Brain somatic mutations in SLC35A2 cause intractable epilepsy with aberrant N-glycosylation

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Neurol Genet 2018;4:e294. doi:10.1212/NXG.0000000000000294

Abstract

Objective
To identify whether somatic mutations in SLC35A2 alter N-glycan structures in human brain tissues and cause nonlesional focal epilepsy (NLFE) or mild malformation of cortical development (mMCD).

Methods
Deep whole exome and targeted sequencing analyses were conducted for matched brain and blood tissues from patients with intractable NLFE and patients with mMCD who are negative for mutations in mTOR pathway genes. Furthermore, tissue glyco-capture and nanoLC/mass spectrometry analysis were performed to examine N-glycosylation in affected brain tissue.

Results
Six of the 31 (19.3%) study patients exhibited brain-only mutations in SLC35A2 (mostly nonsense and splicing site mutations) encoding a uridine diphosphate (UDP)-galactose transporter. Glycome analysis revealed the presence of an aberrant N-glycan series, including high degrees of N-acetylglucosamine, in brain tissues with SLC35A2 mutations.

Conclusion
Our study suggests that brain somatic mutations in SLC35A2 cause intractable focal epilepsy with NLFE or mMCD via aberrant N-glycosylation in the affected brain.
Epilepsy is a major neurologic disorder estimated to affect approximately 50 million people worldwide.\(^1\) Although proper antiepileptic drugs achieve control in 60%–70% of patients with epilepsy, more than one-third fail to attain seizure-free status and are diagnosed with intractable epilepsy.\(^2\) Therein, surgical resection of the epileptic focus in the affected brain is often required to relieve seizures.

The advent of sequencing technology has enabled in-depth genetic studies to identify de novo or rare germline mutations underlying intractable epilepsy.\(^3,4\) We and other groups have shown that low-level somatic activating mutations with a mutational burden (or variant allele frequency, [VAF]) of merely 1% in mTOR pathway genes, which arise only in the affected brain, are a major genetic etiology for intractable focal epilepsies with pathologically or radiologically well-defined lesions, such as focal cortical dysplasia type II (FCDII) and hemimegalencephaly (HME), exhibiting cytomegalic neurons and cortical dyslamination.\(^5\)–\(^9\) In contrast to lesional focal epilepsies, such as FCDII and HME, about 15%–30% of intractable focal epilepsies show no abnormalities on MRI, referred to as nonlesional focal epilepsy (NLFE), or mild cortical abnormalities on pathologic examination, referred to as mild malformation of cortical development (mMCD).\(^10\)–\(^12\) Although these conditions are often responsive to epilepsy surgery,\(^13,14\) the molecular genetic etiology, especially brain somatic mutations, underlying NLFE or mMCD remains elusive.

In this study, we sought to identify somatic mutations in patients with NLFE using deep whole exome sequencing (WES) and targeted amplicon sequencing and to examine the biological and pathologic functions of noted mutations in patient brain tissues.

**Methods**

**Standard protocol approvals, registrations, and patient consents**

All human tissues were obtained with informed consent in accordance with protocols approved by Severance Hospital and the KAIST Institutional Review Board and Committee on Human Research.

We first collected matched brain and peripheral blood tissues from 13 patients with NLFE subjected to epilepsy surgery; none showed an abnormal lesion on MRI (figure 1, A and B and table e-1, links.lww.com/NXG/A124). We performed deep WES (mean depth, >800x) of extracted genomic DNA from the paired brain and peripheral tissues (table e-2). Next, to expand the study cohort, we collected matched brain and peripheral tissues from an additional 18 patients with intractable focal epilepsy: 12 with NLFE and 6 with mMCD or nonspecific gliosis in their pathologies (figure e-1A, e-1B and table e-1, links.lww.com/NXG/A124). For these patients, we performed targeted amplicon sequencing (mean depth, 1,230X) of SLC35A2 in brain tissues using 12 primers overlapping at least 10 bp and covering all exonic regions (figure e-2). To investigate the presence of mammalian target of rapamycin (mTOR) pathway mutations potentially causative of intractable epilepsy, we performed deep targeted hybrid capture sequencing (mean depth, 812X) of 10 known mTOR pathway genes (AKT3, DEPDC5, MTOR, PIK3CA, PIK3R2, PTEN, STRADA, TBC1D7, TSC1, and TSC2) in matched brain and peripheral tissues from the patients with mutations identified in SLC35A2 (table e-3 and table e-4). Furthermore, to determine whether mTOR pathway hyperactivation occurs, we performed coimmunostaining for phosphorylated S6 and NeuN, a neuronal marker, in freshly frozen brain tissue from patients carrying SLC35A2 or MTOR mutations.

