IVS8+11G>A) variation in the proband. We consider this previously unreported variation as non-pathogenic as it was also identified in the unaffected father. Moreover, the Berkeley Drosophila Genome Project Splice Site Predictor (http://www.fruitfly.org/seq_tools/splice.html) predicted that this variation would not affect exon splicing. Long-range PCR and cloning using DNA from the proband was performed, the aim of which was to capture both this polymorphism and the missense mutation identified in the proband in the same fragment.
Large Deletion, Including Exons 1–3 of CDKL5

This 7.5-year-old girl also had an epileptic encephalopathy. She was the third child to nonconsanguineous Italian parents. She was born after an uneventful pregnancy and birth. Her development was always delayed with no clear history of developmental regression. From 2 months of age she had infantile spasms. She continued to have intractable seizures despite anti-epileptic medications, corticosteroids and the ketogenic diet.

At approximately 6 months she developed midline stereotypic hand movements in the form of hand clasp- ing, wringing and hand to mouth movements. She sat unsupported at 2 years of age but has never learnt to crawl or pull herself to stand. She never learnt to say any words. She now occasionally babbles, however, communicates mainly through body language and gestures. She can make choices by touching a desired object and can reach out and grasp an object. There has been no loss of purposeful hand function or communicative abilities. In fact, she has continued to make small developmental gains. In addition, she has a disturbed sleep pattern, suffers with constipation, has difficulty chewing and grinds her teeth.

When reviewed at 7.5 years, she had frequent seizures, mainly clusters of spasms. Her weight was 21.7 kg (<30th percentile) and head circumference was 51.5 cm (50th percentile). She had some facial dysmorphism with full lips, eversion of the lower lip, a prominent columella and horizontal palpebral fissures. She demonstrated midline hand clasp- ing, wringing and finger twisting movements. Her peripheries were warm and well perfused, her back was straight and her breathing pattern was normal. She had generalized hypermobility particularly at the hips, knees, elbows and ankle and pes planus. When looking at people or objects she tended to look from the corners of her eyes.

Sequencing of the CDKL5 coding sequence failed to reveal any changes. Quantitative PCR of genomic DNA showed that exons 1–3 were deleted. Using the ‘Agilent aCGH’ 44K array the deletion was found to extend into the 5’ UTR region of the CDKL5 gene. The ISCN description is arr cgh Xp22.13p22.13 (A_14_P_104234->A_14_P125155) × 1. The deletion is located at 18.44 & 18.55 Mb respectively. It has a minimum size of 0.11Mb and maximum size of 0.19 Mb. The patient was also tested on the ‘Cytochip’ BAC array platform. The results obtained were consistent with the above findings. Neither parent was found to have this deletion.

Missense polymorphic variation (c.2372A>C; p.Q791P)

A coding single nucleotide polymorphism (c.SNP) was detected at position 2372 (c.2372A>C), within exon 16, which results in the amino acid change p.Q791P. This c.SNP was previously detected in 20% of a panel of 50 control chromosomes (Kalscheuer et al., 2003; Tao et al., 2004). This variation was identified in 19 individuals (15 RTT; all female and 3 West syndrome patients; all male and 1 epileptic encephalopathy,
female). Of these patients 12 individuals were known to have seizures.

**Intronic Variation c.2376+118T>A**
The c.2376+118T>A (IVS16+118T>A) variation was identified in 21 patients in this cohort, 18 RTT (all female) and 3 West syndrome patients (all male). Of these patients 13 individuals were identified as having seizures. This variation has been previously reported as a common SNP detected in intron 16 with a minor allele frequency of 33% (Evans et al., 2005).

**Intronic Variation c.2377-31T>C**
The c.2377-31T>C (IVS16-31T>C) variation was identified in a male individual, who had neonatal seizures followed by severe epilepsy in infancy. He has severe mental retardation and a balanced translocation of chromosomes 3 and 14. Her clinically normal mother was also found to be heterozygous for this intronic variation. This sequence variation was not found in dbSNP (http://www.ncbi.nlm.nih.gov/SNP/), the Database of Genomic Variants (http://projects.tcag.ca/variation/) or in the Japanese SNP database (http://snp.ims.u-tokyo.ac.jp/). Moreover, the Berkeley Drosophila Genome Project Splice Site Predictor (http://www.fruitfly.org/seq_tools/splice.html) predicted that this variation would not affect exon splicing. We conclude that this variation is unlikely to be pathogenic.

**Intronic Variation c.978-23T>C**
The c.978-23T>C (IVS11-23T>C) variant was identified in three patients, one female and two males. We note that these two silent variations have been previously reported (Huppke et al., 2005; Tao et al., 2004), forming a rare conserved haplotype (along with the IVS+17A>G variation) that was found in 2 of 267 controls from Caucasian individuals (Tao et al., 2004). The BDGP Splice Site Predictor predicted that neither of these variations would create the potential for abnormal splicing. Therefore it is concluded that this combination of sequence variations is probably non-pathogenic.

