ASPM mutations identified in patients with primary microcephaly and seizures


Background: Human autosomal recessive primary microcephaly (MCPH) is a heterogeneous disorder with at least six genetic loci (MCPH1–6), with MCPH5, caused by ASPM mutation, being the most common. Despite the high prevalence of epilepsy in microcephaly patients, microcephaly with frequent seizures has been excluded from the ascertainment of MCPH. Here, we report a pedigree of multiple affected individuals with microcephaly and seizures.

Objective: To identify the gene responsible for microcephaly and seizures in this pedigree.

Methods: Clinical assessments of three patients and brain MRIs of two patients were obtained. Genome wide linkage screen with 10 k SNP microarray, fine mapping with microsatellite markers, and mutational analysis of the genomic DNA were performed on the pedigree.

Results: We found that the family was linked to the MCPH5 locus on chromosome 1q31.2–q32.1. We screened ASPM and identified a previously unreported nonsense mutation that introduced a premature stop codon in exon 18 of the ASPM gene.

Conclusions: We thus expand the clinical spectrum of ASPM mutations by showing that they can occur in patients with seizures and that the history of seizures alone should not necessarily preclude the diagnosis of primary microcephaly.

Methods:

The consanguineous family originated from Saudi Arabia (fig 1). The first cousin parents had six unaffected children and three children with microcephaly, who were 18.5, 15, and 3.5 years of age, respectively, at the time of latest examination. The HCs of the three affected children were 4 to 5 SDs below the age and sex matched population mean.22 All three affected children had normal motor development. However, IV:1 had severe mental retardation with an IQ of 35, whereas IV:3 showed moderate mental retardation with an IQ of 55.

IV:1 and IV:8 had frequent tonic/clonic seizures with onset at 30 and 32 months of age. Their seizures had no other obvious causes, such as fever or head injury. The EEG of IV:1 at 3 years of age showed bilateral dysrhythmia and grade 3 rolandic spikes. His seizures started as transient paroxysmal attacks with right sided hemiparesis lasting for 5 min, after which he would fall down or sometimes lose consciousness. At 11 years old, his EEG showed left sided epileptic discharges. His seizures occurred 1–2 times per week until he was 16 years old, when they were controlled by medication (carbamazepine). He has been free of seizures since then.

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The pedigree of the family with microcephaly and seizures. IV:1, IV:3, and IV:8 had microcephaly. IV:1 and IV:8 also had seizures. DNA was extracted from peripheral blood lymphocytes by means of a standard non-organic extraction procedure (Qiagen, Valencia, CA). A genome-wide screen for regions of linkage was performed with Affymetrix 10 k SNP GeneChip analysis on all three affected children (IV:1, IV:3, and IV:8), one unaffected sibling (IV:9), and the parents (III:1 and III:2) according to the manufacturer’s specifications (Affymetrix, Santa Clara, CA). For fine mapping, we selected seven polymorphic microsatellite markers surrounding the MCPH5 locus at chromosome 1q31.2–q32.1 between markers rs1377931 and rs724221 (fig 1). The marker order is cen-rs1377931-D1S533-D1S1614-GATA135F02-[MCPH5]-D1S1660-D1S3732-D1S413-D1S412-D1S533-D1S413 (fig 1). The boxed regions indicate the homozygous haplotype shared among all three affected children.

DNA samples were available for individuals labelled “DNA”. The genotypes of seven microsatellite markers between the two SNP markers near the MCPH5 gene, ASPM, were compared. The boxed regions indicate the homozygous haplotype shared among all three affected children.

RESULTS

A single 10.37 Mb region of shared homozygosity and allele sharing among the three affected individuals was identified at chromosome 1q31.2–q32.1 by Affymetrix 10 k SNP GeneChip analysis, overlapping the MCPH5 locus. No other regions of suggestive linkage were seen in the genome. Further refinement of the region by microsatellite marker analysis confirmed linkage to MCPH5. All affected individuals were homozygous for the same haplotype in the region (fig 1). The maximum two point LOD score was 2.43 at all informative markers within the region with h = zero, and the maximum multipoint LOD score was 3.03 at the locus. Mapping of the disease locus in this family to MCPH5 implied that ASPM might be the causative gene, although the finding that two of the three affected children had seizures might suggest the disease is distinct from MCPH5.