For all sequencing data, we applied our analysis pipeline, in-house filtering criteria of putative functional impact, and manual investigation using Integrative Genomic Viewer to identify potential pathogenic mutations (figure e-1, links.lww.com/NXG/A124). Noted somatic mutations were validated on a different sequencing platform, such as site-specific amplicon sequencing (read depth >100,000X). We considered variants as true positive when they appeared with a VAF greater than 1%, 10 times the expected base miscall rate of 0.1%.\(^15\) Furthermore, we estimated the probability value for true positive calls of amplicon sequencing data using a previously described method.\(^16\) Briefly, this method calculates the discrepancy between expected and observed amounts of mismatches in amplicon-based, Illumina platform data sets (up to 10,000X) in which 2 independent blood samples with known single nucleotide polymorphisms (SNPs) were mixed to mimic somatic mutations with 4 different VAFs: 0.5%, 1%, 5%, and 10%. Then, the patterns and levels of background errors generated for the Illumina platform are identified. Based on these data, we could predict the probability value for true positive calls of targeted amplicon sequencing by considering VAFs acquired as background errors and sequencing context.

Finally, to examine whether SLC35A2 mutations affect N-glycosylation status in the affected brain, we performed Tissue Glyco-Capture and nano liquid chromatography / mass spectrometry (nanoLC/MS) analysis, a highly sensitive

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**Glossary**

FCDII = focal cortical dysplasia type II; HexNAc = N-acetyl glucosamine; HME = hemimegalencephaly; mMCD = mild malformation of cortical development; NLFE = nonlesional focal epilepsy; VAF = variant allele frequency; WES = whole exome sequencing.
method to profile brain glycomes,\textsuperscript{17} in 2 SLC35A2 mutation-carrying brain tissues and 3 control brain tissues from patients with SLC35A2 mutation-negative NLFE and metastatic brain tumors. Detailed Methods appears in the supplemental Methods (e-Methods, links.lww.com/NXG/A125).

**Data availability**

Deep whole exome and targeted sequencing data will be deposited in the National Center for Biotechnology Information Sequence Read Archive (ncbi.nlm.nih.gov/sra/). The glycosylation data are available on request.

**Results**

Although no pathogenic or recurrent germline mutations were identified in genes potentially linked to intractable focal epilepsy using targeted hybrid capture sequencing (table e-5 and
<table>
<thead>
<tr>
<th>ID</th>
<th>Sequencing type</th>
<th>Sex</th>
<th>Age at surgery</th>
<th>Syndrome</th>
<th>MRI report</th>
<th>Pathologic diagnosis</th>
<th>Engel classification</th>
<th>Variant allele frequency</th>
<th>Mutation type</th>
<th>Nucleotide changes</th>
<th>Protein changes</th>
</tr>
</thead>
<tbody>
<tr>
<td>EPI219</td>
<td>WES</td>
<td>M</td>
<td>3 y, 5 mo</td>
<td>LGS from IS</td>
<td>No abnormal lesion in brain parenchyma, ventricular system normal</td>
<td>Neurons in white matter, consistent with mMCD</td>
<td>4</td>
<td>23%</td>
<td>Stop_gained</td>
<td>c.589C &gt; T</td>
<td>p.Gln197*</td>
</tr>
<tr>
<td>LGS150</td>
<td>WES</td>
<td>M</td>
<td>5 y, 3 mo</td>
<td>LGS from IS</td>
<td>No abnormal lesion in brain parenchyma, ventricular system normal</td>
<td>Neurons in white matter, consistent with mMCD</td>
<td>1</td>
<td>16%</td>
<td>Stop_gained</td>
<td>c.760 G &gt; T</td>
<td>p.Glu254*</td>
</tr>
<tr>
<td>mMCD13</td>
<td>Amplicon</td>
<td>F</td>
<td>5 y, 1 mo</td>
<td>LGS from IS</td>
<td>No abnormal lesion in brain parenchyma, ventricular system normal</td>
<td>Neurons in white matter, consistent with mMCD</td>
<td>1</td>
<td>10%</td>
<td>Missense</td>
<td>c.703T &gt; G</td>
<td>p.Asn235Gln</td>
</tr>
<tr>
<td>EPI340</td>
<td>Amplicon</td>
<td>M</td>
<td>4 y, 2 mo</td>
<td>LGS</td>
<td>No abnormal lesion in brain parenchyma, ventricular system normal</td>
<td>Neurons in white matter, consistent with mMCD</td>
<td>4</td>
<td>18%</td>
<td>Stop_gained</td>
<td>c.502 G &gt; A</td>
<td>p.Gln168*</td>
</tr>
<tr>
<td>EPI147</td>
<td>Amplicon</td>
<td>F</td>
<td>4 y</td>
<td>LGS</td>
<td>Diffuse cortical dysplasia, right frontal lobe</td>
<td>Minimal gliosis</td>
<td>1</td>
<td>6%</td>
<td>Stop-gained</td>
<td>c.553 G &gt; A</td>
<td>p.Gln185*</td>
</tr>
<tr>
<td>EPI044</td>
<td>Amplicon</td>
<td>M</td>
<td>2 y, 7 mo</td>
<td>LGS from IS</td>
<td>No abnormal lesion in brain parenchyma, ventricular system normal</td>
<td>No abnormality</td>
<td>1</td>
<td>5%</td>
<td>Splice-acceptor</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>