**Discussion**

In recent studies MECP2 mutations have been found in up to 90–95% of patients with classical RTT (Williamson & Christodoulou, 2006) and in a lesser proportion (20–60%) of those with atypical forms of RTT (Bourdon, et al., 2001; Buyse et al., 2000; Cheadle et al., 2000; Hoffbuhr et al., 2002). Further investigations of the remaining group of clinically well defined RTT patients led to the discovery of mutations in a second gene, CDKL5 (Evans et al., 2005; Scala et al., 2005; Tao et al., 2004; Weaver et al., 2004). Disruption of the NTNG1 gene was found in one female with RTT (Borg et al., 2005), but mutations in NTNG1 do not appear to be a significant cause of RTT (Archer, et al., 2006). In addition, mutations in FOXG1 were more recently reported to cause the congenital variant of RTT (Ariani et al., 2008; Mencarelli et al., 2009), and classical RTT in one report (Philippe et al., 2009).

We screened a cohort of patients for mutations in the CDKL5 gene. In our study we identified four novel mutations that we consider probably or potentially pathogenic (Table 1). In addition, we identified seven polymorphic variations, three of which were also seen in unaffected parents, and are therefore likely to be rare polymorphisms. Three SNPs identified in this study were previously reported (Evans et al., 2005; Kalscheuer et al., 2003; Tao et al., 2004), as was the complex allele with two silent variations in cis (Huppke et al., 2005; Tao et al., 2004). None of the intronic variants are likely to affect splicing according to the prediction software used.

Two females with an epileptic encephalopathy clinical picture were found to have missense mutations. One was found to be heterozygous for a c.58G>C mutation in exon 2 leading to a glycine to arginine amino acid change at position 20. The substitution is located in the ATP-binding site of the putative kinase domain of CDKL5. The inclusion of the larger sidechain of arginine in place of the single hydrogen in glycine is therefore likely to disrupt the binding ability.
at that position. A heterozygous mutation in exon 9 (c.586C>T, p.S196L) was identified in the second. We screened both parents of the second case and 300 nonethnically matched control alleles and none were found to have this sequence variation. In addition, this sequence variation was not found in dbSNP (http://www.ncbi.nlm.nih.gov/SNP/), the Database of Genomic Variants (http://projects.tcag.ca/variation/) or in the Japanese SNP database (http://snp.ims.u-tokyo.ac.jp/). Serine at position 196 of the CDKL5 protein is a highly conserved residue located within the kinase domain (Figure 1c), and so could potentially affect the protein kinase activity of CDKL5. In addition, the substitution of the highly polar serine for the highly nonpolar leucine may affect the structure of the protein. We therefore suggest that this mutation is likely to be pathogenic. Functional studies to assess phosphorylation capability of this missense mutation are warranted.

One patient with an epileptic encephalopathy phenotype was found to have a frameshift mutation (c.2504delC; p.P835fs). The resultant peptide is predicted to contain only the first two amino acids encoded by exon 18, with a shortened C-terminal. The C-terminus of CDKL5 is postulated to be of importance to its subcellular localization. A derived truncation of CDKL5 (Δ831) and two nonsense mutations (p.R781X, p.L879X), all of which result in peptides of similar length, show a disruption in export from the nucleus in human HeLa cells, with these forms to be entirely nuclear. In contrast, both wild-type CDKL5 and a longer truncated version of CDKL5 (Δ941), shows a more cytoplasmic distribution, suggesting that the peptide sequence (or part thereof) between 879 and 941 may play a role in the localization of CDKL5 (Rusconi et al., 2008). The C-terminus is also thought to be important in the regulation of CDKL5 kinase activity (Lin et al., 2005). The loss of the entire C-terminal domain of CDKL5 (from amino acid 353 onwards) has elevated protein stability and enhanced autophosphorylation activity. It is uncertain whether the same effects would be seen with this particular mutation (c.2504delC, p.P835fs) as the peptide would still retain a section of the C-terminus.

One patient, a girl who also had an epileptic encephalopathy clinical picture, was found to have a heterozygous deletion of exons 1–3 and up to 190 kb of upstream sequence, without disrupting any other genes upstream of CDKL5. A similar disruption has recently been reported in a girl with severe ISSX (Cordova-Fletes et al., 2009), whereby the balanced translocation resulted in exons 1–3 of CDKL5 being transposed to chromosome 2. Exons 4–21 of the disrupted CDKL5 were shown to be transcribed, although any translated peptide would be partially devoid of the critical N-terminal kinase domain and likely to be nonfunctional. The breakpoint in exon 3 of CDKL5 in the ISSX patient is limited to within 9 to 21 kb downstream of the intron 3 donor splicing site. The breakpoints of the deletion in our patient were not determined, and it would be of interest to examine whether there might be a potential breakpoint hotspot in that region of the chromosome.