To determine whether ASPM might be the causative gene, we performed mutation analysis by sequencing the 28 exons and flanking intron regions of the ASPM gene in all members of the family. A previously unreported homozygous 6189T→G transversion in exon 18 was identified in all three affected individuals (fig 3). This mutation changes the
The mutation segregated with the haplotype. In addition, we also identified four non-synonymous (7480T→R, 7684A→G, 7939C→R, and 9395T→R) and six synonymous (849C→R, 3579T→A, 4449A→G, 5961A→G, and 7674C→R) SNPs in the exons. Six of the SNPs (rs964201, rs3762271, rs6677082, rs4915337, rs2878749, and rs1412640) were described in the dbSNP database, and the other four SNPs were previously reported to occur in individuals with MCPH.9

DISCUSSION

We report here the identification of the first ASPM nonsense mutations in patients with microcephaly and seizures. ASPM and MCPH1 mutations have been reported to associate with MCPH, but none of the patients with ASPM or MCPH1 mutations have been reported to have seizures to date. MCPH has been historically ascertained without other neurological abnormalities including frequent seizures, so that microcephaly with seizures has been generally considered to have a genetic cause distinct from that of MCPH. The brain MRIs of the patients described here were consistent with MCPH. However, it was unusual to observe that two of the three MCPH patients had frequent seizures. Our results provide the first evidence that epilepsy can occur in patients with ASPM mutations.

A total of 24 mutations in the ASPM gene have been reported in MCPH patients.24,25 These mutations are all protein truncating mutations and are scattered throughout the gene except for a ~3 kb gap (nucleotide position 4796–7760) in the 4755 bp exon 18. Interestingly, the 6189T→G mutation we identified in patients with seizures is also a protein truncating mutation, but it falls within the previous mutation free zone. The 6189T→G mutation may induce nonsense mediated decay of the mRNA or result in a 40% truncation of the 3477 amino acid full length protein. Since one of our patients with the same mutation did not have seizures, there appeared to be no correlation between the mutation and the phenotype. On the other hand, it is unlikely that the seizures were due to a second genetic locus in the family, because there was no family history of seizures. Therefore, the manifestations of seizures in two of the three microcephaly patients may suggest that patients with the 6189T→G (Y2063X) mutation in ASPM are more susceptible to seizures, perhaps due to an allelic specific effect. Alternatively, the occurrence of seizures in MCPH patients may generally have been underestimated, because of the strict "no seizures" criterion of the definition of MCPH. Therefore, it is possible that other microcephaly patients with seizures may also have undetected mutations in ASPM or MCPH1. Therefore, perhaps the phenotypic spectrum of MCPH should be broadened to include seizures, and seizure patients who otherwise fit the definition of MCPH should be advised to have mutation testing in known MCPH genes. Given the high prevalence of seizures in microcephaly patients, a large number of families with microcephaly and seizures might have been systematically excluded from linkage studies of MCPH. Including these families will help to refine the mapping of other MCPH loci, where the responsible genes have not been identified.

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Figure 3  The 6189T→G (Y2063X) mutation in ASPM identified in patients with MCPH and seizures. The chromatographs of the DNA sequencing results are shown next to the symbols of the individuals. The arrows point to the nucleotide position 6189T in ASPM, which was mutated to “G” in the three affected children. The parents were heterozygous. IV:2, IV:4, IV:5, and IV:6 were heterozygous carriers. IV:7 and IV:9 were homozygous for the normal allele. The horizontal lines underline the codon. The normal tyrosine codon (TAT) was changed to an amber stop codon (TAG) in the mutant allele.
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**ELECTRONIC-DATABASE INFORMATION**


**Authors’ affiliations**

J Shen, G H Machida, A Bodell, C A Walsh, Howard Hughes Medical Institute, Beth Israel Deaconess Medical Center, Harvard Medical School, Boston, MA 02115, USA

W Eyaid, F Al-Moayyad, Department of Pediatrics, King Fahad National Guard Hospital, Riyadh 11426, Kingdom of Saudi Arabia

C G Woods, Molecular Medicine Unit and Department of Clinical Genetics, University of Leeds, St. James’s University Hospital, Leeds LS9 7TF, UK

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Correspondence to: Dr Christopher A Walsh, Howard Hughes Medical Institute, Department of Neurology, Beth Israel Deaconess Medical Center, New Research Building 266, 77 Avenue Louis Pasteur, Boston, MA 02115, USA; cwwalsh@bidmc.harvard.edu

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