Abbreviations: FCD = focal cortical dysplasia; ILAE = international league against epilepsy; IS = infantile syndrome; LGS = Lennox-Gastaut syndrome; MCD = malformation of cortical development; mMCD = mild malformation of cortical development; NA = non-available; WES = whole exome sequencing.

All identified variants annotated based on NM_005660.1.
values for amplicon sequencing data for matched peripheral mutations ranged from 5% to 18%. Calculating the probability of the identified somatic variants in peripheral tissue samples had less galactosylation (associated with truncated glycans without galactose residues) than control brain samples, which is consistent with a previous study\(^9\) (figure 2B). In particular, we found that mutation-carrying samples had less galactosylation than control brain samples, which is also consistent with a previous study\(^22\) (figure 2B). N-glycan structures were unique, showing high degrees of N-acetylglucosamine (HexNAc), such as Hex\(_3\)HexNAc\(_7\)Fuc\(_1\) and Hex\(_3\)HexNAc\(_8\)Fuc\(_1\), on high sensitive LC/MS analysis (figure 2C). The glycan representing the ion at m/z 1036.90, corresponding to [Hex\(_3\)HexNAc\(_7\)Fuc\(_1\) + 2H]\(^{2+}\), was identified by collision-induced dissociation MS/MS analysis (figure 2C). In sequence, the initial loss of HexNAc residues was clearly observed from the parent ion, indicating that 5 HexNAc residues were linked to the N-glycan core (i.e., Man\(_3\)GlcNAc\(_3\)). These results suggest that somatic loss-of-function mutations in SLC35A2 lead to aberrant N-glycan patterns of Hex\(_3\)HexNAc\(_7\)Fuc\(_1\) in patient brain tissues.

**Discussion**

This study suggests that brain somatic mutations in SLC35A2 explain 19.3% (6 of 31) of intractable focal epilepsies with NLFE or mMCD and result in aberrant N-glycan patterns in mutation-carrying brain tissues. NLFE or mMCD account for 15%–30% of intractable childhood epilepsies. Similar to other intractable childhood epilepsies, patients with NLFE or mMCD often undergo surgical intervention; however, only 30% became seizure free after surgical treatment compared with 62%–80% of patients with lesional focal epilepsy.\(^13\)\(^\text{14}\) Although many research groups have studied the molecular genetic etiology underlying intractable childhood epilepsies, these studies have primarily investigated mechanisms underlying lesional epilepsy, such as malformations of cortical development, tumors, and other circumscribed anomalies. Therefore, the mechanisms underlying NLFE or mMCD have remained obscure.

An association between SLC35A2 and seizure has been suggested. In previous studies, it was reported that de-novo germline mutations or postzygotic mosaic mutation in SLC35A2
Figure 2 Patient brain tissues with somatic mutations in SLC35A2 encoding a UDP-galactose transporter exhibiting aberrant N-glycosylation

(A) Schematic figure showing brain somatic mutations in SLC35A2 identified in this study. Red star: locations of each identified mutation