Presently, the diagnosis of RTT remains a clinical one and is not made solely on the basis of identification of MECP2 or CDKL5 mutations. However, MECP2 and CDKL5 mutations can occur in association with non-RTT phenotypes. To date, over 40 mutations in CDKL5 have been reported (reviewed in Nemos et al., 2009). Genotype-phenotype correlations have been limited because very few of the mutations have been identified in more than 1 patient. It remains unclear why CDKL5 mutations are associated with seizures, as to date, apart from MeCP2, phosphorylation targets of CDKL5 are yet to be identified. Bahi-Buisson and colleagues recently investigated how genotype might influence the epilepsy outcome in patients with CDKL5 mutations (Bahi-Buisson et al., 2008; Bahi-Buisson et al., 2008). They suggested that the course of epilepsy is more severe in patients who carry mutations in the catalytic domain of CDKL5 as opposed to patients with late truncating mutations. Further genotype-phenotype correlations may yield further insights into functionally significant domains within the protein.

Four genes have been associated with phenotypes overlapping with RTT, namely ARX, NTNG1, CDKL5 and FOXG1. Mutations in the ARX gene cause a broad range of more than 8 phenotypes including infantile spasms, X-linked lissencephaly with ambiguous genitalia (XLAG) and X-linked mental retardation (Gecz et al., 2006). NTNG1 has been reported to be a candidate gene for a RTT-like phenotype (Borg et al., 2005), and CDKL5 mutations are a significant cause of spasms and early epileptic encephalopathy (Archer et al., 2006; Bahi-Buisson et al., 2008). An MLPA kit has been devised to screen these three genes to detect large duplications and deletions that would be missed by sequencing. MECP2 deletions occur in up to 30% of females with classical RTT who have no detectable MECP2 mutations by sequencing or dHPLC (Archer et al., 2006; Ariani et al., 2004; Bourdon et al., 2001; Erlandson et al., 2001; Erlandson et al., 2003; Hardwick et al., 2007; Laccone et al., 2004; Ravn et al., 2005; Schollen et al., 2003). MLPA screening of the CDKL5 gene has been reported only twice to date (Mei et al., 2009; Russo et al., 2009). We attempted to use this kit, but despite repeated attempts using DNA that had undergone whole genome amplification using the GenomiPhi amplification kit (GE Healthcare) we were not able to generate reproducible results (data not shown). For this reason, we used qPCR and identified a large deletion in one patient, with exons 1–3 and upstream sequence (also identified by array CGH), which we estimate to be 110–190 kb in size. Interestingly, Nemos and colleagues have very recently reported a patient with a somewhat smaller (43 kb) deletion involving exons 1, 1a and 1b of CDKL5 and...
upstream sequence (Nemos et al., 2009). In addition, Erez and colleagues reported 3 females with deletions ranging between 74 and 157 kb identified initially by array CGH, also involving the first 3 – 4 exons of the CDKL5 gene (Erez et al., 2009). These findings highlight the importance of not relying solely on MLPA results for the identification of large rearrangements of the CDKL5 gene, and this has been our experience with the MECP2 gene as well (Hardwick et al., 2007). It will only be by performing CDKL5 MLPA analysis on a large cohort with confirmatory testing using other methods that the importance of MLPA screening of this gene will be elucidated.

The first CDKL5 abnormalities identified were in patients with ISSX who had X: autosome translocations disrupting the CDKL5 gene (Kalscheuer et al., 2003). Most RTT cases reported to date with CDKL5 mutations have been associated with an early onset seizure variant, the so-called Hanefeld variant (Evans et al., 2005; Scala et al., 2005; Tao et al., 2004; Weaving et al., 2004). Additionally, it is now recognized that CDKL5 mutations may cause a severe infantile onset seizure disorder with poor cognitive development (Archer et al., 2006; Bahi-Buisson et al., 2008). However, our studies suggest that CDKL5 mutations are rarely found in ARX mutation-negative individuals with West syndrome or autistic patients without seizures. We had previously reported a CDKL5 mutation in a female with autism, her identical sister with the early onset seizure variant of RTT, and her brother with epileptic encephalopathy. Despite the twin sisters having the same X-chromosome inactivation pattern in peripheral blood, the possibility remains that the different clinical phenotypes may be the result of skewed X-inactivation in the brain in one twin. In addition, our data and the findings of others (Bahi-Buisson et al., 2008; Elia et al., 2008), strongly suggest that CDKL5 screening of MECP2 mutation-negative RTT patients is more likely to yield pathogenic mutations if they have early onset seizures, particularly an epileptic encephalopathy, and this notion is supported by the recent publications of Mei and colleagues (Mei et al., 2009) and Nemos and colleagues (Nemos et al., 2009). It remains to be seen whether individuals with milder phenotypes (Psoni et al., 2009) will be consistently found to have CDKL5 mutations.

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