The Role of Seizure-Related SEZ6 as a Susceptibility Gene in Febrile Seizures

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Sixty cases of febrile seizures from a Chinese cohort had previously been reported with a strong association between variants in the seizure-related (SEZ) 6 gene and febrile seizures. They found a striking lack of genetic variation in their controls. We found genetic variation in SEZ6 at similar levels at the same DNA sequence positions in our 94 febrile seizure cases as in our 96 unaffected controls. Two of our febrile seizure cases carried rare variants predicted to have damaging consequences. Combined with some of the variants from the Chinese cohort, these data are compatible with a role for SEZ6 as a susceptibility gene for febrile seizures. However, the polygenic determinants underlying most cases of febrile seizures with complex inheritance remain to be determined.

1. Introduction

Febrile seizures affect 3% of infants between the ages of three months and five years of age and are associated with fever in the absence of intracranial infection or other defined cause. Febrile seizures are generally thought to be multifactorial with the genetic component polygenic, as suggested by diminishing risks beyond first degree relatives. As with other genetic forms of epilepsy, there are rare families with presumed autosomal dominant inheritance of febrile seizures [1, 2]. These may lead to gene identification potentially offering leads to genes and gene families that may harbour susceptibility variants for the vast majority of febrile seizures with complex inheritance.

Seizure-related (SEZ) 6 is a protein of 994 amino acids which is thought to play a role in neuronal cell to cell signalling. Normal functioning maintains a balance between dendrite growth and branching to optimize dendritic trees for synaptic connectivity [3]. SEZ6 was originally cloned following upregulation in mouse neurons after seizure induction using pentylenetetrazole (PTZ) stimulation [4]. This raises the question: can disturbances in the amount of transcribed SEZ6 through naturally occurring mutations predispose to seizures? Yu et al. [5] subsequently reported a strong association between SEZ6 and human febrile seizures indicating that SEZ6 is a susceptibility gene for febrile seizures with complex inheritance.

2. Methods

Ninety-four (47 males, 47 females) unrelated cases of simple febrile seizure were screened for SEZ6 mutations in genomic DNA isolated from venous blood. Diagnosis was based on the observation of a seizure which ceased within approximately three minutes and which did not recur within a 24-hour period. For all cases, seizure onset occurred after three
months of age and had ceased in all subjects within five years of age. Ninety-six anonymous blood donors from the same Caucasian population were used as controls. None of the affected children required lumbar puncture, electroencephalography, blood studies, or neuroimaging, consistent with the management recommendations of Duffner et al. [6].

The 17 SEZ6 exons were PCR amplified using the flanking intronic primers listed in Table 1. Primers were designed based on the sequence of SEZ6 transcript variant 1 (NCBI Accession Number NM_178860). Samples were screened by single-stranded conformation polymorphism analysis (SSCA) using the GelScan 3000 (Corbett Research) according to the manufacturer’s instructions. The functional effects of nonsynonymous variants were predicted using the PolyPhen-2 tool (http://genetics.bwh.harvard.edu/pph2/).

### 3. Results

Nine sequence variants were detected within the protein-coding regions of the SEZ6 gene (Table 2). Five of the changes were synonymous and did not change the amino acid, but four of the changes were nonsynonymous and altered the amino acid. Two of the missense changes, in exon 2 (c.142 C>A; p.P48T) and exon 7 (c.1568 G>A; p.R523H), are both low-frequency changes but are present in cases of febrile seizures and in controls. They each affect amino acids which are highly conserved across vertebrate species (Figure 1). Both of these changes were predicted by PolyPhen-2 to be damaging, with scores of 0.955 and 1.000, respectively. Neither change has been reported as a known variant in dbSNP (http://www.ncbi.nlm.nih.gov/snp/).

The remaining two missense changes, the exon 8 c.1636 A>G (causing p.T546A) and exon 12 c.2417 T>C (causing p.M806T), were common, occurring with approximately equal frequency in both febrile seizure cases and controls. They are moderately conserved across vertebrates. Both of these changes were predicted to be benign by

**Figure 1:** Evolutionary conservation of amino acid positions across vertebrates at sites of rare and common nonsynonymous amino acid substitutions within the SEZ6 protein.
PolyPhen-2 analysis. Allele frequencies affecting all coding regions did not markedly differ between febrile seizures (N = 94) and controls (N = 96). There was no evidence in our population, from the sample size examined, for an association of the strength previously reported between SEZ6 genetic variation and febrile seizures. We also detected an insertion in intron 5 of the SEZ6 gene (IVS5+10-11insC) with allele frequencies of 51.6% in patients and 57.3% in controls. This change is intronic and likely benign.