(B) Extracted compound chromatograms (ECCs) of N-glycans from brain tissues. EPI219 and LGS150: subjects carrying somatic mutations in SLC35A2. Control EPI166: patient with intractable focal epilepsy confirmed to have no specific somatic or germline mutations in deep WES. Control MET886 and MET344: specimens from the tumor-free margin of individuals with a metastatic tumor as part of a planned resection. These specimens were pathologically confirmed as normal brain tissue. The ECCs were color coded according to N-glycosylation types: blue for complex-type glycans containing galactose residues, red for truncated-type glycans, green for high mannose glycans, sky blue for hybrid-type glycans, and pink for the glycans involving high degrees of HexNAc residues. Pink round rectangle square: N-glycan structures showing high degrees of N-acetylglucosamine (HexNAc), such as Hex$_3$HexNAc$_7$Fuc$_1$ and Hex$_3$HexNAc$_8$Fuc$_1$. (C) Representative CID MS/MS spectrum of aberrant N-glycan Hex$_3$HexNAc$_7$Fuc$_1$ in the positive ion detection mode. Almost all fragment ions were single-protonated ions [M + H]$^+$; others are indicated as a superscript. Pink square: Hex$_4$HexNAc$_3$Fuc$_1$, glycan, identified by collision-induced dissociation MS/MS, representing the ion at M/Z 1036.90.
cause a congenital disorder of glycosylation and early-onset epileptic encephalopathy with epileptic seizures. Treatment with an oral galactose supplement improved clinical symptoms in 1 case. Although they support our results, these studies are limited in their ability to draw causative links between the SLC35A2 mutation and seizure development. More recently, 1 study reported that somatic mutations in SLC35A2 are associated with intractable neocortical epilepsy. They found somatic mutations in 3 of 18 patients with NLFE and 2 of 38 patients with malformation of cortical development or focal cortical dysplasia. However, no evidence of alterations in glycosylation in affected brain tissues was given. The present study provides stronger evidence that brain somatic mutations in SLC35A2 cause intractable focal epilepsy with NLFE or mMCD through aberrant N-glycosylation only in the affected brain and that SLC35A2 mutations are unlikely to lead to hyperactivation of the mTOR pathway using targeted hybrid capture sequencing and immunostaining for phosphorylated S6. Several studies have explored the effects of N-linked glycosylation on glycoproteins involved in neural physiology, demonstrating essential roles of N-glycan structures in neural circuitry. N-glycans play specific modulatory roles controlling neuronal transmission and the excitability of neural circuits. Of interest, 1 study has shown that N-glycosylation defects elicit epileptic discharges. Therefore, we suggest that N-glycosylation defects caused by SLC35A2 mutations might alter neural transmission and the excitability of neural circuits, thereby resulting in seizures. Future studies using matrix-assisted laser desorption/ionization Fourier transform mass spectrometry with nonspecific proteolysis and deglycosylation will be necessary to address the determination of N-glycosylation sites. Through these experiments, candidates of functionally altered proteins causing intractable epilepsies could be identifiable. Last, identifying target proteins associated with the aberrant N-glycosylation observed in the brain may provide novel therapeutic targets or molecular diagnostic markers for intractable focal epilepsies stemming from NLFE or mMCD.

Author contributions

Study funding
This work was supported by grants from the Korean Health Technology R&D Project, Ministry of Health & Welfare, Republic of Korea (H16C0415 to D.S.K and J.H.L; HI15C1601 to H.C.K).

Disclosure
N. S. Sim has received research support from the Korean Health Technology R&D Project, Ministry of Health & Welfare, Republic of Korea. Y. Seo reports no disclosures. J. S. Lim has received research support from the Korean Health Technology R&D Project, Ministry of Health & Welfare, Republic of Korea. W. K. Kim is/has been employed by SoVarGen and has received research support from the Korean Health Technology R&D Project, Ministry of Health & Welfare, Republic of Korea. H. Son has received research support from the Korean Health Technology R&D Project, Ministry of Health & Welfare, Republic of Korea. H. D. Kim, S. Kim, and H. J. An report no disclosures. H.C. Kang has received research support from the Ministry of Food and Drug Safety, Republic of Korea. S. H. Kim serves/has served on the editorial board of the Journal of Pathology and Translational Medicine. D.S. Kim has received research support from the Korean Health Technology R&D Project, Ministry of Health & Welfare, Republic of Korea. J. H. Lee is/has been employed by and receives stock(stock options/board of directions compensation from SoVarGen and has received research support from the Korean Health Technology R&D Project, Ministry of Health & Welfare, Republic of Korea. Full disclosure form information provided by the authors is available with the full text of this article at Neurology.org/NG.

Publication history
Received by Neurology: Genetics July 27, 2018. Accepted in final form October 3, 2018.

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*Neurol Genet* 2018;4;
DOI 10.1212/NXG.0000000000000294

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