### 4. Discussion

The most common of the SEZ6 variants in the population studied is the IVS5+10-11insC. This is the same variant reported by Yu et al. [5] as occurring in exon 5 at their position 1435 in the cDNA (their GenBank accession number GI:20143984). The discrepancy between the position they report for this polymorphism and the position we report arises from differences in the cDNA sequences used. In both isoforms of SEZ6 currently listed in GenBank (NM_178860 and NM_001098635), the variant is intronic. It is likely that this variant is a benign polymorphism, as evidenced by its high frequency among both cases and controls in our study (Table 2). The variant is also listed in dbSNP (rs58747412), but the entry does not include population frequency data.

Critical examination of the data reported by Yu et al. [5] reveals that in addition to the intronic variant described above, a threonine to alanine missense variant T546A, observed in four of their patients is in fact the SNP rs1976165, which we observed at similar frequency in both patients and controls.

Contrary to the report of Yu et al. we detected the same degree of genetic variation in both the febrile seizure cases and our 96 controls. Their control numbers were not of adequate size, and in their febrile seizure cases, they misinterpreted the presence of naturally occurring genetic variations to be multiple pathogenic mutations present only among the febrile seizure patients.

Data from dbSNP shows that SEZ6 is a highly variable gene, with 17 nonsynonymous coding SNPs listed. Findings of variants in this gene, therefore, need to be interpreted with caution in the absence of additional data (such as protein alignments, in silico pathogenicity predictions, or functional studies) indicating that the variants are indeed deleterious. PolyPhen-2 predictions indicate that only three or perhaps four of the eight coding variants reported by Yu et al. are likely to be deleterious. These and our data reporting two additional potentially damaging rare variants are suggestive of a contribution of SEZ6 to a genetic predisposition to FS in a proportion of cases.

The extent of the evolutionary conservation for some of the variants detected warrants further investigation using much larger sample sizes. Massively parallel sequencing (MPS) [7] now delivers the sensitivity to detect all rare variants. The focus needs to shift to rare variants [8] and statistical developments enabling association tests on rare variants [9]. The polygenic heterogeneity model [10, 11] is likely applicable to febrile seizures as well as for genetic generalised epilepsy. It predicts that rare variants conferring genetic susceptibility will be present in both cases and controls; however, their presence throughout the gene will be significantly higher in cases than in controls if large and adequately powered sample sizes are analysed for the true susceptibility genes.

### 5. Conclusion

Taken together, portions of the data from the present study and from Yu et al. [5] suggest a role for SEZ6 as a susceptibility gene for febrile seizures. There is no reason to restrict
Table 2: Genetic variation detected within SEZ6.

<table>
<thead>
<tr>
<th>Amplicon/exon</th>
<th>Position</th>
<th>Amino acid change</th>
<th>Febrile seizure frequency (%) N = 94</th>
<th>Control frequency (%) N = 96</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rare nonsynonymous missense substitutions</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2.1</td>
<td>c.142 C&gt;A</td>
<td>P48T</td>
<td>0.5</td>
<td>0.5</td>
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<tr>
<td>7</td>
<td>c.1568 G&gt;A</td>
<td>R523H</td>
<td>1.1</td>
<td>0.5</td>
</tr>
<tr>
<td>Common nonsynonymous missense substitutions</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>c.1636 A&gt;G</td>
<td>*T546A</td>
<td>22.4</td>
<td>17.6</td>
</tr>
<tr>
<td>12</td>
<td>c.2417 T&gt;C</td>
<td>**M806T</td>
<td>10.6</td>
<td>15.6</td>
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<tr>
<td>Rare synonymous missense substitutions (benign)</td>
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<tr>
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<td>2.2</td>
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<td>A128A</td>
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<tr>
<td>5</td>
<td>c.1209 C&gt;T</td>
<td>P403P</td>
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<td>0.5</td>
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<tr>
<td>7</td>
<td>c.1557 C&gt;T</td>
<td>G519G</td>
<td>0.5</td>
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<tr>
<td>Common synonymous missense substitutions (benign)</td>
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</tr>
<tr>
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<td>c.1737 C&gt;T</td>
<td>D579D</td>
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<td>Common intronic insertion</td>
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</tr>
<tr>
<td>5</td>
<td>IVS5+10-11insC</td>
<td></td>
<td>51.6</td>
<td>57.3</td>
</tr>
</tbody>
</table>

*rs1976165; **rs12941884.

Numbering of variants in this table is based on the mRNA sequence for SEZ6 transcript variant 1 (NM_178860), with the A of the initiation codon numbered as nucleotide 1.

SEZ6 analyses to febrile seizures since this gene represents a plausible candidate for any seizure disorder based on how it was originally cloned [4]. A significant proportion of febrile seizure cases progress to afebrile seizures [12] suggesting shared genetic determinants between febrile and afebrile seizures. SEZ6 warrants further investigation as a susceptibility gene for both febrile seizures and the epilepsies which show complex inheritance.

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References


